High-Content Chemical and RNAi Screens for Suppressors of Neurotoxicity in a Huntington's Disease Model

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<td>As Published</td>
<td><a href="http://dx.doi.org/10.1371/journal.pone.0023841">http://dx.doi.org/10.1371/journal.pone.0023841</a></td>
</tr>
<tr>
<td>Publisher</td>
<td>Public Library of Science</td>
</tr>
<tr>
<td>Version</td>
<td>Final published version</td>
</tr>
<tr>
<td>Accessed</td>
<td>Thu Apr 04 10:14:55 EDT 2019</td>
</tr>
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High-Content Chemical and RNAi Screens for Suppressors of Neurotoxicity in a Huntington’s Disease Model

Joost Schulte¹*, Katharine J. Sepp¹, Chaohong Wu², Pengyu Hong², J. Troy Littleton¹

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Abstract

To identify Huntington’s Disease therapeutics, we conducted high-content small molecule and RNAi suppressor screens using a Drosophila primary neural culture Huntingtonin model. Drosophila primary neurons offer a sensitive readout for neurotoxicity, as their neurites develop dysmorphic features in the presence of mutant polyglutamine-expanded Huntingtonin compared to nonpathogenic Huntingtin. By tracking the subcellular distribution of mRFP-tagged pathogenic Huntingtin and assaying neurite branch morphology via live-imaging, we identified suppressors that could reduce Huntingtin aggregation and/or prevent the formation of dystrophic neurites. The custom algorithms we used to quantify neurite morphologies in complex cultures provide a useful tool for future high-content screening approaches focused on neurodegenerative disease models. Compounds previously found to be effective aggregation inhibitors in mammalian models were also effective in Drosophila primary cultures, suggesting translational capacity between these models. However, we did not observe a direct correlation between the ability of a compound or gene knockdown to suppress aggregate formation and its ability to rescue dysmorphic neurites. Only a subset of aggregation inhibitors could revert dysmorphic cellular profiles. We identified Ikb1, an upstream kinase in the mTOR/Insulin pathway, and four novel drugs, Camptothecin, OH-Camptothecin, 18β-Glycyrrhetinic acid, and Carbenoxolone, that were strong suppressors of mutant Huntingtin-induced neurotoxicity. Huntingtonin neurotoxicity suppressors identified through our screen also restored viability in an in vivo Drosophila Huntingtonin’s Disease model, making them attractive candidates for further therapeutic evaluation.

Introduction

Huntington’s Disease (HD) is a dominantly inherited fatal neurodegenerative disorder. It results from expansion of a polyglutamine (polyQ) tract in the Huntingtin (Htt) protein which alters its conformation and function [1]. Neuropathological hallmarks of the disease include Htt aggregation, early-onset striatal neurodegeneration, and late-stage cortical thinning [2,3]. Mammalian models of HD indicate that neuron-specific dysregulation of cellular physiology contributes to the underlying neuropathology, although subcortical white matter degeneration may also suggest a glial contribution [4–7]. Mutant Htt has been suggested to disrupt transcription, proteasome activity, axonal transport, synaptic function, signaling cascades (including the mTOR/Insulin pathway) and other physiological processes in a variety of neuronal subtypes [8].

PolyQ tract length accounts for approximately 70% of the variance in the age-of-onset of Huntington’s disease [9], with the remaining variance attributed to disease-modifying agents such as environmental factors or genetic background. Linkage analysis using large affected families is the gold standard for identifying disease modifying loci [10]. However, these investigations require lengthy study periods and considerable resources. In vivo genetic or chemical suppressor screens offer another avenue to rapidly identify suppressors. The suitability of cell-based screening models encompasses several considerations. Htt is ubiquitously expressed, yet deleterious effects of mutant polyQ expansion are observed primarily in the central nervous system of HD patients. In conducting suppressor screens, it is therefore desirable to use neuronal systems. Stable neuronal cell lines can change their characteristics over continued passages, and thus may not retain HD phenotypes. In addition, stable cell lines continually divide, which may alter regulation of cell survival and death pathways that are relevant to the human disease state in quiescent neurons. Primary neuronal disease models have many advantages, since cellular growth and differentiation states are more similar to the in vivo situation, yet they are amenable to high-throughput chemical and genetic suppressor screens.

Huntingtin is conserved in Drosophila, and orthologs of many interacting proteins exist [11–13]. Suppressor screening with first generation exon 1 Htt fragments has generated important candidate disease modifying agents [14,15]. However, protein
context has been shown to be an important component of mutant Htt pathogenesis, and therefore there is a need to conduct additional screens using larger Htt constructs in more physiologically relevant systems [16]. To this end, we have developed a Drosophila primary neural culture system for HD, using a large human Htt fragment (exons 1–12, 588 amino acids in addition to the polyQ tract). The methodology is suited to high throughput small molecule and RNAi suppressor screening, and offers a desirable balance between physiological relevance and technical tractability.

We demonstrate that a 588 amino acid human Htt fragment containing an expanded polyQ tract (138Q) readily forms cytoplasmic aggregates in primary neurons, in addition to causing aberrant neuronal morphology when compared to non-expanded human Htt controls (15Q). From a screen of approximately 2600 small molecules and a whole genome kinase/phosphatase RNAi library, we identified four new compounds that could revert the mutant phenotype (Camptothecin, 10-Hydroxycamptothecin, 18β-Glycyrrhetinic acid, Carbenoxolone) and knockdown of the lkb1 kinase, that can suppress polyQ Htt aggregation and revert morphological profiles towards control states. In addition, we identified several previously studied polyQ Htt aggregation inhibitors. This Drosophila HD model represents an attractive system for future large-scale suppressor screening. In addition, the current candidates provide new avenues to define pathogenic mechanisms in HD.

**Results**

**Drosophila Primary Neural Culture Screening System for Huntington’s Disease**

We have previously described a Drosophila Huntington’s Disease model which displays many characteristics of human HD, including neurodegeneration, disrupted axonal transport, and decreased longevity [17]. To extend our studies of HD pathology, we generated a new monomeric Red Fluorescent Protein (mRFP) N-terminal tag variant for in vivo imaging of Htt distribution (Htt-RFP). The Htt-RFP construct encompasses the caspase-6 cleavage fragment important for Htt toxicity [18] and includes either a non-pathogenic (15Q) or pathogenic (138Q) polyQ tract. This
fragment corresponds to exons 1–12 of human Htt and is 588 amino acids in length (~80 kDa), excluding the polyQ domain and RFP tag. For our studies, we used the GALA/USAS system [19] to drive expression of the constructs in the nervous system using the pan-neuronal GALA driver Elav<sup>C155</sup> (C155). We selected UAS-Htt15QmRFP<sup>C155</sup> and UAS-Htt138QmRFP strains that had comparable expression levels (i.e. Htt15Q<sup>C155</sup> and Htt138Q<sup>C155</sup>) when crossed to C155 as demonstrated by quantitative Western blotting (Figure 1G). Prominent bands of~109 kDa and ~125 kDa were observed for the Htt15Q<sup>C155</sup> and Htt138Q<sup>C155</sup> strains, respectively, in agreement with the predicted molecular weights of the RFP-fusion proteins. Pan-neuronal expression of Htt138Q<sup>C155</sup> using C155 causes pupal lethality, while Htt15Q<sup>C155</sup> controls are viable and have normal longevity (see detailed analysis below). For downstream behavioral analysis, we selected an additional UAS-Htt138QmRFP strain (Htt138Q<sup>C155</sup>) that has reduced Htt138Q protein expression (Figure 1G) and is adult viable. The decreased longevity observed in the Htt138Q<sup>C155</sup> strain is more severe than that observed in our earlier studies [17] and may be related to an increased polyQ length in the new construct (138Q vs. 128Q), a larger Htt N-terminal fragment (588 a.a. vs. 548 a.a.), or differences in Htt expression levels. The severity of the Htt138Q<sup>C155</sup> allele suggests that this model may correspond to juvenile-onset HD observed in humans [20]. In juvenile-onset HD, the CAG repeats often exceed 55 and phenotypes develop prior to adulthood.

To conduct a small molecule and RNAi screen to identify suppressors of Huntington toxicity we prepared primary neuronal cultures from control (C155;Htt15QmRFP<sup>C155</sup>, abbreviated as Htt15Q) and mutant (C155;UAS-Htt138QmRFP<sup>C155</sup>, abbreviated as Htt138Q<sup>C155</sup>) Huntingtin strains that simultaneously expressed membrane-associated-GFP (UAS-Cd8GFP) in all neurons. This dual labeling approach enabled us to track the subcellular distribution of mRFP-tagged Huntingtin, while simultaneously monitoring the general morphology of cultured neurons (Fig. 1 A-F). Visualization of Htt-RFP localization demonstrated that Htt138Q readily forms aggregates which accumulate in cell bodies and neurites, while Htt15Q is soluble and has a more uniform cytoplasmic distribution (Fig. 1, compare 1B, 1E). In addition, we found that Htt138Q-expressing neurons display morphological indicators of reduced neuronal health [21,22], including smaller neuronomes, increased branching, and reduced axonal connectivity, as monitored by membrane-associated-GFP (Fig. 1, compare 1A, 1D). Neurite morphology and Htt aggregation were quantified in cultures plated in 384-well format using custom algorithms developed to process digital images collected via automated microscopy [23]. Population analysis of Htt15Q and Htt138Q replicate wells revealed that eight morphology features (small, medium, large, and average neuronomere size, and short, medium, long, and average neurite length) provided robust data content to generate effective separation of Htt15Q control from Htt138Q mutant neuronal morphology. Differences in Htt aggregation were also readily detectable between mutant and control cultures using these algorithms. To screen for suppressors of HD toxicity we therefore monitored the presence of Htt aggregates, as well as morphology, to evaluate overall neuron health.

**Small Molecule/RNAi Suppressor Screens Using HD Primary Cultures**

We performed dual RNAi and small molecule screens to identify HD toxicity suppressors, and assayed for suppression of Htt138Q aggregate formation, in addition to reversion of mutant Htt138Q morphology towards Htt15Q controls. For RNAi screening, we wanted to identify novel targets for HD therapeutic development, and focused on a kinase/phosphatase RNAi library (468 genes) that would potentially contain targets of high value for chemical inhibition. For small-molecule screening, we tested libraries enriched for FDA-approved drugs, including the NINDS Custom Collection 2, BIOMOL ICCB Known Bioactives Collection and the Prestwick 1 Collection. This allowed screening of ~2600 approved compounds, potentially facilitating the advancement of screen hits to clinical trials. For compound screening, we verified that addition of 0.5% DMSO to primary cultures does not significantly alter neuronal morphology or Htt138Q aggregation characteristics (Table 1). Known suppressors of Htt polyQ aggregation, including C2-8, GW5074, Juglone, Residocil, and Rapamycin, were tested for efficacy in our assay [24–28]. Although all control compounds reduced Htt138Q aggregation, none reverted the morphology profiles of Htt138Q expressing neurons towards Htt15Q controls (Table 1). Instead, these compounds caused reduced axon outgrowth, neuroneme size, and suppressed GFP expression over a wide concentration range, suggesting these compounds have neurotoxic properties.

To identify new potential therapeutic compounds that were not neurotoxic, but that were able to suppress mutant Htt toxicity in our model, we conducted RNAi/compound screens in duplicate. All wells were visually scored independently by two investigators to identify agents that either suppressed aggregation, or reverted mutant Htt138Q neural profiles towards Htt15Q controls. From the visual-based screens, three novel suppressors of Htt polyQ toxicity were identified: 1 RNAi hit (lkb1), and 2 compounds (Camptothecin and 10-Hydroxy-camptothecin). Lkb1 is a known tumor suppressor and a negative regulator of the mTOR/Insulin pathway, which has important roles in autophagy and nutrient sensing [29,30], while the Camptothecins function as DNA Topoisomerase 1 (Top1) inhibitors [31]. In addition to visual inspection of the screen plates, automated microscopy was used to record images of the compound-treated plates for subsequent morphometric analysis using custom algorithms. For automated microscopy, three images per well were taken at different sites for each channel (GFP/RFP) to facilitate hit identification and increase statistical power. Htt138Q aggregation was first quantified, leading to the identification of 62 compounds that significantly suppressed Htt aggregate formation (Fig. 2, Table S1). Subsequently, wells where aggregate formation was inhibited were re-evaluated to determine if any treatments were able to revert the mutant Htt138Q morphology profiles towards that of Htt15Q controls. Of the 62 compounds that were found to inhibit Htt138Q aggregate formation, 8 compounds were identified that improved the Htt138Q induced morphological defects (Fig. 3A, Table 2). Unmasking of the identities of the 8 compounds revealed that 4 compounds were Camptothecins, in agreement with the visual scoring observations. In addition, two Na+/K+-ATPase inhibitors, and a Glutathione-S-Transfersase inhibitor were also identified as being capable of suppressing aggregate formation and rescuing the mutant Htt138Q culture morphologies towards the control state (Table 2). We subsequently validated screen hits, focusing on the targets that overlapped in both the visual scoring and morphometric computational analysis. The Lkb-1 target was validated with three independent dsRNAs (amplicons DRSC16481, DRSC36925, DRSC36926). Each amplicon improved Htt138Q mutant morphology with statistical significance, but did not inhibit aggregate formation (Table 3). The Camptothecin and 10-Hydroxy-camptothecin small molecules are structural analogues, and were found to reduce aggregate formation in addition to partially reverting dystrophic morphology profiles over a range of concentrations (56 μM, 5.6 μM (Fig. 4)). These compounds alter Htt138Q localization within neurons, such that it more closely resembles the distribution of Htt15Q in control cultures (Fig. 4).
Genetic and Pharmacological Validation of Screen Hits

To further examine the RNAi/small molecule screen hits, we assayed in vivo efficacy by testing their ability to rescue lethality in our Drosophila HD model. Htt138Q expression in the nervous system results in late stage pupal lethality when animals are reared on standard media. Animals undergo metamorphosis but fail to eclose. In liquid culture, the longevity of the Htt138Q expressing animals is reduced and larvae perish during the 2nd instar stage, likely due to drowning from decreased motility. Rapamycin, a well characterized mTOR inhibitor [25], suppresses neurodegeneration in various HD models, and we found it enhanced viability of Htt138Q expressing larvae reared in liquid culture in a dose-dependent fashion compared to DMSO-treated controls (Fig. 5A). Using this assay, we found that Camptothecin and 10-Hydroxycamptothecin also increased larval longevity in vivo, but to a lesser extent than Rapamycin (Fig. 5A). 10-Hydroxycamptothecin is more efficacious than Camptothecin, possibly due to solubility differences since Camptothecin readily precipitates when added to cultures. Specific inhibitors of Lkb1 were not available for in vivo testing. Given its role as an upstream regulatory kinase of the mTOR/Insulin pathway, we tested additional pharmacological agents that regulate this pathway, including Metformin (an mTOR pathway activator and oral anti-diabetic drug) [32,33] and 18β-Glycyrrhetinic acid [a putative mTOR inhibitor that acts through PI3K/AKT] [34,35]. Metformin could not revert Htt138Q-induced lethality. However, 18β-Glycyrrhetinic acid was almost as efficacious as Rapamycin (Fig. 5A). We also tested an analogue of 18β-Glycyrrhetinic acid that has increased solubility: Carbenoxolone, and found it to have comparable activity. 18β-Glycyrrhetinic acid is non-toxic and has been used as a commercial sweetener, making it an attractive candidate for future studies for suppressive effects in mammalian HD models. Rapamycin, in contrast, has numerous toxic side-effects that can impact kidney and lung function, cause increased risk of infection, and lead to hyperlipidemia [36–40].

To further examine the role of the Lkb1/Insulin pathway in the suppression of HD toxicity, we conducted genetic interaction studies with lkb1 loss-of-function mutations. While pan-neuronal expression of Htt138Q causes pupal lethality, the introduction of a heterozygous lkb1 null mutation into the Htt138Q background suppresses lethality. We observed no C155/+; UAS-Htt138Q/+ adult escapers at 25°C (n = 83 pupae), however, the introduction

Table 1. Effect of positive control compounds on Htt138Q aggregate formation and neurite morphology (p-values listed) in Drosophila primary neural culture system.

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<tr>
<th>Compound</th>
<th>CAS#</th>
<th>Well Conc. (mM)</th>
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<th>Mutant Htt 138Q aggregation*</th>
<th>Mutant Htt138Q morphology rescue**</th>
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<tr>
<td>DMSO</td>
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<td>15Q</td>
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*p < 0.05 indicates Htt138Q aggregate formation is inhibited (bold, italics).

**p > 0.05 indicates Htt138Q drug-treated culture have morphology similar to Htt15Q control cultures.

doi:10.1371/journal.pone.0023841.t001

High-Content Screens for HD Suppressors

PLoS ONE | www.plosone.org 4 August 2011 | Volume 6 | Issue 8 | e23841

PLoS ONE | www.plosone.org 4 August 2011 | Volume 6 | Issue 8 | e23841
of an Lkb1 heterozygous allele into this background led to an adult escaper frequency of 1.8% (n = 110 pupae) and 3.7% (n = 81 pupae) respectively. Using quantitative Western blot analysis, we found that the introduction of Lkb1 trans-heterozygous alleles does not reduce Htt138Q protein levels (Fig. 5D), suggesting the suppressive effects are not tied to altering Htt expression. This is in contrast to another rescuing deficiency we identified in an independent screen, Df(3L)vin7, which significantly decreases Htt138Q expression and yields an escaper frequency of 25.9% (n = 85 pupae). The Lkb1 heterozygous animals expressing Htt138Q are viable and have relatively normal walking ability, although they do not inflate their wings (Fig. 5C, Movie S1). To further investigate the relationship between Lkb1 and mutant Htt138Q toxicity, we introduced the Lkb1 heterozygous allele into a weaker Htt138Q expressing strain (C155/+; UAS-Htt138QmRFP2/+). From negative geotaxis assays performed on 25-day old flies, we found that introduction of an Lkb1 heterozygous allele into this background led to a 20% reduction in the number of escapers (Fig. 5E). This suggests that the toxicity effects of Htt138Q are suppressed by the Lkb1 allele.

Figure 2. Htt138Q aggregation inhibition screening in primary neural cultures using custom algorithms. (A) Scatter plot indicating the extent of Htt138Q aggregation following treatment with ~2600 small molecules. Log2 ratio of Htt138Q aggregates (small molecule treated well/DMSO treated well from the same screen plate) is plotted. The red line denotes two standard deviations from the mean Log2 ratio observed in the screen data set. Circled wells correspond to compounds that suppress aggregate formation and were subsequently analyzed in downstream validation studies. (B,C) Representative data set images collected via automated microscopy and analyzed with algorithms. (B) Htt15Q control cultures have few aggregates, while mutant Htt138Q cultures (C) have numerous aggregates. The exposure time used for image collection was optimized for htt aggregate detection, which has a higher signal intensity than soluble Htt. This avoided pixel saturation at the upper end of the aggregate dynamic range, ensuring accurate aggregate quantification, although soluble Htt is not readily detectable in automated microscopy images. Image analysis was performed as described in the materials and methods. Scale bar: 200 μm. doi:10.1371/journal.pone.0023841.g002
Htt138Q in neurons, is associated with Lkb-1 signaling. Since RNAi knockdown, as performed in our primary culture screening assay, is representative of a hypomorphic situation, and the in vivo lkb1 rescue studies we conducted were haplo-insufficient, partial knockdown screening can be advantageous to uncover therapeutic targets. Full knockdown of lkb1 would not have revealed beneficial effects, as homozygous lkb1 null mutants are lethal and have cell polarity defects [41].

To investigate the mechanism of action of Camptothecins in suppression of Htt138Q neurotoxicity, we performed genetic loss-
of-function studies with target effector proteins. Since Camptothecins function as Top1 inhibitors, we reasoned that Top1 RNAi knockdown in primary cultures should phenocopy Camptothecin treatment and suppress HD pathology. RNAi knockdown of Top1 or other annotated Drosophila Top genes (Top2, 3a or 3b), either singularly or in combination, did not suppress Htt aggregation (Table 3). Knockdown of the Tops did, however, partially revert the mutant Htt138Q neurite morphology towards controls. To extend these studies in vivo we introduced a heterozygous Top1 null allele into the HD model background, but this had no effect on Htt138Q-induced pupal lethality, as no adult escapers were observed. Given that Camptothecins have a robust effect on Htt138Q aggregation inhibition, while Top-knockdown does not, these results suggest that Camptothecins may act through a Top1-independent pathway to suppress Htt138Q aggregation.

The compounds that suppress Htt138Q aggregate formation, and/or rescue neurite morphology in our system, can be grouped into two classes based on their structures (Figure S1).

### Table 2. Compounds found to inhibit mutant Htt138Q aggregation and revert primary culture morphology towards Htt15Q controls.

<table>
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<th>I.D.</th>
<th>Compound</th>
<th>CAS#</th>
<th>Function</th>
<th>Htt Culture</th>
<th>Htt138Q Aggregate Log2 ratio</th>
<th>Aggregate Suppression Significance** (p-value)</th>
<th>Morphology Statistical Significance*** (p-value)</th>
<th>Library</th>
<th>ICCB Plate I.D., Well #</th>
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*Compounds listed correspond to hits shown in Figure 3A. Bolded compounds are the circled hits.

**P, 0.05 indicates that Htt138Q aggregate formation is inhibited.

***P, 0.05 indicate mutant Htt138Q neurite morphology is reverted towards Htt15Q controls.

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<th>Gene Target</th>
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<th>Morphology Statistical Significance** (p-value)**</th>
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*Htt Aggregates. P, <0.05 indicates suppression of Htt138Q aggregate formation.

**P, 0.05 indicates mutant Htt138Q neurite morphology is reverted towards Htt15Q controls.
structures, while 18β-Glycyrrhetinic acid, Ouabain and Prosccillaridin-A form a second class that share a similar steroid-like backbone. It will be interesting to conduct further structure-function analysis to determine a minimal architecture that is required for these compounds to rescue Htt138Q-induced pathology.

**Figure 4. In vitro validation of small molecule screen hits.** Confocal microscopy images of primary cultures plated on glass coverslips and treated with either DMSO (A,B) or test compounds (C,D). Primary neural cultures expressing Htt138Q have numerous aggregates in neurite processes and surrounding the cell bodies (B), while control Htt15Q expressing cultures do not (A). Htt15Q is soluble and fills most neurite processes. Treatment of Htt138Q expressing cultures with Camptothecin (C) or 10-OH-Camptothecin (D) at 56 μM reduces aggregate formation and increases the proportion of soluble Htt138Q which fills neurite processes. (E) Quantification of altered Htt138Q distribution following Camptothecin treatment. An increase in the number of Htt138Q pixels/neuronal area (Htt-RFP pixels/neuromere and neurite GFP pixels) is observed in mutant cultures, suggesting an increase in Htt138Q solubility after drug treatment. * p < 0.05, n = 4, Scale bar: 100 μm.

doi:10.1371/journal.pone.0023841.g004
Figure 5. In vivo validation of screen hits. (A) Survival frequency scores for HD larvae (Elav<sup>15SS-GAL4; UAS-Htt138Q<sup>+/+</sup>) after 5-day drug dosing in liquid culture. (B) Chemical structures of the Camptothecin and 18β-Glycyrrhetinic acid class of small molecules found to rescue Htt138Q toxicity in vivo. (C-E) Genetic interaction studies to assess the effect of lkb1 kinase reduction on Htt138Q toxicity. (C) Pan-neuronal expression of Htt138Q<sup>1</sup> causes pupal lethality (left) which can be rescued with the introduction of an lkb1 heterozygous background. (D) Quantitative Western blot analysis demonstrating lkb1-rescued HD adults have normal Htt138Q expression levels. A control deficiency, Df(3L)vin, which reduces Htt138Q expression is shown for comparison. (E) Lkb1 mutation rescues the climbing behavior of HD flies. 25 day-old Htt138Q flies (C155;UAS-Htt138QmRFP<sup>2</sup>) have impaired climbing behavior as compared to controls. Introduction of an Lkb1<sup>4A4-2</sup> trans-heterozygous mutation into the Htt138Q<sup>2</sup> background improves climbing ability. * p<0.05.

doi:10.1371/journal.pone.0023841.g005
Discussion

We have used *Drosophila* primary neural cultures isolated from an HD model to screen for RNAi and small molecule suppressors of expanded polyQ Htt-induced toxicity. Cultures expressing a 588 amino acid fragment of human Htt containing an expanded polyQ domain (130Q) display robust cytoplasmic Htt aggregates, and have dystrophic neurites compared to Htt15Q control cultures. To identify suppressors of expanded polyQ Htt toxicity, we screened for compounds and RNAi targets that reduce aggregate formation and revert morphological defects towards the control state. Our screening resulted in the identification of lkβ1, an upstream kinase regulator of the mTOR/Insulin pathway, as a suppressor of mutant Htt toxicity. We also identified multiple compounds that have promising HD therapeutic efficacy: 18β-Glycyrrhetinic acid, Carbenoxolone, and the Camptothecins. Due to the efficiency of conducting screens in cell culture, and the increased physiological relevance of primary neurons, this methodology represents a powerful approach to identify modifiers for other neurodegenerative disorders.

LKB-1 knockdown was found to suppress mutant Htt toxicity in our system, as it rescued the dysmorphic primary neural culture morphology in vitro and restored viability in vivo. LKB-1 has been extensively studied, and mutations in the locus result in the Peutz Jeghers Syndrome (PJS) [42,43]. In *Drosophila*, loss of LKB-1 in the embryonic nervous system blocks apoptosis and results in hyperplasia [44]. How a partial LKB-1 knockdown elicits its beneficial effect in our system is still uncertain, although decreased levels of LKB-1 may reduce apoptosis caused by mutant Htt. LKB-1 lies upstream of many pathways that have previously been implicated in HD, including the mTOR/autophagy pathway [25,45,46] and the Insulin/AMPK signaling network [47,48]. Recently our findings were corroborated in vertebrates as [25,45,46] and the Insulin/AMPK signaling network [47,48]. Implicated in HD, including the mTOR/autophagy pathway [25,45,46] and the Insulin/AMPK signaling network [47,48].

Several compounds that suppressed mutant Htt toxicity in our primary culture system have previously been shown to have neuroprotective effects in mammalian systems, indicating that the assay with *Drosophila* primary cultured neurons has translational capacity. Compound GW5074 inhibited mutant Htt aggregate formation in our system, and also reduced striatal degeneration in our system, and also reduced striatal degeneration in our system, and also reduced striatal degeneration in our system, and also reduced striatal degeneration in our system. Our screening resulted in the identification of lkβ1, an upstream kinase regulator of the mTOR/Insulin pathway, as a suppressor of mutant Htt toxicity. We also identified multiple compounds that have promising HD therapeutic efficacy: 18β-Glycyrrhetinic acid, Carbenoxolone, and the Camptothecins. Due to the efficiency of conducting screens in cell culture, and the increased physiological relevance of primary neurons, this methodology represents a powerful approach to identify modifiers for other neurodegenerative disorders.

Several compounds that suppressed mutant Htt toxicity in our primary culture system have previously been shown to have neuroprotective effects in mammalian systems, indicating that the assay with *Drosophila* primary cultured neurons has translational capacity. Compound GW5074 inhibited mutant Htt aggregate formation in our system, and also reduced striatal degeneration in the NP-3 mouse HD model [28]. Similarly, 18β-Glycyrrhetinic acid, which rescued HD toxicity in vivo in our *Drosophila* assays, has been shown to suppresses neurotoxicity in a PC12 cellular stress model [34].

By analyzing the molecular structures and mechanisms of action of the small molecules identified as mutant Htt suppressors, new avenues to investigate the biology of HD pathogenesis have been uncovered. 18β-Glycyrrhetinic acid, and Carbenoxolone, which were used to pharmacologically manipulate LKB-1 dependent pathways and rescue HD toxicity in vivo, have also been reported to block gap junction activity [50]. Although this mechanism was not further investigated, it is an intriguing approach for future characterization in HD pathology. Recently there have been several reports that mutant Htt expressed in glia can trigger neuronal defects [7,51–53]. In addition, postmortem analysis of HD patient brain samples revealed increased activated astrocytes and reactive microglia in the striatum and cortex compared to similar aged non-diseased brains [54]. Gap junctions allow astrocytes to communicate via elaborate networks, and there is evidence that cell death signals can be propagated through gap junction networks [55]. Therefore, modulating gap junction activity with non-toxic compounds such as 18β-Glycyrrhetinic acid or Carbenoxolone might have neuroprotective benefits. 18β-Glycyrrhetinic acid derivatives are particularly interesting because they have already been evaluated in two clinical trials for other indications (ClinicalTrials.gov Identifier: NCT00398430 and NCT00739525), and are widely used as commercial sweeteners. Recently, an 18β-Glycyrrhetinic acid derivative was found to be efficacious in the treatment of two mouse models of Amyotrophic Lateral Sclerosis (ALS) and an Alzheimer’s Disease model, further supporting the potential therapeutic value of this class of compounds for neurodegenerative diseases [36].

Camptothecins were very effective at suppressing the dystrophic neuronal profiles and mutant Htt aggregation in our assay. Camptothecins are potent anti-cancer drugs that block cell division through several mechanisms including the introduction of DNA replication-dependant double-stranded breaks which trigger apoptosis, and down regulation of Top-1 by activation of proteasome pathways. In quiescent neurons, Camptothecins most likely cause transcriptional repression as a result of collisions between RNA polymerase and immobilized Top-1/Camptothecin complexes linked to the DNA. In our system, the benefit of Camptothecin treatment could theoretically be related to decreased Htt transgene expression, although we did not observe any decrease in Htt-mRFP fluorescence, even after one week of continuous exposure to the drug. Since targeted knockdown of mutant Htt via siRNA has been found to be effective at reversing disease progression in mouse models, small molecule transcriptional repressors may offer another therapeutic avenue to control HD [57]. Although toxicity issues have been reported in neural cultures following Camptothecin treatment, we did not observe morphological defects in our *Drosophila* HD model [38]. Camptothecins have been reported to regulate a number of different pathways, including activation of the ubiquitin/proteasome system and upregulation of mitochondrial biogenesis. These secondary Camptothecin effects could alleviate toxic Htt cellular stress by removing toxic Htt species or restoring energy homeostasis [59–62].

There has been debate in field about the contribution of Htt aggregates to disease pathology for many years. Several studies have shown that Htt aggregates accumulate in fine neuronal processes such as axons and dendrites, and block axon-transport to negatively impact cell health [17,63–65]. Real-time imaging experiments have suggested that soluble Htt, and not aggregates, correlate better with cellular toxicity [66]. Given this controversy, we chose not to use aggregate suppression as the sole metric to identify small molecules and RNAi knockdowns that have potential therapeutic value and included an additional parameter: neurite morphology. We found that neurite processes are sensitive to drugs and RNAi knock-downs that have non-specific toxicity effects. Using this assay we were able to identify compounds and RNAi knockdowns that have potential therapeutic value. Although our studies cannot conclusively demonstrate a physiological link between aggregate inhibition and improved neuronal health, we did discover compounds that improved neurite morphology in addition to reducing mutant Htt aggregation, providing anecdotal evidence that in some cases aggregates may have toxic properties.

*Drosophila* models of neurodegenerative disease have been a powerful tool for understanding mechanisms of neurodegeneration for more than a decade, and have more recently been applied directly to drug discovery as well [67–74]. Aside from genetic tools in *Drosophila* and the host of neurodegenerative disease models available, it is an attractive model for conducting suppressor screens given the lack of gene redundancy often observed in mammals. While single gene knock-down studies often fail to produce robust phenotypes in mammals, this is not the case in...
**Methods**

**Primary Cell Culture**

Euno1-GAL4, GALA virgins were collected en masse and crossed to either UAS-Htt138QmRFP, UAS-mCD8-GFP or UAS-Htt15QmRFP, UAS-mCD8GFP males to generate embryos for primary culture preparation. Neuroblasts were isolated as previously described [22].

**Western Blotting**

Embryonic lysates (n = 4/genotype) were prepared from control and Htt expressing strains (50 mM Tris, pH 8.0, 150 mM NaCl, 0.1% SDS, 1.0% NP-40 (IgePal), 0.1% sodium deoxycholate plus protease inhibitors (cOmplete-mini, Roche)), and protein content was quantified using a BCA kit (Pierce). Protein samples (10 µg/lane) were analyzed using standard SDS-PAGE/Western blotting techniques, and quantified using an Odyssey Infrared Imaging System (Li-Cor). For immunoblotting, antibodies were used at the following concentrations: mouse anti-Tubulin (6-11B-1, Sigma-Aldrich T7451) at 1/60,000, mouse anti-human Htt (MAB 2166, Chemicon) at 1/1,000, and goat-anti-mouse IR800 secondary (LI-COR 926-32210) at 1/3,000.

**Compound screening**

Primary cultures were re-suspended directly in Shields and Sang M3 media (Sigma) supplemented with 10 U/mL penicillin, 10 µg/mL streptomycin, 200 ng/mL insulin, and 5% fetal bovine serum. 100 nL of compounds from arrayed small-molecule libraries (NINDS Custom Collection 2, Prestwick Collection, BIOMOL2 ICCB-Longwood Known Bioactives High Concentration, various concentration from 1–15 mM in DMSO) were applied to 50 µL of cultures 24 hours after plating on optical bottom 384-well plates (Corning 3712). The neuroblast density was 18,500 cells/well. The primary screen was carried out in duplicate and hits were validated with 12 additional replicate wells.

**RNAi Screening**

dsRNAs (250 ng/well) were aliquoted onto microscopy plates and then 10 µL of neuroblasts were applied to a density of 18,500 cells/well. Cultures were incubated for 3 days with dsRNAs to achieve gene knockdown. Shields and Sang M3 media (Sigma) supplemented with 10 U/mL penicillin, 10 µg/mL streptomycin, 200 ng/mL insulin, and 5% fetal bovine serum was then added to cultures to bring assay volume to 50 µL. The *Drosophila* RNAi Screening Center (DRSC) whole genome kinase/phosphatase library (468 genes, 3 ampiclons/gene) was screened in duplicate, and hits were validated using additional dsRNA ampiclons containing no off-targets. For RNAi validation studies, dsRNAs were synthesized from T7-tailed DNA templates using the MEGAscript T7 transcription kit (Ambion). Synthesized dsRNAs were purified with RNasey kits (Qiagen) before use in cell culture experiments. The T7-tailed oligonucleotides used to generate DNA templates from *w*1118 genomic DNA are as follows: Lkb-1: DRSC16481 (GCGGCCAGATCCGTGACTA/CTCCGGCTGACCAGATG); DRSC36925 (GGACATCCAGGTGATTCCAGGGAGAAGCGTG/GCGCCGCTTGATCATG); Top-1: DRSC36056 (GAGAATGTGCAGGGACAGGT/GTCAATGAAGAAGGGCCA); DRSC20295 (GAGAGGAGAGCGGTT/GCGCCCGCTTGTATCAG); Top-2: DRSC36057 (CAGAGCGACAGAGGATCATG/TTTCTGTTATTCCTCTGTTGG); DRSC3459 (TTTGCCAGAGGATATCTCGCTATCAGT); Top3z: DRSC3460 (TTAAGCTTGCTGAAGAA/GCCGACGGCCTTTTTCA); DRSC37672 (TTGTGTCCTGACCGAACAGAT/AGTGGTTTGTAAGCTGGAGAAGAAGCGTG/GCGCCGCTTGATCATG).

**Microscopy**

For high-content screening, mature 7-day old cultures were imaged with an ImageXpress Micro robotic microscope (Molecular Devices, Sunnyvale, CA) using a 10x objective and FITC/ Cy3 filter sets. Images were 1392×1040 pixels, or 897×670 micrometers. Laser-based autofocus was used to locate plate bottoms, and then image-based focusing was used to resolve fluorescently labeled neurons over a 48 µm range. The GFP and mRFP channels were imaged in the same focal plane, with exposure times of 850 and 400 ms respectively. Three sites were imaged per well for each treatment group, and the screen was done in duplicate. For confocal microscopy of primary cultures, neuroblasts were plated on poly-L-lysine coated chambered cover slips (LabTekII, 0.8 cm2/well) at 18,300 cells/well in 50 µL volume. Small molecules were added to cultures 24 hours after plating, incubated for 7 days, and then imaged with a Leica TCS-SP2 confocal LSM microscope.

**Digital Image Analysis of High Content Screening Data Sets**

Neuronal morphological analysis and Htt aggregate quantification for automated microscopy images was performed as previously described [23,77]. In brief, Htt138Q aggregates were quantified as the total number of pixels/image with intensity higher than an empirically set threshold. To quantify neuronal morphologies, cell body clusters (neuromeres) and neurites were extracted from images using our custom algorithms [21]. The *log* transformed areas of cell body clusters were found to fit a Gaussian mixture model (GMM) and therefore were separated into three bins (small, medium, and large). Absolute counts of neuromeres/bin were tabulated for all images. Neurite segment lengths were similarly clustered into three groups (short, medium, and long) using the *K*-means method and then quantified. Cell cluster and neurite counts were converted into percentages to control for any variation in cell number between wells arising from pipetting error. Mean neurone area and neurite length for each image were also calculated to give a total of eight morphological metrics for image morphology quantification. For statistical analysis, *p*-values for each morphological feature were calculated using a two sample *t*-test (e.g. small neurome feature of Htt138Q drug-effect comparing controls to either vehicle or drug).

**Drosophila** [75,76]. We have found that the complex neural morphologies of *Drosophila* primary cultures can also provide sensitive information about the general cell physiological status of a disease model. The algorithms that we have used in this study can help quantify complex morphologies, and can also facilitate the identification of disease modifying genes [23]. Live imaging, as presented here, has the advantage over traditional cell staining experiments in that the fine neurite morphology of cultures is preserved. Deters and washes needed for immunofluorescence-based assays can disrupt fine cellular processes and introduce artifacts, which reduce assay sensitivity and introduce noise. Live-cell imaging also makes it possible to collect different time points in a single experiment, which not only reduces labor but also enables one to track the effect of a compound or gene knockdown over time. Because of the ease and speed of conducting RNAi and compound screens in *Drosophila* primary culture systems, this methodology offers an attractive approach to identify disease-modifying agents for neurodegenerative diseases.
treated cultures versus small neurome feature of Htt15Q DMSO cultures. The resultant morphological p-values for individual features were then integrated into a single p-value using the Fisher method [78] defined by the equation \( p_{\text{combined}} = -\sum x_k \log_2(p_k) \), where \( k \) represents independent tests, \( p_k \) is the p-value of the \( k \)-th feature. The combined statistic has a \( \chi^2 \) distribution with \( 2^k \) degrees of freedom under the joint null hypothesis. This method works well in cases where the evidence against the null-hypothesis is spread across different features. Excluded from analysis were compound-treated wells with <6 images, out-of-focus images, or images that lacked cell profiles altogether.

**In vivo Rescue studies**

For small molecule in vivo rescue studies, Elav\(^{155}\), UAS-Htt138QmRFP, UAS-mCD8-GFP/+ 1st instar larvae were collected en-masse and dispensed into liquid media (10 larvae/well) containing different concentrations of test compounds (n = 3 replicates/concentration). The cultures were reared at 21°C for 5 days, and the mean number or living Htt138Q larvae (i.e. GFP en-masse and dispensed into liquid media (10 larvae/well)

The strong line, pharate lethality at 25°C survives to adulthood and is viable for a number of weeks. Using method [78] defined by the equation

\[
\text{The combined statistic has a } \chi^2 \text{ distribution with } 2^k \text{ degrees of freedom under the joint null hypothesis. This method works well in cases where the evidence against the null-hypothesis is spread across different features. Excluded from analysis were compound-treated wells with <6 images, out-of-focus images, or images that lacked cell profiles altogether.}

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**Negative Geotaxis Assay**

Lkb1\(^{1444-2}\) was crossed into the Elav\(^{155}\), UAS-Htt138QmRFP\(^2\) which is adult viable and has weaker Htt138Q expression. Virgin female Drosophila were collected and flipped onto media with 2 times per week until the start of the assay. 25 day-old flies (10–15 flies/vial, 4 vials/genotype) were gently tapped to the base of vials, and climbing behavior was video-recorded for 10 seconds (trial). The percentage of flies to reached the top of a vial was tabulated and averaged after 4 trials. Vials were back-lit with a light box to enhance the resolution of the fly climbing trajectories. Statistical analysis was performed using a t-test.

**Supporting Information**

**Figure S1** Selective compounds tested for their ability to suppress Htt138Q neuronal toxicity. (TIF)

**Table S1** Compounds found to inhibit Htt138Q aggregate formation in Drosophila primary neuronal culture screen. (DOC)

**Movie S1** Elav\(^{155}\), GAL4; UAS-Htt138QmRFP\(^2\)/lkb1\(^{1444-2}\) rescued adult Drosophila. While Elav\(^{155}\), GAL4;UAS-Htt138QmRFP\(^2\)+/+ adults are pharate lethal, introduction of a heterozygous lkb1\(^{1444-2}\) allele suppresses Htt138Q toxicity and results in the emergence of viable escapers. Escapers have normal walking ability, but are unable to unfurl and inflate their wings. (MPG)

**Acknowledgments**

The authors thank C. Sharmu, M. Booker, S. Mohr at the Institute of Chemistry and Cell Biology-Longwood (ICCB-L) and the Drosophila RNAi Screening Center (DRSC) at Harvard Medical School for their advice and use of screening facilities and compound/RNAi libraries. The lkb1\(^{1444-2}\) and lkb1\(^{14B1-11}\) alleles were obtained from the St, Johnston lab, and other stocks were obtained from the Bloomington Stock Center.

**Author Contributions**

Conceived and designed the experiments: JS KJS. Performed the experiments: JS KJS. Analyzed the data: JS KJS CW PH. Contributed reagents/materials/analysis tools: JTL. Wrote the paper: JS KJS. Designed the software used in the analysis: CW PH.

**References**


