Ionotropic GABA and glycine receptor subunit composition in human pluripotent stem cell-derived excitatory cortical neurones

Citation for published version:

Digital Object Identifier (DOI):
10.1113/jphysiol.2014.278994

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Publisher's PDF, also known as Version of record

Published in:
Journal of Physiology

Publisher Rights Statement:
Free via Open Access

General rights
Copyright for the publications made accessible via the Edinburgh Research Explorer is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy
The University of Edinburgh has made every reasonable effort to ensure that Edinburgh Research Explorer content complies with UK legislation. If you believe that the public display of this file breaches copyright please contact openaccess@ed.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.

Download date: 26. Jan. 2020
Ionotropic GABA and glycine receptor subunit composition in human pluripotent stem cell-derived excitatory cortical neurones

Owain T. James1,2,3, Matthew R. Livesey1,3, Jing Qiu1, Owen Dando1,2, Bilada Bilican3,5,6, Ghazal Haghi1,5, Rinku Rajan1,5, Karen Burr3,5,6, Giles E. Hardingham1,4, Siddharthan Chandran2,3,5,6, Peter C. Kind1,2,4 and David J. A. Wyllie1,4

1Centre for Integrative Physiology, University of Edinburgh, Edinburgh EH8 9XD, UK
2Centre for Brain Development and Repair, Institute for Stem Cell Biology and Regenerative Medicine, National Centre for Biological Sciences, Bangalore 560065, India
3Euan MacDonald Centre for MND Research, University of Edinburgh, Edinburgh EH16 4SB, UK
4Patrick Wild Centre, University of Edinburgh, Edinburgh EH8 9XD, UK
5Centre for Clinical Brain Sciences, University of Edinburgh, Edinburgh EH16 4SB, UK
6MRC Centre for Regenerative Medicine, University of Edinburgh, Edinburgh EH16 4SB, UK

Key points

- This study reports a functional assessment of the subunit composition of inhibitory ionotropic GABA\textsubscript{A} receptors (GABA\textsubscript{AR}s) and glycine receptors (GlyRs) expressed by excitatory cortical neurones derived from human embryonic stem cells (hECNs).
- GABA\textsubscript{AR}s expressed by hECNs are predominantly composed of \(\alpha_2/3\beta_3\gamma_2\) subunits; such a composition is typical of that reported for GABA\textsubscript{AR}s expressed in rodent embryonic cortex.
- Analysis of GlyRs expressed by hECNs indicates they are likely to contain \(\alpha_2\) and \(\beta\) subunits – a composition in rodents that is associated with a late embryonic/early postnatal period of development.

Abstract We have assessed, using whole-cell patch-clamp recording and RNA-sequencing (RNA-seq), the properties and composition of GABA\textsubscript{A} receptors (GABA\textsubscript{AR}s) and strychnine-sensitive glycine receptors (GlyRs) expressed by excitatory cortical neurones derived from human embryonic stem cells (hECNs). The agonists GABA and muscimol gave EC\textsubscript{50} values of 278 \(\mu\text{M}\) and 182 \(\mu\text{M}\), respectively, and the presence of a GABA\textsubscript{AR} population displaying low agonist potencies is supported by strong RNA-seq signals for \(\alpha_2\) and \(\alpha_3\) subunits. GABA\textsubscript{AR}-mediated currents, evoked by EC\textsubscript{50} concentrations of GABA, were blocked by bicuculline and picrotoxin with IC\textsubscript{50} values of 2.7 and 5.1 \(\mu\text{M}\), respectively. hECN GABA\textsubscript{AR}s are predominantly \(\gamma\) subunit-containing as assessed by the sensitivity of GABA-evoked currents to diazepam and insensitivity to Zn\textsuperscript{2+}, together with the weak direct agonist action of gaboxadol; RNA-seq indicated a predominant expression of the \(\gamma_2\) subunit. Potentiation of GABA-evoked currents by propofol and etomidate and the lack of inhibition of currents by salicylidine salicylhydrazide (SCS) indicate expression of the \(\beta_2\) or \(\beta_3\) subunit, with RNA-seq analysis indicating strong expression of \(\beta_3\) in hECN GABA\textsubscript{AR}s. Taken together our data support the notion that hECN GABA\textsubscript{AR}s have an \(\alpha_2/3\beta_3\gamma_2\) subunit composition – a composition that also predominates in immature rodent cortex. GlyRs expressed by hECNs were activated by glycine with an EC\textsubscript{50} of 167 \(\mu\text{M}\). Glycine-evoked (500 \(\mu\text{M}\)) currents were blocked by strychnine (IC\textsubscript{50} = 630 \(\text{nM}\)).

O. T. James and M. R. Livesey contributed equally to this work and are listed in alphabetical order.
and picrotoxin (IC$_{50}$ = 197 µM), where the latter is suggestive of a population of heteromeric receptors. RNA-seq indicates GlyRs are likely to be composed of α2 and β subunits.

(Received 17 June 2014; accepted after revision 6 August 2014; first published online 28 August 2014)

**Corresponding author** D. J. A. Wyllie: Centre for Integrative Physiology, University of Edinburgh, Hugh Robson Building, George Square, Edinburgh EH8 9XD, UK. Email: dwyllie1@staffmail.ed.ac.uk

**Abbreviations** D-AP5, (2R)-amino-5-phosphonovaleric acid; CNQX, 6-cyano-7-nitroquinoxaline-2,3-dione; DIV, days in vitro; GABAAR, γ-aminobutyric acid receptor type A; GFAP, glial fibrillary acidic protein; GlyR, glycine receptor; hECN, human excitatory cortical neuron; hPSC, human pluripotent stem cell; PCR, polymerase chain reaction; RNA-seq, RNA sequencing; VGLUT1, vesicular glutamate transporter 1.

### Introduction

γ-Aminobutyric acid (GABA) type A receptors (GABA$_A$Rs) are the principal inhibitory neurotransmitter receptors in the mammalian adult brain. GABA$_A$Rs are a pentameric ligand-gated anion channels that can be potentially composed of 19 known subunits (α1–6, β1–6, γ1–3, δ, ε, θ and ρ1–3), giving rise to a large number of potential receptor stoichiometries (Olsen & Sieghart, 2009). Alongside GABA$_A$Rs, strychnine-sensitive glycine receptors (GlyRs) form another major class of pentameric ligand-gated anion channel that can be potentially composed of 5 subunits, α1–4 and β (Lynch, 2009). GABA$_A$R and GlyR subunits are each associated with a high degree of spatial and developmental regulation within the CNS (Malosio et al. 1991; Laurie et al. 1992; Fritschy et al. 1994; Flint et al. 1998). In this regard, GABA$_A$R composition is currently limited to approximately 30 known variants. Moreover, subunit identity typically imparts various pharmacological specificities to the GABA$_A$R complex and, collectively, these properties make GABA$_A$Rs a key pharmacological target for a range of neurological disorders (Olsen & Sieghart, 2009). The increasing knowledge regarding the functions of GlyRs within the developing CNS indicates that these receptors too are likely to be relevant pharmacological targets (Avila et al. 2013a).

The technological advance in the ability to generate human excitatory cortical neurones (hECNs) from pluripotent stem cells (hPSCs) gives the potential to study human-specific physiology and disease in vitro. We have previously reported a protocol that generates cultures of predominantly hECNs by 4 weeks of differentiation from anterior neural precursors derived from various stem cell lines (Bilican et al. 2014). The translational impact of this technology is ultimately determined by the ability of hECNs to display properties that reflect neurones in their native environment (Yang et al. 2011; Sandoe & Eggan, 2013). Indeed, we have previously identified that hECNs are a useful model to study the maturation of AMPAR composition and the reduction in intracellular Cl$^-$ concentration that is observed in native neuronal development (Livesey et al. 2014). The present study characterises the likely subunit composition of GABA$_A$R and GlyRs expressed by hECNs and illustrates that their subunit composition are likely to be similar to those that have been described for inhibitory ionotopic receptors expressed in immature rodent cortex.

### Methods

**In vitro hECN preparation**

A detailed description of the derivation of hECNs can be found in Bilican et al. (2014). Briefly, hECNs were differentiated from anterior neural precursors that were derived from the H9 human embryonic stem cell line (WiCell), which was obtained under ethical/IRB approval of the University of Edinburgh. Experiments were carried out on cells that had been differentiated and maintained in culture for 28–42 days in vitro (DIV), or 49–56 DIV. At these time points, around 70% of cells were neuronal (β3-tubulin$^+$), with little contamination from neural precursor cells (nestin$^+$), astrocytes (GFAP$^+$) or GABA-ergic (GAD65/67$^+$) interneurons (Bilican et al. 2014; Livesey et al. 2014). Neurones were consistent with an excitatory (VGLUT1$^+$) identity that also exhibited properties of neurones of the upper and lower layers of the cortex (see Bilican et al. 2014; Livesey et al. 2014).

**Electrophysiology**

The whole-cell patch-clamp configuration was used to record currents from hECNs using an Axon Multiclamp 700B amplifier (Molecular Devices, Sunnyvale, CA, USA). Patch electrodes (~4–7 MΩ) were filled with an ‘internal’ recording solution comprising (in mM): potassium gluconate 155, MgCl$_2$ 2, Na-HEPES 10, Na-PiCreatine 10, Mg$_2$-ATP 2 and Na$_3$-GTP 0.3, pH 7.3 (300 mOsmol $^{-1}$). Coverslips containing hECNs were placed in the recording chamber, which was superfused with an ‘external’ recording solution composed of (in mM): NaCl 152, KCl 2.8, HEPES 10, CaCl$_2$ 2, glucose 10, pH 7.3 (320–330 mOsmol $^{-1}$) using a gravity-feed system at room temperature (20–23°C) with a flow rate of approximately
4 ml min $^{-1}$. Time for complete bath solution exchange was approximately 5 s, but agonist onset times were dependent on position of perfusion line and cell; the rise-time of agonist-evoked whole-cell currents was $< 2$ s and all responses were measured at steady state. We observed that faster solution exchange rates were frequently associated with hECNs detaching from coverslips. The 'external' solution exchange rates were adjusted as required, which gave a large driving force ($\sim 80$ mV), resulting in inward flux of Cl$^-$ ions. Series resistances ($R_s$) were between 10 and 30 M$\Omega$ and compensated between 50 and 80%. Experiments were terminated if series resistance shifted more than 20%.

Before each experiment, three bath applications of a given concentration of agonist that gave equivalent current amplitudes within 15% of the initial amplitude were obtained to establish a stable response. Similarly, a response to a control concentration of agonist was applied at the end of the recording to ensure stability. Data were only taken if the amplitude of the final control response was within 15% of the initial controls. Selective agonists, antagonists and allosteric modulators were purchased either from Tocris Bioscience (Bristol, UK) or Abcam (Cambridge, UK).

**RNA-sequencing**

For RNA-seq, RNA was isolated from four biological replicates using the Roche HP RNA Isolation kit according to manufacturer’s instructions. Total RNA was assessed for quality (Agilent Bionalyzer) and quantity (Invitrogen Qubit) before library preparation. Illumina libraries were prepared from 1 μg of total RNA using TruSeq RNA Sample Prep Kit v2 with a 10 cycle enrichment step as per the manufacturer’s recommendations. Final libraries were pooled in equimolar proportions before Illumina sequencing on a HiSeq 2500 platform using 100 base paired-end reads in rapid mode. Raw reads were processed using RTA 1.17.21.3 and Casava 1.8.2 (Illumina). Reads were mapped to the primary assembly of the human reference genome contained in Ensembl release 75. A genome index was built with Bowtie, version 1.0.0; default options; (Langmead et al. 2009), and then reads mapped with TopHat, version 2.0.10, (Kim et al. 2013); for TopHat, coverage-based search for junctions was disabled, otherwise default values were used for all options. Gene expression was then estimated with Cufflinks, version 2.2.0, (Trapnell et al. 2010; Roberts et al. 2011) using gene annotations from Ensembl release 75. Cufflinks was run in expression estimation mode only (-G flag), and corrections for multi-read mapping (-u flag) and bias (-b flag) were enabled; otherwise default values were used for all options. Estimates of GABA$_A$R and GlyR subunit mRNA expression were then extracted in units of fragments per kilobase of exon per million mapped fragments, and normalised as expression relative to that of the highest expressed subunit.

**Data analysis**

Recordings were low-pass filtered at 2 kHz, digitised at 10 kHz via a BNC-2090A (National Instruments, TX, USA) interface, and recorded to computer using the WinEDR V2.7.6 Electrophysiology Data Recorder (J. Dempster, University of Strathclyde, UK, http://spider.science.strath.ac.uk/sipbs/software_ses.htm)

Agonist concentration–response curves were fitted individually for each cell using the Hill equation:

$$ I = \frac{I_{\text{max}}}{1 + (EC_{50}/[A])^{n_H}}, $$

where $I$ is the current response to agonist concentration [A], $n_H$ is the Hill coefficient, $I_{\text{max}}$ is the maximum current and $EC_{50}$ is the concentration of agonist that produces a half-maximal response. Each data point was normalised to the fitted maximum of the concentration–response curve, then pooled, averaged and re-fitted again with the same equation, with the maximum and minimum for each curve being constrained to asymptote to 1 and 0, respectively (Frizelle et al. 2006; Wrighton et al. 2008).

Concentrations of antagonists required to inhibit agonist-evoked responses by 50% (IC$_{50}$) were determined by fitting inhibition curves with the equation:

$$ I = \frac{I_{[B]0}}{1 + ([B]/IC_{50})n_H}, $$

where $n_H$ is the Hill coefficient, $I_{[B]0}$ is the predicted current in the absence of antagonist and [B] is the concentration of the antagonist. Data points were again normalised to the fitted maximum, before pooling, averaging and re-fitting as described above.

Data are presented as mean ± standard error of the mean (SEM). The number of experimental replicates (cells) is denoted as ‘n,’ while ‘N’ represents number of de novo preparations of batches from which ‘n’ is obtained. Statistical analysis was conducted as described in the text with the significance levels indicated as: $P < 0.05 \, (**),$ $P < 0.01 \, (***)$ and $P < 0.001 \, (***)$.

**Results**

**GABA$_A$ receptor characterisation**

The potency of GABA$_A$R agonists varies considerably between GABA$_A$R isoforms (Mortensen et al. 2011; Karim et al. 2013). Thus, to characterise initially the functional properties of GABA$_A$Rs expressed by
hECNs (28–42 DIV) differentiated from anterior neural precursors derived from H9 human embryonic stem cells (Bilican et al. 2014; see Methods) we conducted concentration–response experiments using GABA and the GABA_A-selective agonist muscimol. We previously established that hECNs robustly respond to GABA at this time point (Livesey et al. 2014). After establishing stable control responses to bath applications of GABA (100 μM), or muscimol (300 μM), increasing concentrations of agonist were applied sequentially to generate concentration–response curves (Fig. 1A). Mean EC_{50} values for GABA- and muscimol-activated currents were found to be 278 ± 11 μM (n = 12, N = 2) and 182 ± 10 μM (n = 6, N = 2), respectively (Fig. 1B).

GABA (EC_{50})-evoked current responses were blocked by GABAAR antagonists bicuculline and picrotoxin (Fig. 1C) in a concentration-dependent manner (Fig. 1D) giving respective IC_{50} values of 2.7 ± 0.2 μM (n = 5, N = 2) and 5.1 ± 0.2 μM (n = 4, N = 2).

We next performed a series of pharmacological assays to assess the presence of γ and/or δ subunit–containing GABA_ARs. Applications of γ-selective allosteric potentiator diazepam (30 nM and 3 μM) to GABA (EC_{10}; 35 μM)-mediated currents potentiated the control GABA response by 10 ± 6% (P = 0.1 vs. control) and 46 ± 10% (P < 0.001 vs. control, Welch’s t test, n = 17, N = 3), respectively, indicating the presence of the γ subunit (Fig. 2A). In contrast, applications of Zn^{2+} (10 μM and 300 μM), which selectively inhibits GABA_ARs composed of α and β subunits only (Draguhn et al. 1990), did not inhibit
GABA (EC_{50})-evoked currents (10 \mu M, 6 \pm 3 \%, P = 0.053 vs. control; 300 \mu M, 11 \pm 5 \%, P = 0.052 vs. control; unpaired t tests; n = 9, N = 1; Fig. 2B). Furthermore, the potent \delta-containing GABA \textsubscript{A}R-selective agonist gaboxadol (3 \mu M and 300 \mu M; Storustovu & Ebert, 2006) gave only nominal currents (6.0 \pm 2.3\% and 14.6 \pm 3.7\%; both data P < 0.001 vs. GABA (3 \mu M); unpaired t tests; n = 6–7, N = 1, respectively) compared to the maximum response that could be elicited by GABA (3 mM; Fig. 2C), confirming that a population of GABA \textsubscript{A}Rs that contain \delta subunits is negligibly expressed. We confirmed that the low potency of GABA we observed was not a consequence of the specific culture conditions that we employed. Indeed GABA potency was not influenced by the culture of hECNs in atmospheric O\textsubscript{2} 48 h prior to recording (222 \pm 13 \mu M, n = 3, N = 1), the absence of brain-derived neurotrophic factor and glial cell-derived neurotrophic factor media supplements (222 \pm 36 \mu M, n = 5, N = 2), or maintaining hECNs for extended (49–56 DIV) culture periods (204 \pm 17 \mu M, n = 5, N = 2). Moreover, even for hECNs maintained for extended culture periods gaboxadol (300 \mu M)-evoked currents remained very low (9.7 \pm 4.1\%, n = 4, N = 1) with respect to GABA-evoked currents and indicated that hECNs maintained in culture for prolonged time periods (49–56 DIV) did not begin to express a \delta-containing receptor population.

The presence of \beta subunits in hECN GABA\textsubscript{A}Rs was confirmed by the potentiation by the intravenous anaesthetic propofol (10 \mu M) of GABA (EC\textsubscript{30}; 120 \mu M)-evoked currents which resulted in robust potentiation of the control current responses by 144 \pm 29 \% (Fig. 3A and B; P = 0.002 vs. control, unpaired t test, n = 8, N = 2; Sanna et al. 1995; Hill-Venning et al. 1997). Furthermore, direct activation of GABA\textsubscript{A}Rs was observed when propofol (100 \mu M) was applied on its own (98 \pm 21 \% relative to GABA (EC\textsubscript{30}; 120 \mu M)-evoked control; n = 7, N = 2; Fig. 3A and C). The intravenous anaesthetic etomidate (3 \mu M), which is selective for \beta2/3 subunit-containing GABA\textsubscript{A}Rs (Hill-Venning et al. 1997), also potentiated GABA (EC\textsubscript{30}; 120 \mu M)-evoked currents by 75 \pm 20 \% (Fig. 3A and B; P = 0.01 vs. control, unpaired t test, n = 6, N = 1) while application on its own and at a higher concentration (300 \mu M) directly activated GABA\textsubscript{A}Rs (116 \pm 23 \% relative to GABA (EC\textsubscript{30}; 120 \mu M)-evoked control; n = 6, N = 1). Taken together, these data suggest the presence of a large complement of \beta2/3-containing GABA\textsubscript{A}Rs. The absence of \beta1-containing GABA\textsubscript{A}Rs was indicated by the fact that...
the selective inhibitor of $\beta_1$-containing GABA$_A$Rs, SCS (Thompson et al. 2004), failed to antagonise GABA (EC$_{50}$; 120 $\mu$M)-evoked currents (Fig. 3A and B; SCS vs. control, $P = 0.27$ vs. control, unpaired $t$ test, $n = 8, N = 2$).

As illustrated above GABA-evoked currents are potentiated by diazepam which suggests that $\alpha_4$ and $\alpha_6$ subunits are absent from the GABA$_A$R population in hECNs since typically benzodiazepines are active at $\alpha_1$, $\alpha_2$, $\alpha_3$, or $\alpha_5$-containing GABA$_A$Rs (Olsen & Sieghart, 2009). To rule out the possibility of the expression of $\alpha_4$ and $\alpha_6$ subunits, GABA (EC$_{50}$; 120 $\mu$M)-elicited currents were shown to be insensitive to the $\alpha_4/\alpha_6$ subunit containing GABA$_A$R inhibitor furosemide (100 $\mu$M; $P = 0.43$ vs. control, unpaired $t$ test, $n = 6, N = 2$; Fig. 3D and E; Knoflach et al. 1996; Wafford et al. 1996).

Furthermore, the observed low GABA and muscimol
The majority of the GABA AR population expressed by hECNs (Mortensen et al. 2011; Karim et al. 2013). To identify the nature of the α subunit we examined the actions of zolpidem (50 nM and 500 nM), which exhibits selectivity for α1-containing GABAARs with lesser potency at α2- and α3-containing GABAARs and negligible activity at α5-containing GABAARs (Sanna et al. 2002). Co-application of zolpidem to GABA (EC10: 35 μM)-evoked currents resulted in only a mild potentiation of control currents (Fig. 3D and E; 50 nM: 46 ± 10 %; 500 nM: 70 ± 10 %, n = 8, N = 2), indicating the majority of the GABAAR population expressed by hECNs most likely contain α2 and/or α3 subunits.

To assess quantitatively the expression of GABAAR subunits we examined the relative expression of subunit mRNA transcripts via RNA-seq analysis (35 DIV). Figure 4A shows the relative expression of α, β and γ subunits with levels normalised to the highest expressed subunit mRNA (β3). These data are consistent with the pharmacological analysis of GABAARs expressed by hECNs described above. For α subunits, we found prominent mRNA expression of the α2 and α3 subunits and very little detection of α4 and α6 subunits, whilst the α1 and α5 subunit mRNAs were expressed to a moderate extent. The β3 subunit is prominently expressed over β1 and β2 subunits. Pharmacological data do not point to the identity of the γ subunit(s) that are functionally expressed by hECNs; however, the RNA-seq data indicate the strongest expression of the γ2 subunit mRNA. In agreement with the pharmacological analysis, levels of δ subunit mRNA expression were considered to be nominal.

### Strychnine-sensitive glycine receptor characterisation

GlyR characterisation was initially performed with RNA-seq analysis of GlyR subunit mRNA transcripts in hECNs (35 DIV; Fig. 4B). Both α2 and β subunits are abundantly expressed at the mRNA level, whilst α1 and α3 subunits are only nominally or weakly expressed, respectively, relative to the α2 subunit. As expected, the presence of α4 subunit mRNA was not detected given its status as a pseudogene in humans (Lynch, 2009).

Functional expression of GlyRs was examined by the ability of hECNs (7–35 DIV) to respond to bath applications of glycine (500 μM). With increasing periods following differentiation the mean GlyR-mediated current density profile displays a marked increase (Fig. 5A; 3.3 ± 2.2 pA pF⁻¹ to 49.4 ± 8.4 pA pF⁻¹, P < 0.001, unpaired t test, n = 7, N = 2), indicating a strong temporal up-regulation of functional GlyRs expressed by hECNs. Furthermore by 28 DIV all cells examined gave currents (Fig. 5A) and in all cases examined these were blocked by the GlyR antagonist strychnine (20 μM).

The potency of glycine-evoked currents was assessed by concentration–response experiments (Fig. 5B), from which a curve-fitting of mean data yielded an EC50 of 167 ± 20 μM (Fig. 5C). Glycine-evoked (500 μM) currents were blocked fully by strychnine in a concentration-dependent manner with an IC50 of 630 ± 59 nM (n = 5, N = 2; Fig. 5D and E). Note that an increased agonist concentration, rather than the typical EC50, was used to elicit suitable current responses to measure antagonist effects. The composition of the expressed GlyRs was probed using picrotoxin, which exhibits selectivity for homomeric over heteromeric GlyR forms, as the inclusion of the β subunit into the GlyR results in a reduction in sensitivity to picrotoxin (Pribilla et al. 1992; Wang et al. 2006; Lynch, 2009). Inhibition of GlyRs by picrotoxin (Fig. 5D and E) gave an IC50 of 197 ± 22 μM (n = 5, N = 2), indicating the low potency of this antagonist at hECN GlyRs and suggesting that the majority of these receptors are heteromeric assemblies contain α and β subunits.
Discussion

We have employed a variety of techniques to identify the principal subunit composition of ionotropic GABA<sub>AR</sub>Rs and GlyRs expressed by hECNs. The identification of GABA<sub>AR</sub> subunit regulation and expression is relevant to neurodevelopment and neurological disease and thus the ability of hPSC-derived neurones to express GABA<sub>AR</sub>Rs that reflect those seen in native neurones is essential if such in vitro preparations are to be used for human-specific development and disease modelling.

Our data establish that the predominant GABA<sub>AR</sub> α subunits expressed by hECNs (DIV 28–45) are α<sub>2</sub> and/or α<sub>3</sub> subunits, which is consistent with an expression profile predominantly exhibited by embryonic rodent cortical neurones (Laurie <i>et al.</i> 1992; Fritschy <i>et al.</i> 1994). Given that GABA-evoked currents were not inhibited by furosemide, hECN GABA<sub>AR</sub>Rs are considered to lack α<sub>4</sub> and α<sub>6</sub> subunits. Furthermore, the mild modulatory action of zolpidem suggests the absence of the α<sub>1</sub> subunit which is perhaps to be expected given that this subunit is associated with a more mature neuronal phenotype (Laurie <i>et al.</i> 1992; Fritschy <i>et al.</i> 1994). In agreement with our pharmacological analysis, RNA-seq also showed only moderate expression of α<sub>1</sub> subunits together with negligible expression of both α<sub>4</sub> and α<sub>6</sub> subunits compared to the relative abundance of transcripts for both α<sub>2</sub> and α<sub>3</sub> subunits. We considered that the functional expression of the α<sub>5</sub> subunit, which is associated with high agonist potency, was unlikely given

![Figure 5](https://example.com/figure5.png)

**Figure 5.** Agonist and antagonist pharmacology of hECN GlyRs

- **A,** weekly percentage response to bath applications of glycine and the mean glycine-mediated current density. 
  - Current density: 125 pA, 50 s. 
  - Mean (±SEM) agonist concentration–response curves: glycine data: EC<sub>50</sub> = 167 ± 20 μM; n<sub>H</sub> = 1.59 ± 0.1; n = 7, N = 2. 
  - Mean antagonist concentration–response curves: picrotoxin data: IC<sub>50</sub> = 197 ± 22 μM; n<sub>H</sub> = 0.9 ± 0.06; n = 5, N = 2. 
  - Mean strychnine data: EC<sub>50</sub> = 690 ± 59 nM; n<sub>H</sub> = 1.17 ± 0.06; n = 5, N = 2.
the relatively low levels of mRNA detected and the low agonist potencies of GABA and muscimol. Indeed, low potency is indicative of GABA$_{A}$Rs that contain either $\alpha_2$ or $\alpha_3$ subunits (Mortensen et al. 2011; Karim et al. 2013).

High expression of the GABA$_{A}$R $\beta_3$ subunit has been associated with rodent immature cortical neurones (Laurie et al. 1992), though the $\beta_2$ subunit is often also reported to be substantially expressed in cortical neurones (Fritschy et al. 1994). Potentiation of GABA-evoked currents by the low concentrations of intravenous anaesthetics etomidate and propofol, direct activation by high concentrations of etomidate and propofol, a lack of SCS inhibition and a high level of mRNA expression for the $\beta_3$ subunit collectively demonstrate that hECNs are likely to predominantly express $\beta_3$ subunit-containing GABA$_{A}$Rs, although a contribution of $\beta_2$ to GABA$_{A}$R stoichiometry cannot be ruled out.

The vast majority of GABA$_{A}$Rs in the CNS are $\gamma_2$ subunit containing (Olsen & Sieghart, 2009). RNA-seq data indicate that hECNs predominantly express the $\gamma_2$ subunit, in agreement with the pharmacological findings that GABA-evoked currents were potentiated by $\gamma$ subunit-selective diazepam. Subsets of $\delta$ subunit-containing GABA$_{A}$Rs are selectively expressed by certain cortical adult neuronal phenotypes and importantly are commonly associated with GABA$_{A}$R-mediated tonic inhibition (Olsen & Sieghart, 2009). Nevertheless, our data indicate that hECNs lack $\delta$ subunit-containing GABA$_{A}$Rs as gABoxadol gave rise to only low amplitude currents compared to those seen with GABA. Furthermore, the finding that $\text{Zn}^{2+}$ did not inhibit GABA-evoked currents is consistent with the absence of GABA$_{A}$Rs containing only $\alpha_1/\beta$ subunits.

We have demonstrated that both RNA-seq analysis and selective GABA$_{A}$R pharmacology converge on a predominant GABA$_{A}$R composition of $\alpha_2/3\beta_3\gamma_2$. Such isoforms are observed in recombinant expression systems to have low agonist potency relative to other isoforms and we similarly demonstrate that GABA$_{A}$R expressed upon hECNs exhibit relatively low agonist potency (Karim et al. 2013). This GABA$_{A}$R isoform is the most likely to be widely expressed in the immature rodent cortex (Laurie et al. 1992; Olsen & Sieghart, 2009). Nevertheless, our data cannot rule out the presence of other GABA$_{A}$R isoforms expressed at a low level. However, inspection of Brainspan (Atlas of the Developing Human Brain http://www.brainspan.org/rnaseq/search) indicates that the levels of mRNA we report from the RNA-seq analysis of hECNs (35 DIV) are qualitatively similar to those seen in human cortical neurones between 12 and 21 weeks post conception. Thus, hECNs provide a system to investigate the properties of human GABA$_{A}$R pharmacology and furthermore permit investigation of the role of GABA$_{A}$Rs in the maturing cortical neurones (Wang & Kriegstein, 2009).

In rodents, transient functional GlyR expression is a key feature of early neocortical development (Flint et al. 1998; Avila et al. 2013a). Indeed, hECNs maintained for 28–42 DIV exhibited strong responses to glycine that were blocked by the GlyR antagonist strychnine. Glycine concentration–response experiments indicated glycine potency was lower than previously reported recombinant values (Pribilla et al. 1992) but is generally higher than glycine potencies observed in native cortical preparations (Flint et al. 1998; Okabe et al. 2004; Kilb et al. 2008; but see Avila et al. 2013b). The reasons for these differences are unknown, but may be related to systematic differences in the solution exchange times of these studies, where slower exchange times are more likely to give shallower observed concentration–response curves. In this regard, the ability to examine deactivation kinetics of GlyRs expressed by hECNs in isolated patches using fast agonist application may yield further details of GlyR identity (Mangin et al. 2003; Pitt et al. 2008; Krashia et al. 2011; Marabelli et al. 2013).

GlyRs expressed by rodent forebrain neurones have been described as developing from an embryonic homomeric to postnatal heteromeric ($\beta$ subunit-containing) composition (Lynch, 2009). To investigate the functional GlyR composition we used the antagonist picrotoxin, which inhibits homomeric over heteromeric GlyRs (Lynch, 2009). Given the observed low sensitivity of GlyRs to picrotoxin, our results suggest that the principal GlyR identity of hECNs is likely to a heteromeric $\alpha/\beta$ assembly. Pharmacological tools to identify unambiguously the nature of the $\alpha$ subunit within the heteromer are lacking (but see Han et al. 2004); however, RNA-seq analysis indicates that $\alpha_2$ subunit mRNA is the most abundantly expressed. As is the case for GABA$_{A}$R subunit expression, levels of mRNA expression for GlyRs in our RNA-seq analysis are consistent with a development age of around 12–21 weeks post conception (Atlas of the Developing Human Brain http://www.brainspan.org/rnaseq/search).

Finally, it is of interest to note that there is trans- ferent expression of heteromeric $\alpha_2/\beta$ GlyRs by rodent Cajal–Retzius cells in early postnatal development (Okabe et al. 2004). This class of neurone is considered to form a significant population in our hECN cultures (Bilican et al. 2014) and in this respect hECNs may provide a useful human model of GlyR development.

**References**


Frizelle PA, Chen PE & Wyllie DJ (2006). Equilibrium constants for (R)-[1S]-1-(4-bromo-phenyl)ethylamino-[2,3-dioxo-1,2,3,4-tetrahydroquinoline-xalin-5-yl]-methyl-phosphonic acid (NVP-AAM077) acting at recombinant NR1/NR2A and NR1/NR2B N-methyl-d-aspartate receptors: Implications for studies of synaptic transduction. Mol Pharmacol 70, 1022–1032.


GABA_{A}Rs and GlyRs in human stem cell-derived cortical neurones


**Additional Information**

**Competing interests**

The authors declare no conflict of interest.

**Author contributions**

Conception and design of the experiments: O.T.J., M.R.L., J.Q., O.D., G.E.H., S.C., P.C.K. and D.J.A.W. Collection, analysis and interpretation of data: O.T.J., M.R.L., J.Q., O.D., B.B., G.H., R.R., K.B. and D.J.A.W. Drafting the article or revising it critically for important intellectual content: O.T.J., M.R.L., O.D., G.E.H., S.C., P.C.K. and D.J.A.W. It is confirmed that all authors approved the final version of the manuscript and that all persons designated as authors qualify for authorship, and all those who qualify for authorship are listed. All experiments were performed in the laboratories of G.E.H., S.C., P.C.K. and D.J.A.W at the University of Edinburgh, Edinburgh, UK.

**Funding**

This research was funded by The Wellcome Trust (Grant 092742/Z/10/Z to D.J.A.W., S.C. and G.E.H.), the Medical Research Council (Senior Non-clinical Research Fellowship to G.E.H.), the Euan MacDonald Centre and the NC3Rs CRACK IT Programme (S.C.) and seedcorn funding from the Patrick Wild Centre/RS Macdonald Trust (P.C.K. and D.J.A.W).

**Acknowledgements**

We thank Karim Gharbi and Timothee Cezard (Edinburgh Genomics, University of Edinburgh) for their help in conducting RNA-seq analysis and the members of our lab for their many constructive comments during the course of this study.

**Authors’ present addresses**

G. Haghi: New World Laboratories, 500 Cartier Blvd, Laval, H7V 5B7, Quebec, Canada. B. Bilican: Novartis Institutes for Biomedical Research, 100 Technology Square, Cambridge, MA 02139, USA.