Biased Type 1 Cannabinoid Receptor Signaling Influences Neuronal Viability in a Cell Culture Model of Huntington Disease^S

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ABSTRACT

Huntington disease (HD) is an inherited, autosomal dominant, neurodegenerative disorder with limited treatment options. Prior to motor symptom onset or neuronal cell loss in HD, levels of the type 1 cannabinoid receptor (CB₁) decrease in the basal ganglia. Decreasing CB₁ levels are strongly correlated with chorea and cognitive deficit. CB₁ agonists are functionally selective (biased) for divergent signaling pathways. In this study, six cannabinoids were tested for signaling bias in in vitro models of medium spiny projection neurons expressing wild-type (ST*Hdh*^{Q7/Q7}) or mutant huntingtin protein (ST*Hdh*^{Q111/Q111}). Signaling bias was assessed using the Black and Leff operational model. Relative activity [Δ logR (τ/K_A)] and system bias ($\Delta\Delta$ logR) were calculated relative to the reference compound WIN55,212-2 for G $\alpha_{i/o}$, G α_s , G α_q , G $\beta\gamma$, and β -arrestin1 signaling following treatment with 2-arachidonoylglycerol (2-AG), anandamide (AEA), CP55,940,

Introduction

Huntington Disease. Expression of mutant huntingtin protein (mHtt) causes a myriad of molecular and cellular changes that ultimately cause progressive worsening of the symptoms of

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Δ⁹-tetrahydrocannabinol (THC), cannabidiol (CBD), and THC+CBD (1:1), and compared between wild-type and HD cells. The *E*_{max} of Gα_{i/o}-dependent extracellular signal-regulated kinase (ERK) signaling was 50% lower in HD cells compared with wild-type cells. 2-AG and AEA displayed Gα_{i/o}/Gβγ bias and normalized CB₁ protein levels and improved cell viability, whereas CP55,940 and THC displayed β-arrestin1 bias and reduced CB₁ protein levels and cell viability in HD cells. CBD was not a CB₁ agonist but inhibited THC-dependent signaling (THC+CBD). Therefore, enhancing Gα_{i/o}-biased endocannabinoid signaling may be therapeutically beneficial in HD. In contrast, cannabinoids that are β-arrestin-biased—such as THC found at high levels in modern varieties of marijuana—may be detrimental to CB₁ signaling, particularly in HD where CB₁ levels are already reduced.

Huntington disease (HD). Early in HD progression, levels of type 1 cannabinoid receptor (CB1) mRNA and protein decrease in medium spiny projection neurons of the caudate and putamen (Denovan-Wright and Robertson, 2000; Glass et al., 2000; Van Laere et al., 2010). CB_1 transcription is inhibited by mHtt (McCaw et al., 2004; Laprairie et al., 2013). The reduction in CB1 and loss of CB1 function have been shown to contribute to the cognitive, behavioral, and motor deficits of HD pathology in animal models of HD (Blázquez et al., 2011; 2015; Chiarlone et al., 2014). Furthermore, rescue of CB_1 gene expression in the striatum using viral transduction prevents the loss of excitatory synaptic markers and reduces dendritic spine loss in animal models of HD (Naydenov et al., 2014). The benefit of adenoassociated viral CB₁ delivery in HD provides strong proof for the concept of treating HD through enhancing CB₁ function. However, gene-based therapies specifically for CB₁ or other single alterations in gene expression, will probably not be used clinically for HD in the near future because of the invasive nature of delivery and because the potential adverse effects of gene therapy are still being investigated. The more effective gene-based therapies for HD will target the underlying cause of the disease,

ABBREVIATIONS: AEA, anandamide; Akt, protein kinase B; ANOVA, analysis of variance; BRET, bioluminescence resonance energy transfer; cal-AM, calcein-AM; CBD, cannabidoi; CB₁, type 1 cannabinoid receptor; CP, CP55,940; CREB, cAMP response element-binding protein; CTx, *Cholera* toxin; 8-OH-DPAT, 7-(dipropylamino)-5,6,7,8-tetrahydronaphthalen-1-ol; D2, type 2 dopamine receptor; ERK, extracellular signal-regulated kinase; EthD-1, ethidium homodimer-1; GABA, γ -aminobutyric acid; GFP², green fluorescent protein 2; HD, Huntington disease; mHtt, mutant huntingtin protein; N-CB₁, amino terminus of CB₁; O-2050, (6aR,10aR)-3-(1-methanesulfonylamino-4-hexyn-6-yl)-6a,7,10,10a-tetrahydro-6,6,9-trimethyl-6Hdibenzo[b,d]pyran; p, phosphorylated; PAMs, positive allosteric modulators; PLC, phospholipase C; Rluc, *Renilla* luciferase; THC, Δ^9 -tetrahydrocannabinol; URB597, [3-(3-carbamoylphenyl] *N*-cyclohexylcarbamate; WAY-100,635, *N*-[2-[4-(2-methoxyphenyl)-1-piperazinyl]ethyl]-*N*-(2-pyridyl)cyclohexanecarboxamide; WIN, WIN55,212–2.

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the *mHtt* gene and encoded protein, and not secondarily lost cellular components (Kumar et al., 2015). In contrast, pharmacological strategies aimed at elevating CB_1 levels and/or signaling through remaining pool of CB_1 receptors has significant therapeutic potential for the treatment and management of HD.

Pharmacological Targeting of CB₁. CB₁ is activated by cannabinoids, which are a structurally diverse group of ligands that includes endogenously occurring cannabinoids (endocannabinoids) such as anandamide (AEA) and 2-arachidonoylglycerol (2-AG), phytocannabinoids from Cannabis sativa such as Δ^9 -tetrahydrocannabinol (THC), and synthetic cannabinoids such as CP55,940 (CP) and WIN55,212-2 (WIN) (Pertwee, 2008). Activation of CB_1 in the brain results in inhibition of neurotransmitter release from presynaptic glutamatergic and GABAergic neurons and activation of prosurvival signaling cascades such as extracellular signal-regulated kinase (ERK) and protein kinase B (Akt) (Fernández-Ruiz, 2009). We have reported that AEA, and structurally related compounds, increase the expression of CB_1 via CB_1 through $G\alpha_{i/o}$ and $G\beta\gamma$ signaling in a cell culture model expressing normal huntingtin $(STHdh^{Q7/Q7})$ and cells expressing mHtt $(STHdh^{Q111/Q111})$ (Laprairie et al., 2013). Importantly, this cell culture model endogenously expresses CB1 and other components of the endocannabinoid system. Increasing levels of CB₁ improved neuronal viability in this cell culture model (Laprairie et al., 2013), lending further support to the strategy of enhancing signaling through the pool of CB_1 that are retained in the presence of mHtt and elevating CB_1 levels in these cells despite transcriptional repression via mHtt.

Not all cannabinoids increase CB1 levels. THC and CP treatment promote β -arrestin-dependent CB₁ internalization and reduce CB₁-dependent downstream signaling (Laprairie et al., 2014). Functional selectivity (i.e., signaling bias) describes the receptor- and ligand-dependent enhancement of certain signal transduction pathways and the simultaneous diminution of other signal transduction pathways at a single receptor (Luttrell et al., 2015). Functional selectivity occurs via a GPCR ligand that preferentially activates one effector (e.g., $G\alpha_{i/o}$) more potently and efficaciously than another (e.g., β -arrestin) through ligand-specific changes in GPCR conformation or dimerization with other GPCRs (Christopoulos, 2014). Signaling bias could be exploited for enhancement of CB₁ function in HD, at the same time limiting detrimental adverse on-target effects (Laprairie et al., 2014). Cannabinoids display signaling bias (Laprairie et al., 2014; Khajehali et al., 2015). Endocannabinoids acting at CB₁ are $G\alpha_{i/o}$ -biased, whereas THC and CP are β -arrestinbiased in STHdh^{Q7/Q7} cells (Laprairie et al., 2014). In this study, we wanted to determine how the bias of different classes of cannabinoid affected neuronal viability. We hypothesized that $G\alpha_{i/o}$ -biased cannabinoids improve neuronal viability, whereas β -arrestin-biased cannabinoids reduce—or have no effect oncell viability. The functional selectivity of six cannabinoids [AEA, 2-AG, THC, cannabidiol (CBD), WIN, and CP] between $G\alpha_{i/0}$, $G\alpha_s$, $G\alpha_q$, $G\beta\gamma$, and β -arrestin pathways was examined in STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells and compared with cannabinoid-dependent changes in ATP level, γ -aminobutyric acid (GABA) release, metabolic activity, and cell death.

Materials and Methods

Drugs. Drugs were dissolved in ethanol (THC) or DMSO [2-AG, 8-OH-DPAT (5HT_{1A} agonist), AEA, CP, CBD, gallein ($G\beta\gamma$ inhibitor),

haloperidol (D₂ antagonist), O-2050 (CB₁ antagonist), quinpirole (D₂ agonist), WAY-100,635 (5HT_{1A} antagonist), WIN] and diluted to final solvent concentrations of 0.1%. 2-AG, AEA, CP, CBD, O-2050, and WIN were purchased from Tocris Bioscience (Bristol, UK). 8-OH-DPAT, haloperidol, quinpirole, THC, and WAY-100,635 were purchased from Sigma-Aldrich (Oakville, ON, CAN). The G $\beta\gamma$ modulator gallein was purchased from MilliporeSigma (Billerica, MA). *Pertussis* toxin (PTx) and *Cholera* toxin (CTx) (Sigma-Aldrich) were dissolved in dH₂O (50 ng/ml) and added directly to the media 24 hours prior to cannabinoid treatment. Pretreatment of cells with PTx and CTx inhibits G $\alpha_{i/o}$ and G α_s , respectively (Milligan et al., 1989). In the case of CTx, this occurs via downregulation of G α_s following ADPribosylation (Milligan et al., 1989; McKenzie and Milligan, 1991). All experiments included a vehicle treatment control.

Cell Culture. STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells are derived from the conditionally immortalized striatal progenitor cells of embryonic day 14 C57BlJ/6 mice (Coriell Institute, Camden, NJ) (Trettel et al., 2000). STHdh^{Q111/Q111} cells express exon 1 of the mutant human huntingtin gene containing 111 CAG repeats knocked into the mouse huntingtin locus (Trettel et al., 2000). STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells endogenously express CB₁ and dopamine D₂ receptor (Paoletti et al., 2008; Laprairie et al., 2014). Cells were maintained at 33°C, 5% CO₂ in Dulbecco's modified Eagle's medium supplemented with 10% fetal bovine serum, 2 mM L-glutamine, 10⁴ IU ml⁻¹ penicillin/streptomycin, and 400 μ g ml⁻¹ geneticin. Cells were serum-deprived for 24 hours prior to experiments to promote differentiation (Trettel et al., 2000; Laprairie et al., 2014).

Plasmids and Transfection. Human CB₁-green fluorescent protein² (GFP²) C-terminal fusion protein was generated using the pGFP²-N3 plasmid (PerkinElmer, Waltham, MA), as described previously (Bagher et al., 2013). Human arrestin2 (β -arrestin1)-*Renilla* luciferase II (Rluc) C-terminal fusion protein was generated using the pcDNA3.1 plasmid and provided by Dr. Denis J Dupré (Dalhousie University, NS). The GFP²-Rluc fusion construct, and Rluc plasmids have also been described (Bagher et al., 2013). The G α_q dominant negative mutant [Glu 209 Δ Leu, Asp 277 Δ Asn (Q209L,D277N)] pcDNA3.1 plasmid was obtained from the cDNA Resource Center (Missouri S&T, Rolla, MO) (Lauckner et al., 2005).

Cells were grown in six-well plates and transfected with 200 ng of the Rluc fusion plasmid and 400 ng of the GFP^2 fusion plasmid according to previously described protocols (Laprairie et al., 2014) using Lipofectamine 2000 according to the manufacturer's instructions (Invitrogen, Burlington, Canada). Transfected cells were maintained for 48 hours prior to experimentation.

BRET². Interactions between CB₁ and β -arrestin1 were quantified via BRET² (Packard BioScience Company, Meriden, CT) according to previously described methods (James et al., 2006; Laprairie et al., 2014). Bioluminescence resonance energy transfer (BRET) efficiency (BRET_{Eff}) was determined such that Rluc alone was used to calculate BRET_{MIN} and the Rluc-GFP² fusion protein was used to calculate BRET_{MAX} using previously described methods (James et al., 2006).

On- and In-Cell Western. On-Cell Western (LI-COR Biosciences, Lincoln, NE) analyses were completed as described previously (Laprairie et al., 2014) using primary antibody directed against N-CB₁ (1:500, cat. no. 101500; Cayman Chemical Company, Ann Arbor, MI). All experiments measuring CB₁ included an N-CB₁ blocking peptide (1:500) control, which was incubated with N-CB1 antibody (1:500). Immunofluorescence observed with the N-CB1 blocking peptide was subtracted from all experimental replicates. In-Cell Western (LI-COR Biosciences) analyses were conducted as described previously (Laprairie et al., 2014). Primary antibody solutions were directed against: the amino terminus of CB1 (N-CB1) (1:500), phosphorylated (p)ERK1/2(Tyr205/185) (1:500), ERK1/2 (1:500), pCREB(S133) (1:500), cAMP response element-binding protein (CREB) (1:500), pPLC\u03b23(S537) (1:500), PLC\u03b23 (1:1000), pAkt (S473) (1:500), protein kinase B (Akt) (1:1000), or β-actin (1:2000; Santa Cruz Biotechnology, Dallas, TX). Secondary antibody solutions were: $\label{eq:cwr00dye} \mbox{ or } IR^{CW800dye} \mbox{ or } IR^{CW800dye} \mbox{ (1:500; Rockland Immunochemicals, Pottstown, PA)}.$

ATP Quantification, γ-Aminobutyric Acid Enzyme-Linked Immunosorbent Assay, and Cell Viability Assays. The CellTiter-Glo ATP quantification assay was used according to the manufacturer's instructions (Promega, Madison, WI). The GABA enzyme-linked immunosorbent assay was conducted according to the manufacturer's instructions for mouse cell culture media (Novatein Biosciences, Boston, MA). GABA levels were reported as ΔGABA relative to GABA in vehicletreated cells. Viability assays [calcein-AM (cal-AM), ethidium homodimer-1 (EthD-1)] were conducted according to the manufacturer's instructions (Live/Dead Cytotoxicity Assay, Life Technologies, Burlington, Canada). Cal-AM fluorescence is an indicator of cellular esterase activity and mitochondrial respiration. Cal-AM fluorescence (460/510 nm) is reported as % esterase activity relative to vehicletreated STHdh^{Q7/Q7} cells (100%). EthD-1 fluorescence is an indicator of membrane permeability and cell death. EthD-1 fluorescence (530/620 nm) is reported as % membrane permeability relative to ${
m STH}dh^{{
m Q7/Q7}}$ cells treated with 70% methanol for 30 minutes (100%). All measurements of viability (ATP, GABA, calcein-AM, EthD-1) were made 18 hours following cannabinoid treatment.

Statistical Analyses. All experiments were conducted alongside WIN as a reference ligand. Although it is often considered ideal to choose the endogenous receptor agonist as a reference ligand (Kenakin and Christopoulos, 2013), WIN was chosen as a reference ligand for these studies because: 1) it is a widely used reference compound to study CB₁-dependent signaling (Lauckner et al., 2005); 2) it acted as an agonist in all assays with nonsignificant differences in EC₅₀ observed between assays; and 3) we wanted to determine whether the two endogenous cannabinoids, AEA and 2-AG, were inherently biased either in wild-type (STH $dh^{Q7/Q7}$) or mHtt-expressing (STH $dh^{Q111/Q111}$) cells. Concentration-response curves for ERK, BRET² (CB₁/ β -arrestin1), CREB, phospholipase C (PLC) β 3, and Akt are presented as % of WIN E_{max} in STHdh^{Q7/Q7} cells (Griffin et al., 2007).

Concentration-response curves were fit to nonlinear regression with variable slope (four-parameter) model to determine pEC_{50} and E_{max} (Table 1), or global nonlinear regression using the operational model (Black and Leff, 1983; Ehlert et al., 2011; Kenakin et al., 2012) (eq. 1) to estimate the transduction coefficient $[\log R(\tau/K_A)]$, change in transducer coefficient relative to the reference ligand ($\Delta log R$), and bias factor (AAlogR) (Prism v. 5.0, GraphPad Software Inc., San Diego, CA), as indicated. In eq. (1) E is the response, E_{\max} is the maximal response, [A] is agonist concentration, n is transducer slope, τ is agonist efficacy, and $K_{\rm A}$ is the agonist's affinity for the receptor (Kenakin et al., 2012). To obtain a global least-squares fit of the data to the operational model, nwas constrained to 1 and $\log K_A$ was shared between both STHdh^{Q7/Q7} and STHdh^{Q111/Q111} datasets and constrained to be greater than -15(Griffin et al., 2007; Ehlert, 2015). Relative activity ($\Delta \log R$) was calculated in Prism as the difference between transduction coefficients $[\log R (\tau/K_A)]$ values for two ligands, a "test" ligand, and a reference ligand (here WIN) as measured between sample-matched replicates (Kenakin et al., 2012) (eq. 2). In eq. (3) bias factor (i.e., log bias, $\Delta\Delta \log R$) is the difference between response 1 (R1) and response 2 (R2) (Kenakin et al., 2012). All calculations of $\Delta\Delta \log R$ are reported using pERK response ($G\alpha_{i/o}$) as R₁. Statistical analyses were two-way analysis of variance (ANOVA) (Prism). Post-hoc analyses were performed using the Bonferroni test. Homogeneity of variance was confirmed using the Bartlett test. The level of significance was set to P < 0.01 where ANOVA was used or P < 0.05 where nonoverlapping confidence intervals (CI) were used to determine significance. Results are reported as the mean \pm S.E.M. from at least four independent experiments.

$$E = \frac{E_{max}[A]^{n} \tau^{n}}{[A]^{n} \tau^{n} + ([A] + K_{A})^{n}}$$
(1)

$$\Delta log R = \log(\tau/K_A)_{Test \ compound} - log(\tau/K_A)_{Ref \ compound}$$
(2)

$$log bias = \Delta \Delta log R = \Delta \Delta log (\tau/K_A)_{R1-R2}$$

$$= \Delta log(\tau/K_A)_{R1} - \Delta log(\tau/K_A)_{R2}$$
(3)

3.2 + 2.7Data are expressed as mean \pm S.E.M. 5.6 2.7_{\uparrow} 6.4(%) +| +| UU⁺ ZZ Akt Response $(G\beta\gamma)$ $E_{\rm max}$ (30.333.2 $\begin{array}{c} 76.0\\111\\102\\115\\111\\111\\111\\48.3\\40.1\end{array}$ $0.5 \\ 0.6$ pEC_{50} +1 +1 zz 6.06.13.3 + 2.8 $\begin{array}{c} +++5.3\\ +-5.3\\ ++2.3\\ ++5.1\\ 5.2\\ +\\ 5.2\\ +\end{array}$ Determined using nonlinear regression analysis (four parameters) in GraphPad v. 5.0. E_{max} (%) is the maximal agonist effect relative to E_{max} for WIN in STH4th ^{QTQ7} cells for each measurement. (%) PLC β 3 Response (G α q) +| +| O O Z Z +| +| E_{\max} ($\begin{array}{c} 105 \\ 102 \\ 71.8 \\ 70.8 \\ 87.4 \\ 87.4 \end{array}$ $101 \\ 90.2 \\ 71.4 \\ 67.9$ 55.451.1 $\begin{array}{c} & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & & & & \\ & &$ pEC_{50} $\begin{array}{c} 6.2 \\ 6.2 \\ 6.4 \\ 6.5 \\ 6.5 \\ 6.5 \\ 6.5 \\ \end{array}$ $6.4 \\ 6.4$ N.C. N.C. N.C. N.C. N.C. N.C. 24.1^{+} 13.1_{1} 4.4_{1} (%) CREB Response $(G\alpha s)$ $E_{\rm max}$ (' +| +| +| +| $\frac{115}{105}\\ \frac{443}{432}$ 445 348 204 194 $\begin{array}{c} 0.2 \\ 0.3 \\ 0.5 \\ 0.7 \end{array}$ $\begin{array}{c} 0.6 \\ 0.8 \\ 0.9 \\ 1.1 \end{array}$ pEC_{50} +| +| +| ± 1 zzzzz 6.7 7.0 6.6 6.6 6.4 $6.2 \\ 6.2$ $\begin{array}{c} 4.3 \\ 5.1 \\ \dot{\uparrow} \\ 3.9 \\ 3.8 \\ 3.8 \\ 3.8 \\ 9.8 \\ 9.8 \\ 9.8 \\ \end{array}$ 3.6 $3.0 \\ 3.4$ BRET Response (β -arrestin1) E_{\max} (%) U +| +| $\begin{array}{c} 128 \\ 126 \\ 101 \\ 96.7 \\ 96.7 \\ 65.0 \\ 98.8 \\ 98.8 \\ 107 \end{array}$ $90.2 \\ 102$ $0.5 \\ 0.5$ pEC_{50} +| +| 6.27.46.96.16.16.16.16.16.0+ 4.7 + + 4.7 + + 3.6 + + 5.9 + + 2.4 + + 7.7 +2.3+(%) N.N.N. ERK Response (G α i/o) +| $E_{\rm max}$ (51.5 88.0 88.0 75.2 117 117 40.3 33.8 33.8 17.61.1 pEC_{50} N.C. N.C. +1 5.0STHdh^{Q111/Q111} STHdh^{Q7/Q7} STHdh^{Q111/Q111} STHdhQ111/Q111 STHdhQ7/Q7 STHdh Quivenin STHdh Quive $STHdh^{Q7/Q7}$ $STHdh^{Q111/Q111}$ $STHdh^{Q7/Q7}$ THC + CBDTHC CBD 2-AG AEA MIN СЪ

 $ho EC_{50}$ and $E_{
m max}$ of cannabinoid ligands at $m CB_1$ in $m STHdh^{Q7/Q7}$ and $m STHdh^{Q111/Q111}$ cells

FABLE 1

N.C., not converged. *P < 0.01 compared with $STHdh^{Q7/Q7}$ within ligand and measurement; $^{+}P < 0.01$ compared with WIN within cell type and measurement, as determined using two-way analysis of variance followed by Bonferroni post-hoc st (n = 4). test (n =

Results

Cannabinoid-Dependent Signaling in the Presence of mHtt. STHdh^{Q7/Q7} (Fig. 1, A–E) and STHdh^{Q111/Q111} (Fig. 1, F–J) cells were treated with 10 nM–10 μ M WIN, CP, 2-AG, AEA, THC, CBD, or THC+CBD (1:1), and G $\alpha_{i/o}$ - (ERK1/2), β -arrestin1, $G\alpha_{s^-}$ (CREB), $G\alpha_{q^-}$ (PLC β 3), and $G\beta\gamma$ -dependent (Akt) signaling were measured. The coupling of each of these signaling pathways to CB₁ and their respective G proteins or β -arrestin1 has been tested previously (Laprairie et al., 2014) and is presented in (Supplemental Fig. 1 for a subset of cannabinoids. The agonist effects of all cannabinoids



Fig. 1. Functional selectivity of cannabinoids in wildtype and mHtt-expressing cells. STHdh^{Q7/Q7} (A–E) and STHdh^{Q111/Q111} (F–J) cells were treated with 10–10,000 nM WIN, CP, 2-AG, AEA, THC, CBD, or THC+CBD (1:1) and ERK1/2 phosphorylation (10 minutes) (A,F), β -arrestin1 recruitment (30 minutes) (B,G), CREB phosphorylation (30 minutes) (C,H), PLC β 3 phosphorylation (10 minutes) (D,I), or Akt phosphorylation (10 minutes) (E,J) were measured and expressed relative to WIN $E_{\rm max}$ in STHdh^{Q7/Q7} cells. ERK1/2, CREB, PLC β 3, and Akt phosphorylation were measured via in-cell Western. β -arrestin1 recruitment was measured via BRET². Concentration-response curves were fit to the Black-Leff global nonlinear regression using the operational model. N = 4.

tested were CB_1 -dependent, with the exception of CBD (see below).

For pERK1/2 (G $\alpha_{i/o}$), the E_{max} observed for all cannabinoids was reduced by approximately 50% in STHdh^{Q111/Q111} cells compared with STHdh^{Q7/Q7} cells, with no change in pEC₅₀ observed between STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells (Table 1; Fig. 1, A and F). This is consistent with our earlier finding that the E_{max} for pERK relative to total ERK (i.e., raw data without reference ligand) following arachidonoyl-2'chloroethylamide treatment is 50% lower in STHdh^{Q111/Q111} cells expressing mHtt compared with STHdh^{Q111/Q111} cells expressing mHtt compared with STHdh^{Q111/Q111} cells (Laprairie et al., 2013). The pERK E_{max} values were greater in WIN- and AEA-treated STHdh^{Q7/Q7} cells; CBD and THC+CBD displayed no agonist activity in STHdh^{Q7/Q7} cells (Table 1; Fig. 1A). In contrast, the pERK E_{max} values were not different in 2-AG-, AEA-, WIN-, and CP-treated STHdh^{Q111/Q111} cells, and the pERK E_{max} was lower in THCand THC+CBD-treated STHdh^{Q111/Q111} cells compared with WIN; CBD did not elicit an agonist response (Table 1; Fig. 1F). THC+CBD-treated STHdh^{Q111/Q111} cells also displayed a lower pEC₅₀ in the pERK assay (Table 1; Fig. 1F).

CB₁ is known to interact with β -arrestin1, which mediates receptor internalization, recycling, and degradation (Sim-Selley and Martin, 2002; Laprairie et al., 2014). Unlike pERK, no differences in $E_{\rm max}$ and pEC₅₀ were observed for β -arrestin1 assays. CP displayed higher pEC₅₀ and $E_{\rm max}$ values than WIN, whereas no differences in pEC₅₀ and $E_{\rm max}$ were observed between WIN, 2-AG, and THC, and AEA displayed lower $E_{\rm max}$ values for β -arrestin1 recruitment in both cell lines (Table 1; Fig. 1, B and G). CBD was not an agonist of β -arrestin1 recruitment. In the THC+CBD-treated cells, the $E_{\rm max}$ and pEC₅₀ of BRET_{Eff} were both reduced compared with THC-treated cells (Table 1). These data are consistent with our previous finding that CBD is a negative allosteric modulator of THC-dependent effects at CB₁ (Laprairie et al., 2015).

The observed E_{max} and pEC₅₀ for pCREB (G α_{S}) was not different in STHdh^{Q7/Q7} cells treated with WIN, CP, CBD, or THC+CBD, relative to STHdh^{Q111/Q111} cells (Table 1; Fig. 1, C and H). AEA and 2-AG did not evoke a pCREB response. CP, CBD, and THC+CBD treatment resulted in E_{max} values for pCREB higher than WIN treatment in both cell lines. pCREB pEC₅₀ and E_{max} values were higher in CP- and CBD-treated cells compared with THC+CBD-treated cells (Table 1; Fig. 1, C and H). Because CB₁-dependent G α_{S} signaling is uncommon, this was examined further (see below).

CB₁ can also couple $G\alpha_q$ to modulate Ca²⁺- and PLC β 3dependent signaling (Lauckner et al., 2005). No differences were observed for PLC β 3 phosphorylation between STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells (Table 1; Fig. 1, D and I). pPLC β 3 E_{max} values were greater in WIN-, 2-AG-, and AEA-treated cells compared with CP- and THC-treated cells, with no change in pEC₅₀ (Table 1; Fig. 1, D and I). CBD was not an agonist of PLC β 3 phosphorylation.

In the case of pAkt (G $\beta\gamma$), no differences were observed between STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells (Table 1; Fig. 1, E and J). pAkt $E_{\rm max}$ values were greater in WIN-, 2-AG-, and AEA-treated cells compared with CP-treated cells, which were in turn greater compared with THC-treated cells (Table 1; Fig. 1, E and J). pAkt pEC₅₀ values did not differ between agonists. CBD was not an agonist of Akt phosphorylation.

Operational Model Analysis of Cannabinoid Transduction Coefficients (logR) and Relative Activity (AlogR) in the Presence of mHtt. The operational model global nonlinear regression (eq. 1) was used to analyze concentration-response data for cannabinoid signaling bias in STH $dh^{Q7/Q7}$ and STH $dh^{Q111/Q111}$ cells. CBD only displayed agonist activity for pCREB and these data were therefore omitted from global nonlinear regression analyses of pERK, β -arrestin1, pPLC β 3, and pAkt assays. The transduction coefficient $[\log R (\tau/K_A)]$ for the ERK response was lower in THC- and THC+CBD-treated cells compared with WINtreated cells, and was lower in THC- and THC+CBD-treated $STHdh^{Q111/Q111}$ cells compared with $STHdh^{Q7/Q7}$ cells (Table 2). logR for β -arrestin1 was also lower in THC- (only $STHdh^{Q111/Q111}$) and THC+CBD-treated cells compared with WIN-treated cells, was lower in THC- and THC+CBD-treated $STHdh^{Q111/Q111}$ cells compared with $STHdh^{Q7/Q7}$ cells, and was higher in THC- and THC+CBD-treated cells compared with the ERK response (Table 2). logR for the CREB response was higher in CP-treated cells, and lower in THC+CBDtreated cells, compared with WIN, was lower in WIN-treated STH $dh^{Q111/Q111}$ cells compared with STH $dh^{Q7/Q7}$ cells, and was lower in WIN-treated cells compared with the ERK response (Table 2, 3). logR for the PLC β 3 response was lower in CP- (only STHdh^{Q7/Q7}), AEA-, THC-, and THC+CBDtreated cells, compared with WIN, was lower in CP-, AEA-, and THC-treated STH $dh^{Q111/Q111}$ cells compared with STHdh^{Q7/Q7} cells, and was lower in AEA- and THC-treated cells compared with the ERK response (Table 2, 3). Finally, logR for the Akt response was lower in CP-, THC-, and THC+CBDtreated cells, was lower in THC- and THC+CBD-treated $STHdh^{Q111/Q111}$ cells compared with $STHdh^{Q7/Q7}$ cells, and was lower in THC-treated STHdh^{Q7/Q7} cells compared with the ERK response (Table 2, 4).

Relative activity $(\Delta \log R)$ was calculated using WIN as the reference ligand (eq. 2). WIN was chosen as a reference ligand, rather than the endocannabinoids 2-AG and AEA (Kenakin and Christopoulos, 2013), because it displayed activity in all assays, and we wanted to quantify the relative activity and bias of 2-AG and AEA in STHdhQ7/Q7 and STHdhQ111/Q111 cells. The AlogR for ERK response was lower in THC- and THC+CBD-treated cells compared with WIN ($\Delta \log R = 0$) (Table 2). The $\Delta \log R$ for β -arrestin1 was lower in 2-AG-, AEA-, THC-, and THC+CBD-treated cells compared with WIN, and compared with the ERK response (Table 2). The $\Delta \log R$ for β -arrestin1 was lower in THC-treated STHdh^{Q111/Q111} cells, and higher in THC+CBD-treated STHdhQ111/Q111 cells. compared with STHdh^{Q7/Q7} cells (Table 2). The Δ logR for the CREB response was higher in CP- (both cell types) and THC+CBD-treated STHdh^{Q111/Q111} cells, and lower in THC+CBD-treated STH $dh^{Q7/Q7}$ cells, compared with WIN (Table 3). The $\Delta \log R$ for the CREB response was higher in CP- (both cell types) and THC+CBD-treated STHdh^{Q111/Q111} cells compared with the ERK response, and was greater in THC+CBD-treated STHdh^{Q111/Q111} cells compared with ${\rm ST}Hdh^{\rm Q7/Q7}$ cells (Table 2, 3). The $\Delta {\rm logR}$ for the ${\rm PLC}\beta 3$ response was lower in CP- (only STH $dh^{Q7/Q7}$), 2-AG- (only STHdh^{Q7/Q7}), AEA- (only STHdh^{Q111/Q111}), THC- and THC+CBDtreated cells compared with WIN, and compared with the ERK response for CP, 2-AG, and AEA treatments (Table 2, 3). The $\Delta \log R$ for the PLC β 3 response was lower in THC-and THC+CBD-treated STHdh^{Q111/Q111} cells compared with TABLE 2

Transduction coefficients and relative activity of cannabinoid ligands at CB_1 in $STHdh^{Q7/Q7}$ and $STHdh^{Q111/Q111}$ cells: ERK and BRET Responses Determined using the operational model global nonlinear regression analysis (eqs. 1 and 2) in GraphPad v. 5.0. Data are expressed as mean with 95% confidence interval.

			ERK Response (Gai/o)				BRET Response $(\beta$ -arrestin1)			
		$\log R (\tau/K_A)$		$\Delta {\rm logR} \; (\tau/{\rm K_A})^a$		logR (τ/K_A)		$\Delta {\rm logR} \; (\tau/{\rm K_A})^a$		
WIN	$STHdh^{Q7/Q7}$	6.35	(6.33–6.37) Reference ligand		6.41	(6.36 - 6.46)	Reference ligand			
	$STHdh^{Q111/Q111}$	6.33	(6.28 - 6.38)	Reference ligand		6.41	(6.38 - 6.44)	Reference ligand		
CP	$STHdh^{Q7/Q7}$	6.30	(6.26 - 6.34)	-0.04	(-0.09-0.01)	6.46	(6.41 - 6.52)	0.05	(-0.03-0.13)	
	$STHdh^{Q111/Q111}$	6.22	(6.17 - 6.27)	-0.11	(-0.22-0.02)	6.47	(6.42 - 6.49)	0.06	(-0.01-0.11)	
2-AG	$STHdh^{Q7/Q7}$	6.28	(6.20 - 6.36)	-0.07	(-0.14 - 0.00)	6.15	(5.91 - 6.37)	-0.23	(-0.24-0.22)*†	
	$STHdh^{Q111/Q111}$	6.28	(6.21 - 6.35)	-0.05	(-0.11-0.01)	6.27	(6.36 - 6.38)	-0.13	$(-0.23-0.03)^*$	
AEA	$STHdh^{Q7/Q7}$	6.35	(6.34 - 6.36)	0.00	(-0.01-0.01)	6.09	(5.82 - 6.37)	-0.31	(-0.33-0.29)*†	
	$STHdh^{Q111/Q111}$	6.42	(6.36 - 6.48)	0.09	(-0.02-0.20)	6.22	(6.07 - 6.37)	-0.18	(-0.26-0.10)*†	
THC	$STHdh^{Q7/Q7}$	4.48	(4.43 - 4.54)*	-1.83	(-2.97-0.69)*	6.41	(6.40-6.42)†	0.00	(-0.01-0.01)†	
	$STHdh^{Q111/Q111}$	3.26	(3.22-3.30)*^	-3.01	$(-4.43 - 1.59)^*$	4.98	$(4.94 - 5.02)*^{\dagger}$	-1.43	$(-1.47 - 1.39)*^{\dagger}$	
CBD	$STHdh^{Q7/Q7}$		N.C.		N.C.		N.C.		N.C.	
	$STHdh^{Q111/Q111}$		N.C.		N.C.		N.C.		N.C.	
THC + CBD	$STHdh^{Q7/Q7}$	2.06	$(1.91 - 2.21)^*$	-4.29	$(-5.95-2.63)^*$	0.83	(-1.91-1.95)*†	-5.58	(-5.60-5.56)*	
	$STHdh^{Q111/Q111}$	0.35	$(-2.01-3.69)*^{\circ}$	-1.40	$(-2.77-0.33)^*$	4.83	(4.77-4.89)*^†	-1.58	$(-1.64 - 1.52)*^{\dagger}$	

N.C., not converged.

*P < 0.05 compared with WIN within cell type and measurement; $^{P} < 0.05$ compared with STHdh^{Q7/Q7} within ligand and measurement; $^{\dagger}P < 0.05$ compared with ERK (G $\alpha_{i/o}$) within cell type, as determined using nonoverlapping confidence intervals (n = 4).

 $^{a}\Delta \log R (\tau/K_{A})$ calculated as $\log R (\tau/K_{A})$ test ligand $-\log R (\tau/K_{A})$ reference ligand within cell type, where **WIN** is the reference ligand and $\Delta \log R (\tau/K_{A})$ 'WIN' = 0.

STHdh^{Q7/Q7} cells (Table 2, 3). Finally, the $\Delta \log R$ for the Akt response was lower in CP- (only STHdh^{Q7/Q7}), AEA- (only STHdh^{Q7/Q7}), THC-, and THC+CBD-treated cells compared with WIN, and compared with the ERK response for CP and THC (Table 2, 4). $\Delta \log R$ values for the Akt response were lower and higher in THC- and THC+CBD-treated STHdh^{Q111/Q111} cells, respectively, compared with STHdh^{Q7/Q7} cells (Table 2, 4).

Summarizing the data in Table 2, we observed that the rank order of τ/K_A and relative activity ($\Delta \log R$) for pERK was AEA > WIN > CP (STHdh^{Q7/Q7}) > 2-AG > CP (STHdh^{Q111/Q111}) > THC \geq THC+CBD. For β -arrestin1 this order was CP > THC \geq WIN > 2-AG = AEA > THC (STHdh^{Q111/Q111}) > THC+CBD. For pCREB this order was CP > WIN (STHdh^{Q7/Q7}) > CBD (STHdh^{Q111/Q111}) > THC+CBD (STHdh^{Q111/Q111}) > CBD (STHdh^{Q111/Q111}) > WIN (STHdh^{Q111/Q111}) > CBD (STHdh^{Q111/Q111}) > WIN (STHdh^{Q111/Q111}) > CBD (STHdh^{Q111/Q111}) > KEA (STHdh^{Q111/Q111}) > CP (STHdh^{Q111/Q111}) > AEA (STHdh^{Q1/Q7}) > 2-AG (STHdh^{Q1/Q7}) > CP (STHdh^{Q111/Q111}) > AEA (STHdh^{Q1/Q7}) > THC+CBD. And for pAkt the order was AEA \geq 2-AG = WIN > CP > THC + CBD.

Operational Model Analysis of Cannabinoid-Dependent System Bias ($\Delta\Delta \log R$) in the Presence of **mHtt.** Bias values ($\Delta\Delta \log R$) were calculated from the relative activity data $(\Delta \log R)$ to characterize functional selectivity in STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells (eq. 3) (Fig. 2, A–D). Because CB_1 is classically considered a $G\alpha_{i/o}$ -coupled receptor (Kondo et al., 1998; Lauckner et al., 2005), all comparisons were made using $G\alpha_{i/o}$ -dependent ERK1/2 signaling (pERK) as $\Delta \log R_1$. On the basis of these data, CP evoked $G\alpha_{S}$ - and β -arrestin1-biased signaling compared with $G\alpha_{i/o}$, and $G\alpha_{i/o}$ biased signaling compared with $G\alpha_q$ or $G\beta\gamma$ in both cell types tested here (i.e., $G\alpha_S > \beta$ -arrestin1 $> G\alpha_{i/o} > G\alpha_q > G\beta\gamma$) (Fig. 2, A–D). 2-AG evoked $G\alpha_{i\prime o}$ -biased signaling compared with β -arrestin1 (in STHdh^{Q7/Q7} cells) and $G\alpha_q$ (more so in STHdh^{Q111/Q111} cells), and G $\beta\gamma$ -biased signaling compared with $G\alpha_{i/o}$ (in STHdh^{Q7/Q7} cells) (i.e., $G\beta\gamma > G\alpha_{i/o} >$ β -arrestin1 > G α_{α}) (Fig. 2, A–D). Like 2-AG, AEA evoked $G\alpha_{i/0}$ -biased signaling compared with β -arrestin1 and $G\alpha_{i}$ (more so in STHdh^{Q111/Q111} cells), and $G\beta\gamma$ -biased signaling compared with $G\alpha_{i/o}$ (in STHdh^{Q7/Q7} cells) (i.e., $G\beta\gamma > G\alpha_{i/o} >$ β -arrestin1 > G α_q) (Fig. 2, A–D). THC evoked β -arrestin1-, $G\alpha_{q}$, and $G\beta\gamma$ -biased signaling compared with $G\alpha_{i/o}$, in both

TABLE 3					
(Continued	from	Table 2:	CREB	and PLCB3	Responses)

		CREB Response (Gas)				PLC β 3 Response (G α q)			
		$\log R (\tau/K_A)$		$\Delta {\rm logR}~(\tau/{\rm K_A})^a$		$\log\!R~(\tau/\rm K_A)$		$\Delta {\rm logR}~(\tau/{\rm K_A})^a$	
WIN	STHdh ^{Q7/Q7} STHdh ^{Q111/Q111}	3.43	$(3.32 - 3.54)^{\dagger}$	Reference ligand		6.54	(6.32-6.72)	Reference ligand	
CP	$STHdh^{Q7/Q7}$	6.47	$(2.20-2.24)^{*}$ $(6.46-6.48)^{*}$	3.01	(2.91–3.11)*†	5.77	$(5.67-5.87)^{*\dagger}$	-0.77	(-0.92-0.62)*†
2-AG	STHdh ^{Q7/Q7}	5.07	(5.06–5.08)* N.C.	2.85	(2.55–3.04)*† N.C.	$6.32 \\ 6.01$	$(4.35 - 8.29)^{\wedge}$ (4.66 - 7.36)	$-0.21 \\ -0.53$	$(-0.48-0.06)^{\prime\prime}$ $(-0.88-0.18)^{*\dagger}$
AEA	$STHdh^{Q111/Q111}$ $STHdh^{Q7/Q7}$		N.C. N.C.		N.C. N.C.	$5.76 \\ 6.31$	(4.99-6.53) (6.08-6.54)	$-0.71 \\ -0.23$	(-1.46-0.04) (-0.47-0.01)
muc	STHdh ^{Q111/Q111}		N.C.		N.C.	5.41	$(4.52-5.94)*^{\dagger}$	-1.13	$(-1.99-0.27)^{*\dagger}$
THC	$STHah$ $Q111/Q111$ $STHdh^{Q111/Q111}$		N.C. N.C.		N.C.	$\frac{5.45}{4.33}$	$(3.80-4.86)^{*++}$	-1.09 -2.18	$(-2.69-1.67)^{*}$
CBD	$STHdh^{Q1/Q1}$ $STHdh^{Q111/Q111}$	$\frac{3.34}{2.27}$	(3.29 - 3.39) (2.24 - 2.30)	-0.09 0.03	(-0.22-0.04) (-0.01-0.07)		N.C. N.C.		N.C. N.C.
THC + CBD	$\begin{array}{l} \mathrm{ST}Hdh^{\mathrm{Q7/Q7}} \\ \mathrm{ST}Hdh^{\mathrm{Q111/Q111}} \end{array}$	0.26 3.28	$(-0.40-1.92)^{*}$ $(3.27-3.30)^{*}^{\dagger}$	-3.19 1.06	$(-3.21-3.17)^{*}$ $(1.04-1.08)^{*}^{\dagger}$	$\begin{array}{c} 0.57 \\ 4.25 \end{array}$	(-1.43-1.91)* (3.55-4.95)*^	$-5.97 \\ -2.27$	(-6.20-5.74)* (-2.95-1.59)*^

TABLE 4						
(Continued	from	Table	2:	Akt	Res	oonse)

		Akt Response $(G\beta\gamma)$					
			$\log R (\tau/K_A)$	$\Delta {\rm logR} ~(\tau/{\rm K_A})^a$			
WIN	${ m ST}Hdh^{{ m Q7/Q7}}$	6.18	(5.98-6.40)	Ref	erence ligand		
	$STHdh^{Q111/Q111}$	6.21	(6.13–6.29) Reference ligar				
CP	$STHdh^{Q7/Q7}$	5.94	(5.92 - 5.96)*†	-0.24	(-0.26-0.22)*†		
	$STHdh^{Q111/Q111}$	5.84	(5.31 - 6.37)	-0.37	(-0.91-0.17)		
2-AG	$STHdh^{Q7/Q7}$	6.22	(6.19 - 6.25)	0.02	(-0.01-0.05)		
	$STHdh^{Q111/Q111}$	6.14	(5.96 - 6.32)	-0.07	(-0.25-0.11)		
AEA	$STHdh^{Q7/Q7}$	6.32	(6.27 - 6.37)	0.14	$(-0.03-0.25)^{*}$		
	$STHdh^{Q111/Q111}$	6.25	(5.73 - 6.77)	0.04	(-0.47 - 0.55)		
THC	$STHdh^{Q7/Q7}$	5.35	(5.32 - 5.38)*†	-0.83	(-0.86-0.80)*†		
	$STHdh^{Q111/Q111}$	4.00	$(3.87 - 4.13)*^{\circ}$	-2.21	(-2.32-2.10)*^†		
CBD	$STHdh^{Q7/Q7}$		N.C.		N.C.		
	$STHdh^{Q111/Q111}$		N.C.		N.C.		
THC + CBD	$STHdh^{Q7/Q7}$	0.31	(-1.39 - 2.01)*†	-5.87	$(-5.97-5.77)^*$		
	$STHdh^{Q111/Q111}$	3.59	(3.50-3.68)*^	-2.62	$(-2.72-2.52)*^{}$		

cell types (i.e., β -arrestin1 > G $\alpha_q = G\beta\gamma > G\alpha_{i/0}$) (Fig. 2, A–D). CBD treatment only produced a significant activation of G α_s -dependent CREB phosphorylation, and bias values could not be calculated for this ligand. The combination THC+CBD evoked G α_s -biased signaling compared with G $\alpha_{i/o}$ - and G $\alpha_{i/o}$ -biased signaling compared with β -arrestin1, G α_q , or G $\beta\gamma$ (more so in STHdh^{Q7/Q7} cells) (i.e., G $\alpha_s > G\alpha_{i/o} > \beta$ -arrestin1 = G $\alpha_q = G\beta\gamma$) (Fig. 2, A–D).

Each cannabinoid analyzed here displayed unique functional selectivity for different signaling pathways. Overall, the bias factor of 2-AG and AEA was shifted toward $G\alpha_{i/o}$ -dependent ERK phosphorylation, and the bias factor of THC+CBD was shifted away from $G\alpha_{i/o}$ -dependent ERK phosphorylation, in STHdh^{Q111/Q111} cells. The reduced pERK $E_{\rm max}$ in mHtt-expressing STHdh^{Q111/Q111} cells compared with STHdh^{Q7/Q7} cells (Table 1) may result from lower CB₁ levels (50%) (Laprairie et al., 2013). An important advantage of using the operational model to estimate the relative activity and ligand bias is that this model negates the effects of differences in receptor density (Kenakin et al., 2012). Therefore, differences in bias between STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells were probably mHtt-dependent and not the result of changes in agonist potency or efficacy.

Cannabinoid-Specific Changes in Cellular Function and Viability. Treatment of STHdh^{Q7/Q7} cells with WIN, 2-AG, AEA, or THC resulted in a small increase in ATP, whereas treatment with CP, CBD, or THC+CBD resulted in a decrease in ATP (Fig. 3A). In STHdh^{Q111/Q111} cells, basal ATP levels were approximately 50% lower than basal ATP levels in STHdh^{Q7/Q7} cells. ATP levels increased in STHdh^{Q111/Q111} cells treated with WIN, 2-AG, AEA, or THC and decreased with CP or CBD (Fig. 3E). THC+CBD treatment resulted in higher ATP levels in ST $Hdh^{Q111/Q111}$ cells. CP and CBD were the only cannabinoids tested that evoked $G\alpha_S$ -biased (CREB) signaling in STHdh cells. The lower ATP levels observed in cells treated with CP or CBD may have resulted from cAMP production. However, given that cells expressing mHtt are deficient in ATP (Sadri-Vakili et al., 2006; Laprairie et al., 2013), cannabinoids that exaggerate this state may exacerbate cellular pathology.

Excessive glutamate release from cortical neurons and GABA release from striatal medium spiny projection neurons are both observed in HD (Benn et al., 2007; Botelho et al.,

2014). Compounds that limit neurotransmitter release may, therefore, be beneficial in HD, whereas compounds that enhance neurotransmitter release may exacerbate HD pathophysiology. GABA release was inhibited by WIN, 2-AG, AEA, CP, and THC in STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells (Fig. 3, B and F). CBD treatment was associated with enhanced GABA release in STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells and the EC₅₀ and E_{max} of this response were reduced in the presence of THC (THC+CBD) (Fig. 3, B and F). Therefore, CBD treatment may enhance excessive neurotransmitter release in HD, whereas other cannabinoids tested here limited neurotransmitter release.

Cell viability was measured by cal-AM fluorescence, which is an indicator of esterase activity and mitochondrial respiration that is positively correlated with viability, and EthD-1 fluorescence, which is an indicator of membrane permeability and cell death and therefore negatively correlated with viability (MacCoubrey et al., 1990). Basal cal-AM fluorescence (% esterase activity) was 60% less in STHdh^{Q111/Q111} cells compared with STHdh^{Q7/Q7} cells (Fig. 3, C and G). Cal-AM fluorescence was decreased by 40% in STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells treated with CP or THC and increased by 40% in STHdh^{Q111/Q111} cells treated with WIN, 2-AG, AEA, or CBD (Fig. 3, C and G). Basal EthD-1 fluorescence (% membrane permeable cells) was 40% greater in STHdh^{Q111/Q111} cells compared with STHdh^{Q7/Q7} cells (Fig. 3, D and H). EthD-1 fluorescence was increased by 30% in STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells treated with CP or THC (Fig. 3, D and H). EthD-1 fluorescence was decreased by 20% in AEAand CBD-treated ST $Hdh^{Q7/Q7}$ cells, and by 40% in WIN-, 2-AG-, AEA-, and CBD-treated ST $Hdh^{Q111/Q111}$ cells (Fig. 3, D and H). The effect of CBD predominated over that of THC for both cal-AM and EthD-1 fluorescence in both cell lines. Therefore, in these viability assays, the CP and THC (which both displayed β -arrestin1 bias) appeared harmful, whereas other cannabinoids improved viability in STHdh^{Q111/Q111} cells.

Functional CB₁ residing at the plasma membrane undergo internalization following ligand binding and β -arrestin recruitment (Blair et al., 2009). Total CB₁ levels were higher in WIN-, 2-AG-, and AEA-treated STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells, compared with vehicle, whereas total CB₁ levels were lower in CP- and THC-treated STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells (Fig. 4A). The fraction of CB₁ at the



Fig. 2. Calculated bias factor of cannabinoids in wild-type and mHtt-expressing cells. Ligand bias ($\Delta \Delta \log R$) was calculated using eq. (2) as the difference between the ERK ($G\alpha_{i/o}$) response and a second response X: (A) β -arrestin1, (B) $G\alpha_s$, (C) $G\alpha_q$, or (D) $G\beta\gamma$. Data are displayed as the mean with the minimum and maximum (box) and 95% confidence intervals (error bars). *P < 0.01 compared with 0 (i.e., no bias), †P < 0.01 compared with STHdh^{Q7/Q7} cells within ligand. N = 4.

plasma membrane and total CB_1 was assayed in $STHdh^{Q7/Q7}$ and STHdh^{Q111/Q111} cells treated with various cannabinoids for 12 hours (Fig. 4, A and B). The fraction of CB₁ at the plasma membrane was lower in WIN-, 2-AG-, CP-, and THC-treated cells, and higher in CBD-treated cells (Fig. 4B). CP and THCand to a lesser extent WIN and 2-AG-displayed greater β -arrestin1 bias than AEA or CBD. The mechanism of cannabinoid-dependent induction of CB1 expression has been described previously (Laprairie et al., 2013). Here, it is important to note that treatment with cannabinoids that evoked $G\alpha_{i/o}$ -and $G\beta\gamma$ -biased signaling (2-AG, AEA) was associated with higher CB₁ levels, whereas treatment with CP and THC (β -arrestin1-biased cannabinoids) was associated with lower CB₁ levels, suggesting that cannabinoids that are functionally selective for β -arrestin1 may reduce the available pool of CB₁ receptors. The effects of THC and CBD were neutralized by one another (Fig. 4, A and B).

Mechanism of CP- and CBD-Dependent $G\alpha_S$ Signaling. CBD is known to modulate the activity of many cellular GPCRs, including CB_1 , the type 2 cannabinoid receptor (CB_2) (Hayakawa et al., 2008), the serotonin 5HT_{1A} receptor (Russo et al., 2005), G protein-coupled receptor 55(Ryberg et al., 2007), and the μ - and δ -opioid receptors (Kathmann et al., 2006). Here, CBD treatment resulted in CB_1 -independent CREB phosphorylation (Fig. 5). CREB phosphorylation was highest 30 minutes after CBD treatment and was sustained for the duration of the experiment (60 minutes) (Fig. 5A). Treatment of $STHdh^{Q7/Q7}$ cells with the $5HT_{1A}$ agonist 8-OH-DPAT resulted in a dose-dependent increase in CREB phosphorylation that was competitively inhibited by the $5HT_{1A}$ antagonist WAY-100,635 and CBD (Fig. 5B). Treatment of STHdh^{Q7/Q7} cells with CBD alone also resulted in a dosedependent increase in CREB phosphorylation, with less potency and efficacy that the full agonist 8-OH-DPAT (Fig. 5C). CBD-dependent CREB phosphorylation was not inhibited by the CB_1 antagonist O-2050, but was inhibited by WAY-100,635 (Fig. 5C), indicating that CBD activated CREB via 5HT_{1A}. It is not known whether the partial agonism of 5HT_{1A} by CBD is functionally antagonistic of serotonergic signaling in vivo and whether this would play a role in CBD-based treatments of neurologic disorders.

Unexpectedly, we observed a switch in signaling following continued drug exposure for CP. At 10 minutes CP treatment produced $G\alpha_{i/o}$ -dependent ERK phosphorylation that returned to basal levels by 25 minutes; and at 30 minutes CP treatment produced $G\alpha_s$ -dependent CREB phosphorylation (Fig. 5A). STHdh cells endogenously express the type 2 dopamine receptor (D₂) (Paoletti et al., 2008) and heterodimerization of CB₁ and D₂ is known to lead to a switch in coupling from $G\alpha_{i/0}$ to $G\alpha_s$ following treatment with CP (Glass and Felder, 1997; Kearn et al., 2005). Therefore, we hypothesized that CP could be functionally selective for CB₁/D₂ heterodimer signaling to explain the switch from $G\alpha_{i/o}$ to $G\alpha_s$. Cotreatment of STHdh^{Q7/Q7} cells with CP and 1 μ M quinpirole (a D_2 agonist) shifted the concentration-response curve for CREB phosphorylation right, as did cotreatment with O-2050 (a competitive antagonist of CB_1), whereas cotreatment with 10 µM haloperidol (a D2 antagonist) shifted the concentration-response curve left (Fig. 5D). Quinpirole and haloperidol did not effect CREB phosphorylation alone (Fig. 5D). From these data, we suggest that CP selectively enhanced either physical heterodimerization between CB₁/D₂



Fig. 3. Changes in functionality and viability in wild-type and mHttexpressing cells treated with cannabinoids. STHdh^{Q7/Q7} (A–D) and STHdh^{Q111/Q111} (E–H) cells were treated with 10–10,000 nM WIN, CP, 2-AG, AEA, THC, CBD, or THC+CBD (1:1) for 30 minutes, and ATP (A,E), change in GABA release compared with vehicle treatment (Δ GABA) (B,F), % cellular esterase activity compared with vehicle treatment (C,G), and % membrane-permeable cells compared with vehicle treatment (D,H) were measured. [ATP] was determined using the CellTiter Glo assay (Promega). [GABA] in cell culture media was determined using GABA enzyme-linked immunosorbent assay (Novatein Bio, Woburn MA). % Cellular esterase activity (calcein-AM cleavage) and % membrane permeable cells (ethidium homodimer-1 penetration) were determined using the Live/Dead cytotoxicity assay (Invitrogen/ThermoFisher Scientific, Grand Island, NY). Concentration-response curves were fit using nonlinear regression models. N = 4.

or functional signaling through these receptors with a subsequent switch from $G\alpha_{i/0}$ to $G\alpha_s$ (Kearn et al., 2005).

Discussion

Correlations between Functional Selectivity and Cellular Viability. In this study, we described the biased signaling properties of six cannabinoids in the ST*Hdh* cell culture model of striatal medium spiny projection neurons. System bias shifted toward $G\alpha_{i/o}$ for 2-AG and AEA in ST*Hdh*^{Q111/Q111} (mHtt-expressing) cells compared with ST*Hdh*^{Q7/Q7} cells. Treatment of ST*Hdh*^{Q111/Q111} cells with cannabinoids that signaled via CB₁ and were functionally selective for $G\alpha_{i/o}$ and $G\beta\gamma$ (2-AG, AEA) was associated with the greatest improvement in ATP production, inhibition of GABA release, cellular metabolic activity (esterase activity),

and cell death (membrane permeability). In contrast, ligands that preferentially enhanced β -arrestin1-recruitment (THC and CP) reduced cellular viability in both STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells as determined by the same measures. We have previously observed that derivatives of AEA normal-ize CB₁ levels in STHdh^{Q111/Q111} cells via $G\alpha_{i/o}$, $G\beta\gamma$, Akt, and nuclear factor (NF)- κ B, and that normalization of CB₁ was associated with improved cell function and viability (Laprairie et al., 2013, 2014). Recently, three studies have demonstrated that increasing CB₁ levels in medium spiny projection neurons in the R6/2 mouse model of HD via adenovirus-mediated overexpression normalizes brain-derived neurotrophic factor levels, reduces striatal atrophy, and prevents decreases in dendritic spine density and levels of excitatory synaptic markers, such as synaptophysin and vesicular glutamate transporter, but does not improve deficits in motor coordination (Chiarlone et al., 2014; Naydenov et al., 2014; Blázquez et al., 2015). In accordance with this, knockdown or knockout of CB1 in medium spiny projection neurons of R6/2, N171-82Q, or $Hdh^{Q150/Q150}$ HD mice further reduces the pool of CB_1 and exacerbates deficits in motor control, enhances striatal atrophy, and reduces survival (Blázquez et al., 2011; Mievis et al., 2011; Horne et al., 2013). Further, individuals with HD and a variant of the CB₁ gene (CNR1 rs4707436) that is associated with lower levels of CB₁ begin displaying motor-related symptoms of HD earlier than individuals with HD and normal CNR1 (Kloster et al., 2013). Together, these studies and our



Fig. 4. Long-term exposure to cannabinoids affected CB₁ localization and levels. STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells were treated with 1.0 μ M 2-AG, AEA, WIN, CP, THC, CBD, or THC+CBD (1:1) for 12 hours, and total CB₁ levels (A) and the fraction of CB₁ at the plasma membrane (B). (A) Total CB₁ levels were determined using In-Cell Western and expressed relative to β -actin levels. N = 8. (B) The fraction of CB₁ at the plasma membrane was determined using On- and In-Cell Western. N = 8. *P < 0.01 compared with vehicle-treated cells within cell type, $\dagger P < 0.01$ compared with STHdh^{Q7/Q7} cells within treatment group, as determined using two-way ANOVA followed by Bonferroni post-hoc analysis.



Fig. 5. CB₁-independent CREB signaling. (A) Time course of ERK and CREB signaling. STHdhQ7/Q7 cells were treated with 1 μ M WIN55,212-2, CP55940, or CBD for 0–60 min, and ERK (left y-axis) or CREB (right y-axis) phosphorylation was measured via In-Cell Western. N = 4. (B,C) 5HT_{1A}-dependent CREB signaling. STHdhQ^{7/Q7} cells were treated with 0.1–100,000 nM 8-OH-DPAT, WAY-100,635, or CBD, $\pm 1 \ \mu$ M CBD, 100 nM WAY-100,635, or 500 nM O-2050 for 30 minutes, and CREB phosphorylation was measured via In-Cell Western. N = 4. (D) D₂-dependent CREB signaling STHdhQ^{7/Q7} cells were treated with 0.1–100,000 nM 8-OH-DPAT, WAY-100,635, or CBD, $\pm 1 \ \mu$ M CBD, 100 nM WAY-100,635, or 500 nM O-2050 for 30 minutes, and CREB phosphorylation was measured via In-Cell Western. N = 4. (D) D₂-dependent CREB signaling STHdhQ^{7/Q7} cells were treated with 0.1–100,000 nM CP, quinpirole, or haloperidol, $\pm 10 \ \mu$ M haloperidol, $1 \ \mu$ M quinpirole, or 500 nM O-2050 for 30 minutes and CREB phosphorylation was measured via In-Cell Western. N = 4. (B) models. N = 4. All data are expressed relative to WIN E_{max} in STHdhQ^{7/Q7} cells.

data provide support for $G\alpha_{i/o}$ - and $G\beta\gamma$ -selective activation of CB_1 to maintain CB_1 levels and the cellular function and viability of cells expressing mHtt (Blázquez et al., 2011, 2015; Mievis et al., 2011; Horne et al., 2013; Chiarlone et al., 2014; Naydenov et al., 2014).

Use of THC and CBD in HD. Despite a lack of clinical evidence, patients suffering from HD may be seeking medical marijuana or acquiring it from other sources in an attempt to relieve some of the symptoms of their disease (Müller-Vahl et al., 1999; Meisel and Friedman, 2012; Koppel et al., 2014). Most medically available and tested illicit marijuana contains a high concentration of THC relative to other cannabinoids, such as CBD (De Backer et al., 2012). Here, we observed that THC reduced cellular function and viability in cells expressing mHtt whether THC was used alone or in a 1:1 combination with CBD. Likewise, treatment of R6/1 and R6/2 mouse models with 10 mg/kg THC is associated with worsening of HD signs and symptoms (Dowie et al., 2010). However, others have reported improvement in motor control and reduced striatal atrophy in R6/1 and R6/2 HD treated for 6 weeks with 2 mg/kg THC beginning at 4 weeks of age (Blázquez et al., 2011), suggesting that the deleterious effects of THC in HD are doseand time course-dependent. CBD alone displayed mixed beneficial and negative effects in STHdh^{Q7/Q7} and STHdh^{Q111/Q111} cells. CBD is known to act through a number of effectors, including as a negative allosteric modulator at CB1 and a partial agonist at 5HT_{1A} (Pazos et al., 2013; Laprairie et al., 2015). It is unclear which effects of CBD predominate in vivo normally and in HD and how the combinations of any or all of the at least 65 cannabinoids found in marijuana (McPartland et al., 2015) influence one another's pharmacokinetics and pharmacodynamics (Sagredo et al., 2011; Valdeolivas et al.,

2012). Further, the utility of CBD in HD remains controversial, with some studies reporting no effects in animal models and human trials (Consroe et al., 1991; Valdeolivas et al., 2012), or positive effects in animal models (Sagredo et al., 2007, 2011). Overall, the use of THC or marijuana may exacerbate the signs and symptoms of HD via further down-regulation of CB₁ and reduced cellular viability.

Conclusions

 $G\alpha_{i/0}$ - and $G\beta\gamma$ -selective CB_1 ligands are probably the most therapeutically useful cannabinoids in the treatment of HD. However, highly potent synthetic cannabinoids, such as WIN, may produce unwanted psychoactive effects and their chronic use would probably result in receptor desensitization or downregulation (Sim-Selley and Martin, 2002; Blair et al., 2009). Endocannabinoids, which we observed to enhance $G\alpha_{i/o}$ and $G\beta\gamma$ -dependent signaling in the STHdh cell culture system, are rapidly metabolized in vivo and consequently have limited efficacy when they are directly administered (Devane et al.., 1992; Kondo et al., 1998). The inhibitor of endocannabinoid catabolism URB597 has demonstrated limited efficacy at improving motor control deficits in R6/2 HD mice (Dowie et al., 2010), but additional studies are needed to understand how elevating endocannabinoid levels affects the signs and symptoms of HD in vivo. An alternative means of enhancing endogenous CB₁ signaling is with the use of positive allosteric modulators (PAMs) of CB1. PAMs bind to a site on the receptor that is distinct from the site of endogenous ligand binding (i.e., the orthosteric site) and enhance the binding and efficacy of the endogenous ligands that are produced and regulated through intrinsic control mechanisms (Pamplona et al.,

2012; Wootten et al., 2013). CB₁ PAMs may increase $G\alpha_{i/o}$ dependent pro-survival signaling occurring via endocannabinoids without producing the psychotropic effects associated with synthetic cannabinoid agonists, because they are unable to directly activate CB₁. Our in vitro study of cannabinoid functional selectivity leads us to conclude that enhancement of endocannabinoid-dependent CB₁ activation may be a means of treating the signs and symptoms of HD by targeting CB₁.

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Authorship Contributions

Participated in research design: Laprairie, Bagher, Kelly, and Denovan-Wright.

Conducted experiments: Laprairie.

Contributed new reagents or analytic tools: Kelly, Denovan-Wright. Performed data analysis: Laprairie, Denovan-Wright.

Wrote or contributed to the writing of the manuscript: Laprairie, Bagher, Kelly, Denovan-Wright.

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