NanoBiT Complementation to Monitor Agonist-Induced Adenosine A₁ Receptor Internalization

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Abstract
Receptor internalization in response to prolonged agonist treatment is an important regulator of G protein–coupled receptor (GPCR) function. The adenosine A₁ receptor (A₁AR) is one of the adenosine receptor family of GPCRs, and evidence for its agonist-induced internalization is equivocal. The recently developed NanoBiT technology uses split NanoLuc Luciferase to monitor changes in protein interactions. We have modiﬁed the human A₁ AR on the N-terminus with the small high-affinity HiBiT tag. In the presence of the large NanoLuc subunit (LgBiT), complementation occurs, reconstituting a full-length functional NanoLuc Luciferase. Here, we have used complemented luminescence to monitor the internalization of the A₁AR in living HEK293 cells. Agonist treatment resulted in a robust decrease in cell-surface luminescence, indicating an increase in A₁AR internalization. These responses were inhibited by the A₁AR-selective antagonist 1,3-dipropyl-8-cyclopentylxanthine (DPCPX), with an antagonist afﬁnity that closely matched that measured using ligand binding with a ﬂuorescent A₁ receptor antagonist (CA200645). The agonist potencies for inducing A₁ AR internalization were very similar to the afﬁnities previously determined by ligand binding, suggesting little or no ampliﬁcation of the internalization response. By complementing the HiBiT tag to exogenous puriﬁed LgBiT, it was also possible to perform NanoBRET ligand-binding experiments using HiBiT–A₁AR. This study demonstrates the use of NanoBiT technology to monitor internalization of the A₁AR and offers the potential to combine these experiments with NanoBRET ligand-binding assays.

Keywords
GPCR, adenosine, receptor internalization, NanoBiT, nanluciferase complementation

Introduction
G protein–coupled receptors (GPCRs) are the largest family of membrane-signaling proteins and are able to modulate signals from a wide range of endogenous ligands.¹ Prolonged stimulation by an agonist results in the internalization of many GPCRs, and this process can occur via different pathways, including caveolae-dependent and clathrin-mediated processes.²,³ For the latter, G protein–coupled receptor kinases (GRKs) phosphorylate serine and threonine residues within the intracellular loops and C-terminal tail of the receptor following agonist-stimulated receptor activation.⁴ β-Arrestins are able to bind to the phosphorylated receptor and can initiate downstream signaling pathways that are independent of G proteins.⁵ β-Arrestins also compete stERICALLY with G proteins for binding to the receptor, resulting in receptor desensitization, and recruit speciﬁc adaptor proteins that are required for clathrin-mediated endocytosis.⁶ The GPCRs are internalized in clathrin-coated vesicles and transferred into early endosomes, where it is now known that a second wave of intracellular signaling can occur.⁷,⁸

The adenosine A₁ receptor (A₁AR) is part of the wider adenosine GPCR subfamily, grouped by their ability to bind their endogenous ligand, adenosine.¹,⁹ The A₁AR

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predominantly couples to the G_\text{i} family of heterotrimeric G proteins, which inhibit adenylyl cyclase–mediated cAMP (cyclic adenosine monophosphate) production. There is contrasting evidence, however, concerning the nature of GRK-mediated A_1AR phosphorylation,\(^{10–13}\) as well as the nature and extent of A_1AR internalization in response to chronic stimulation by agonists.\(^{12–15}\) The A_1AR is able to internalize through both clathrin- and caveolae-dependent endocytosis.\(^{13,16}\) Previous studies of human A_1AR internalization observed that the receptor had a slow rate of internalization of several hours.\(^{15,17–19}\) Ruiz et al. found this was also true of the rat A_1AR receptor, which required more than 12 h of stimulation to internalize 50% of rat A_1ARs in cortical neurons.\(^{20}\) These A_1AR data contrast drastically with data for the other G_\text{i}-coupled adenosine receptor, the A_3 receptor, which internalizes more rapidly, and within minutes of agonist stimulation.\(^{12,21,22}\)

Previous studies on A_1AR internalization have been conducted using either radiolabeled A_1AR ligands\(^{14,15}\) or confocal microscopy.\(^{11,19}\) These techniques offer specific advantages, such as the ability to monitor A_1AR internalization in ex vivo tissues with radioligand binding, or the ability to directly visualize internalization with microscopy. These methods are, however, intensive and low throughput.

Recently, NanoLuc Binary Technology (NanoBiT; Promega, Southampton, UK) has been developed that splits the bright NanoLuc Luciferase\(^{23}\) into two segments, a large 18 kDa fragment (termed LgBiT) and a much smaller 1.3 kDa fragment (termed SmBiT; a small complementation tag).\(^{24}\) These fragments have low intrinsic affinity for each other [equilibrium dissociation constant (K_D), 190 \(\mu\)M] and complement to form the full bioluminescent protein NanoLuc. SmBiT–LgBiT complementation has successfully been used to monitor protein–protein interactions of membrane receptors, including the recruitment of G proteins and β-arrestins to GPCRs.\(^{25,26}\) In the development of the NanoBiT system, other small complementary peptides were identified that have different affinities for LgBiT. Therefore HiBiT–LgBiT complementation has a high-throughput method to monitor loss of A_1ARs from the cell surface in living cells.

**Materials and Methods**

**Materials**

Adenosine and 5’-N-ethylcarboxamidoadenosine (NECA) were purchased from Sigma-Aldrich (Gillingham, UK). 1,3-Dipropyl-8-cyclopentylxanthine (DPCPX), 2-chloro-N\(^6\)-cyclopentyladenosine (CCPA), 2’-methyl-2-chloro-N\(^6\)-cyclopentyladenosine (2-MeCCPA), and 2-phenylamino-adenosine (CV-1808) were obtained from Tocris (Bristol, UK). 2-Amino-6-[2-(4-chlorophenyl)-1,3-thiazol-4-yl]methyl-sulfanyl]-4-[4-(2-hydroxyethoxy)phenyl]pyridine-3,5-dicarbonitrile (capadenosin) was purchased from Haoyuan Chemexpress (Shanghai, China). The fluorescent antagonist CA200645 was purchased from HelloBio (Bristol, UK). Purified LgBiT, restriction enzymes, FuGENE HD Transfection Reagent, and furimazine were purchased from Promega.

**Constructs and Cell Lines**

To create the HiBiT–A_1AR construct, the full-length NanoLuc sequence was removed from the pcDNA3.1 NLuc–A_1AR vector\(^{27}\) using KpnI and BamHI restriction sites. This left the pcDNA3.1 vector containing the A_1AR with a mutated start codon (Met→Leu). Primers containing the HiBiT sequence (bold letters), a GSSGGSSG linker (5’: cATGTTGAGCCGCTGGCGTTCGTCAAAAGAATTAGCAGGGATGGTCTGAGCGCTGACGGTG; and 5’: gatccACCGCTAGCCGCCGAACCTCCTCGC TAATCTTCTGAACGAGCCACCGGTCACCAT, respectively) and the respective KpnI and BamHI overhangs (lowercase letters) were phosphorylated using T4 Polynucleotide Kinase (NEB, Hitchin, UK) and annealed for 30 min at 37°C. The annealed primers were then ligated into the digested pcDNA3.1 A_1AR vector using T4 ligase (NEB), creating the full-length fusion protein HiBiT–A_1AR. Correct insertion was confirmed by DNA sequencing using the School of Life Sciences Sequencing Facility at the University of Nottingham.

HEK293 cells were maintained in Dulbecco’s modified Eagle medium (DMEM) containing 10% fetal calf serum (FCS) and 2 mM L-glutamine at 37°C in a 5% CO₂ atmosphere. A mixed-population HiBiT–A_1AR stable cell line was generated using FuGENE HD (Promega), according to the manufacturer’s instructions, and the cells were subjugated to 3 weeks of selection with 1 mg/mL G418.

**NanoBiT Internalization Assay**

HEK293 cells stably expressing HiBiT–A_1AR were plated onto white 96-well plates (Greiner Bio-One, Monroe, NC) previously coated with 10 \(\mu\)g/mL poly-D-lysine. 100 \(\mu\)L DMEM containing cells in suspension (30,000 cells/well) was added to each well, and the plate incubated at 37°C in a 5% CO₂ atmosphere for 24 h. The next day, the medium was removed from each well and replaced with 50 \(\mu\)L HEPES-buffered saline solution (HBSS; 145 mM NaCl, 5 mM KCl, 10 mM HEPES, 1.3 mM CaCl₂ dihydrate, 1.5 mM NaHCO₃, 2 mM sodium pyruvate, 1 mM MgSO₄·7H₂O, 10 mM D-glucose; pH 7.45) and the relevant concentration of
ligand. For end-point assays, cells were incubated at 37 °C for 2 h. Purified LgBiT was diluted in HBSS (10 nM final concentration) and added to each well in the presence of furimazine (1:400 final concentration). The plate was incubated for 15 min in the dark at 37 °C, allowing complementation to occur. Luminescence was measured on the PHERAstar FS plate reader (BMG Labtech, Offenburg, Germany) using the LUM Plus module.

Bioluminescence Imaging

HEK293 cells stably expressing HiBiT–A1AR were seeded onto a poly-D-lysine-coated (10 µg/mL) 35 mm four-chamber MatTek dish (Ashland, MA) at a density of 120,000 cells/mL. The dish was incubated at 37 °C in a 5% CO2 atmosphere for 24 h. The next day, the medium was removed and replaced with 400 µL HBSS containing furimazine (1:400 final concentration). Purified LgBiT was added, and the plate incubated at 37 °C for 20 min. Bright-field and bioluminescence imaging was performed on the Olympus LV200 inverted microscope (Olympus, Southend, UK). Bright-field images were captured with a 50 ms exposure. Bioluminescence images were captured with a 45 s exposure, using a Hamamatsu EM-CCD (electron-multiplying charge-coupled device; Hamamatsu, Hamamatsu City, Japan) with a gain of 100.

NanoBRET Ligand-Binding Assay

HEK293 HiBiT–A1AR cells were seeded onto poly-D-lysine-coated white 96-well plates as described above. The next day, the medium was removed from each well and replaced with 50 µL HBSS containing 10 nM LgBiT; the plate was incubated for 15 min in the dark at 37 °C, allowing complementation to occur. The HBSS with unbound LgBiT was removed and replaced with 50 µL HBSS containing the fluorescent A1 receptor antagonist ligand CA20064528 in the absence or presence of 10 µM DPCPX. The plate was incubated in the dark at 37 °C for 2 h. Furimazine (1:400 final concentration) was added to each well, and the plate incubated for 15 min at 37 °C. The resulting bioluminescence resonance energy transfer (BRET) was measured using the PHERAstar FS plate reader (BMG Labtech), which simultaneously measured filtered light emissions at 460 nm (80 nm bandpass) and >610 nm (longpass). The BRET ratio was calculated by dividing the >610 nm emission by the 460 nm emission.

Data Analysis

Data were presented and analyzed using Prism 7 software (GraphPad, San Diego, CA).

The potency of ligands that internalized HiBiT–A1AR was determined from fitting data to a one-site sigmoidal concentration–response curve defined by the following three-parameter logistic equation:

\[
\% \text{ receptor at cell surface} = 100 - \left( \frac{100 \times [A^n]}{[A^n] + IC_{50}^n} \right)
\]

where \([A]\) is the concentration of the ligand \(n\) is the Hill coefficient, and \(IC_{50}^n\) is the concentration of ligand required to internalize 50% of receptors.

In the experiments in which three fixed concentrations of DPCPX were used, the \(K_D\) of DPCPX was estimated from the shift in the NECA response by 10 nM DPCPX using the Gaddum equation:

\[
CR = 1 + \left( \frac{[B]}{K_B} \right)
\]

where \(CR\) is the concentration ratio of NECA required to stimulate an identical response in the presence or absence of 10 nM DPCPX \([B]\), and \(K_B\) is the affinity of DPCPX.

The time course of internalization in response to 10 µM NECA at HiBiT–A1AR was fitted with a one-phase exponential decay curve using the following equation:

\[
Y = (Y_0 - NS) e^{-kt} + NS
\]

where \(Y\) is the luminescence at time \(t\) minutes, \(Y_0\) was the luminescence at time 0, \(NS\) is the background luminescence, and \(k\) is the rate constant of the decrease in luminescence per minute.

Saturation NanoBRET experiments were simultaneously fitted to obtain the total and nonspecific components using the following equation:

\[
\text{BRET Ratio} = \frac{B_{\text{max}} \times [B]}{[B] + K_D} + \left( \frac{M \times [B]}{[B] + C} \right)
\]

where \(B_{\text{max}}\) is the maximal level of specific binding, \([B]\) is the concentration of fluorescent ligand in nM, \(K_D\) is the equilibrium dissociation constant, \(M\) is the slope of the linear nonspecific binding component, and \(C\) is the \(y\)-axis intercept.

Data are presented as the mean ± SEM of triplicate determinations in a single experiment. In the text, \(n\) refers to the number of separate experiments. Statistical significance was defined as \(p < 0.05\) using Student’s unpaired \(t\) test.

Results

NanoBiT has provided a platform for assessing protein–protein interactions in vitro in real time. Here, we have used the NanoBiT complementation technology to monitor the presence of the human A1 receptor, tagged on its N-terminus with HiBiT, at the cell surface of living cells.
following addition of purified LgBiT (Fig. 1a). This approach can also be extended to detect the loss of HiBiT–A1AR following agonist stimulation as a method to detect receptor internalization (Fig. 1b).

Expression of the HiBiT–A1AR at the plasma membrane was first confirmed using NanoBiT complementation. HEK293 cells, stably transfected with HiBiT–A1AR, were incubated with purified LgBiT in the presence of the NanoLuc substrate, furimazine. As an 18 kDa protein, LgBiT is cell impermeable and thus will complement only with HiBiT–A1AR present on the plasma membrane. Increasing concentrations of LgBiT resulted in a higher luminescence signal (Fig. 2a; \( n = 4 \)). These results indicated that HiBiT–A1AR was able to traffic to the plasma membrane and complement with exogenously applied purified LgBiT. It should be noted that neither HiBiT–A1AR nor LgBiT alone produced a strong luminescent signal (Fig. 2a). Wide-field bioluminescent imaging also confirmed clear membrane expression of HiBiT–A1AR in HEK293 cells (Fig. 2b). From these experiments, it was determined that 10 nM LgBiT would provide a sufficient luminescence response window for all subsequent assays.

To confirm that the complementation of HiBiT–A1AR with exogenously applied LgBiT did not alter the ability of the A1AR to bind ligands, ligand-binding studies were performed using NanoBRET with a fluorescent A1 receptor antagonist \( ^{28,33} \) (Fig. 1a). Following complementation of HiBiT–A1AR with purified LgBiT, the binding of the fluorescent A1 receptor antagonist CA200645 to the complemented A1 receptor was monitored using NanoBRET \( ^{28} \) (Figs. 1 and 3). In these assays, clear specific binding of CA200645 to the A1AR was observed. The negative log of the dissociation constant \( (pK_D) \) of CA200645 was calculated to be 7.17 ± 0.03 \( (K_D = 63.8 \text{ nM}; n = 4; \text{Fig. 3}) \). This was similar to the \( K_D \) value reported previously \( (K_D = 33.8 \text{ nM}) \) for CA200645 to the full-length NanoLuc-tagged A1AR. \(^{27} \)
With successful membrane expression of HiBiT–A<sub>1</sub>AR confirmed, it was then established if NanoBiT could be used to monitor receptor internalization (Fig. 1b). Cells were incubated at 37 °C and treated with 10 µM NECA for increasing periods of time to stimulate an internalization response. Longer incubation periods resulted in a decrease in luminescence (Fig. 4), correlating to an increase in the proportion of HiBiT–A<sub>1</sub>ARs that have internalized (Fig. 1b). The resulting half-life of internalization was 31 ± 6 min (n = 4). From these data, a 2 h ligand incubation time was chosen for all subsequent end-point experiments, because receptor internalization had plateaued by this point.

NECA stimulated a concentration-dependent loss of HiBiT–A<sub>1</sub>ARs from the cell surface of HEK293 cells (pIC<sub>50</sub> = 5.67 ± 0.21; n = 10; Fig. 5a and Table 1). The A<sub>1</sub>-selective antagonist DPCPX was able to inhibit the NECA-stimulated internalization response (Fig. 5a).
Fitting the Gaddum equation to the responses measured in the presence and absence of 10 nM DPCPX produced an affinity of DPCPX \( (pKD = 8.28 \pm 0.12; n = 6) \), which closely matches the affinity of DPCPX calculated in the human NLuc–A1AR.27

A panel of adenosine A1 receptor agonists were screened for their ability to internalize HiBiT–A1AR. In addition to NECA, the A1 receptor agonists CCPA and 2-MeCCPA were found to be full agonists in this assay, able to stimulate a robust internalization of HiBiT–A1AR (Fig. 5b and Table 1). The atypical A1AR agonist capadenoson and the adenosine A2 receptor ligand CV-1808 were found to elicit partial internalization responses (Fig. 5b and Table 1).

### Discussion

NanoBiT has provided the opportunity to measure GPCR–effector interactions in real time in living cells with a high degree of sensitivity.25,26,31,32 Here, we have used the high-affinity HiBiT tag to detect cell surface expression of the adenosine A1 receptor and quantified the loss of receptors at the cell surface in response to agonist treatment as a measure of receptor internalization.

The HiBiT–A1AR was successfully expressed on the surface of HEK293 cells and could be visualized with bioluminescent imaging following addition of exogenous purified LgBiT. Furthermore, the complemented NLuc–A1AR retained the ability to bind fluorescent adenosine A1AR antagonists, yielding binding constants that were similar to those determined previously using A1ARs expressing the full-length NLuc tag.27,28 The strong luminescence signal provided by fully complemented HiBiT–LgBiT, however, provided a large assay window to detect small changes in the surface expression of the A1AR. This can be observed in Figure 4 as the loss of luminescence in response to increasing incubation periods with the agonist NECA.
binding.\textsuperscript{15,17,18} These studies observed a slow rate of $A_1$AR internalization, with a $t_{1/2}$ for internalization of several hours. Using NanoBiT, it was possible to detect $A_1$AR internalization (Fig. 4) at much earlier time points than was previously reported.\textsuperscript{17–19} In addition, both radioligand binding and confocal microscopy are low-throughput techniques and are not amenable to performing full concentration–response curves for a panel of $A_1$AR agonists.

In contrast, NanoBiT provided an ideal platform for detecting the internalization of $A_1$AR in living cells in response to a wide panel of ligands. The high signal-to-noise ratio of the assay made it possible to monitor full-agonist and partial-agonist responses during relatively short periods of time (Fig. 5b). The potencies of the agonist responses were generally similar to the affinities of the ligands at the human $A_1$AR, as measured previously with NanoBRET.\textsuperscript{27} Thus, the similarity in values obtained for NECA and CCPA for the two assays suggests that there is no signal amplification in the internalization response for these two agonists. This contrasts with the higher receptor–effector coupling observed for these ligands for cAMP inhibition or pERK1/2 phosphorylation.\textsuperscript{34,35}

The one exception was the partial $A_1$AR agonist capadenoson,\textsuperscript{36,37} in which the pEC$_{50}$ (5.23) for internalization was more than an order of magnitude lower than its pKi value (6.85), determined from inhibition of NanoBRET binding with CA200645 at the human $A_1$AR.\textsuperscript{27} This very low potency for internalization of capadenoson compared to its binding affinity for the orthosteric ligand-binding site suggests that there may be a more complex mechanism of action involved. This may involve differential affinities for multiple $A_1$AR agonist receptor conformations and the potential for signaling bias.\textsuperscript{35,38,39}

The internalization stimulated by NECA could be antagonized by the $A_1$AR antagonist DPCPX in a concentration-dependent manner. The resulting analysis suggested an affinity for DPCPX that was in keeping with the known affinity of this ligand for the human $A_1$AR.\textsuperscript{27,40} In addition, there was no hint of inverse agonism with DPCPX in this assay (Table 1).

These experiments were performed in HEK293 cells, which express both adenosine $A_{2A}$ and $A_{2B}$ receptors endogenously.\textsuperscript{41} It is unlikely that the internalization responses measured in this study were affected by the presence of the adenosine $A_{2A}$ or $A_{2B}$ receptors, given that the potencies of the ligands used in this study are in the same rank order as the binding affinities of the human $A_1$AR.\textsuperscript{27,40,42} and the determined affinity for DPCPX was in keeping with the known affinity at the human $A_1$AR.

It should be noted that the assay described here has been configured specifically to monitor the extent of loss of $A_1$ receptors from the cell surface in response to agonist treatment. From the data obtained, we cannot comment on the extent to which $A_1$ agonists also alter $A_1$ receptor protein degradation and turnover. It should be noted, however, that NanoBiT represents a versatile technology with a broad dynamic range that can be applied to detect and quantify protein expression\textsuperscript{43} and degradation.\textsuperscript{43} For example, Riching et al. have exploited the high sensitivity of HiBiT–LgBiT complementation to detect targets with low levels of native expression and measure their subsequent degradation following PROTAC treatment.\textsuperscript{43} A similar approach using a HiBiT tag on the C-terminus of the $A_1$ receptor and its expression in cells that also express cytosolic LgBiT would allow $A_1$ receptor turnover and degradation to be monitored.

In conclusion, this study reports the use of NanoBiT to monitor $A_1$AR internalization in a plate-based assay based on complemented nanoluciferase luminescence. This approach can readily be applied to other GPCRs or indeed any cell surface membrane receptors (e.g., receptor tyrosine kinases or cytokine receptors) through the introduction of the HiBiT tag at the extracellular terminus of the protein of interest.

Declaration of Conflicting Interests

The authors declared no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

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