Gα protein signaling bias at 5-HT1A receptor

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Abstract
Serotonin 1A receptor (5-HT1AR) is a clinically relevant target because of its involvement in several central and peripheral functions including sleep, temperature homeostasis, processing of emotions, and response to stress. As a G Protein Coupled Receptor (GPCR) activating numerous Gαi/o/z family members, 5-HT1AR can potentially modulate multiple intracellular signaling pathways in response to different therapeutics. Here, we applied a cell-based BRET assay to quantify how ten structurally diverse 5-HT1AR agonists exert biased signaling by differentially stimulating Gαi/o/z family members. Our concentration-response analysis of the activation of each Gαi/o/z protein revealed unique potency and efficacy profiles of selected agonists when compared to the reference 5-HT. Overall, our analysis of signaling bias identified groups of ligands sharing comparable G protein activation selectivity and also drugs with unique selectivity profiles. We observed, for example, a strong bias of F-15599 toward the activation of Gαi3 that was unique among the agonists tested: we found a biased factor of +2.19 when comparing the activation of Gαi3 versus Gαi2 by F-15599, while it was -0.29 for 8-OH-DPAT. Similarly, vortioxetine showed a biased factor of +1.06 for Gαz versus GαoA, while it was -1.38 for vilazodone. Considering that alternative signaling pathways are regulated downstream of each Gα protein, our data suggest that the unique pharmacological properties of the tested agonists could result in multiple unrelated cellular outcomes. Further investigation is needed to reveal how this type of ligand bias could affect cellular responses and to illuminate molecular mechanisms underlying therapeutic profile and side effects of each drug.
**Significance statement:**

Serotonin 1a receptor (5-HT1AR) activates several members of the G_{i/o/z} protein family. Here, we examined ten structurally diverse and clinically relevant agonists acting on 5-HT1AR and identified distinctive bias patterns among G proteins. Considering the diversity of their intracellular effectors and signaling properties, this data reveal novel mechanisms underlying both therapeutic and undesirable effects.
Introduction

G Protein Coupled Receptors (GPCRs) are the largest group of membrane receptors in mammals. About 35% of approved drugs regulate GPCRs, thus they are a vital target for drug discovery (Campbell and Smrcka, 2018; Sriram and Insel, 2018). GPCRs are seven transmembrane proteins that couple and transduce signals by activating heterotrimeric G proteins and β-arrestins which further regulate various downstream signaling pathways. The activation of intracellular effectors by GPCR ligands is sometimes thought to be balanced, despite the fact that a limited number of studies explored this issue. However, biased ligands with the ability to preferentially stimulate a signaling pathway over another one have also been identified (Kenakin, 2019; Urban et al., 2007). The first evidence of signaling bias emerged from the observation that individual serotonergic receptors could control distinct intracellular pathways (Roth and Chuang, 1987). Later, drug discovery efforts suggested that G protein biased agonists targeting μ-opioid receptors could maintain analgesic effects while reducing adverse outcomes (DeWire et al., 2013; Raehal et al., 2005; Schmid et al., 2017). On the contrary, β-arrestin biased agonists targeting angiotensin II type-1 receptors have been proposed to reduce blood pressure and increase cardiac performance (Violin et al., 2010). More recently, Gαs-biased compounds activating β2-adrenergic receptors with no apparent involvement of β-arrestin-mediated signaling have been identified as potential candidates for treating asthma (Kim et al., 2021). As a consequence, the functional selectivity between Gα proteins and β-arrestins has become a classical example of clinically relevant ligand bias (Gurevich and Gurevich, 2020). However, ligand bias producing selective activation of Gα protein subtypes is an event that has been rarely
investigated (Von Moo et al., 2022; Voss et al., 2022). It has been demonstrated that biased agonist acting on adenosine 1 receptor and selective to GoB exhibit less cardiorespiratory depression compared to non-biased G protein agonists (Wall et al., 2022). As a result, it might be possible to understand the molecular process underlying drug efficacy and potency by looking into biased G protein signaling pathways. In mammals, 16 genes encode for Gα proteins that are classified into four subfamilies according to their sequence homology: Gαs, Gαq, Gα12/13, and Gαi/o/z (Wettschureck and Offermanns, 2005). Given that GPCR-G protein coupling can be selective toward a subset of G proteins, different ligands acting on the same receptor could potentially control alternative downstream signaling cascades (Berg et al., 1998; Fleetwood et al., 2021; Kim et al., 2022; Wright and Bouvier, 2021; Zheng et al., 2010).

The neurotransmitter serotonin (5-hydroxytryptamine; 5-HT) plays essential roles in the central and peripheral nervous systems (Mann, 1999; Nichols and Nichols, 2008; Sharp and Barnes, 2020; Svob Strac et al., 2016). Among the GPCRs endogenously activated by 5-HT, 5-HT1A receptor (5-HT1AR) is widely expressed and it has been implicated in many central and peripheral physiological functions including sleep, pain, temperature homeostasis, processing of emotions, and response to stress (Albert and Vahid-Ansari, 2019; Bjorvatn and Ursin, 1998; Garcia-Garcia et al., 2014; Haleem, 2019; Pehrson et al., 2022; Polter and Li, 2010; Razakarivony et al., 2021; Voronova, 2021). In the brain, 5-HT1AR acts as either a somatodendritic autoreceptor to control activity-dependent 5-HT release (Sprouse and Aghajanian, 1987) or as a postsynaptic heteroreceptor to reduce neuronal excitability and firing rates (Garcia-Garcia et al., 2014; Riad et al., 2000). Previous studies have shown that signaling cascades activated by 5-HT1AR are
exquisitely sensitive to pertussis toxin (PTX) suggesting coupling to $G_{\alpha_{i/o/z}}$ family members with minimal activity toward members of the $G_{\alpha_s}$, $G_{\alpha_q}$, and $G_{\alpha_{12/13}}$ protein families (Kooistra et al., 2021; Pandy-Szekeres et al., 2022; Raymond et al., 1999). Since 5-HT1AR preferentially couples to members of the numerous $G_{\alpha_{i/o/z}}$ and several natural and synthetic agonists are available, this receptor provides an excellent model to explore the potential $G_{\alpha}$ protein bias. Furthermore, many approved drugs acting on 5-HT1AR elicit different therapeutic effects and adverse responses (Celada et al., 2013). Nevertheless, the question of whether these diverse outcomes depend on the biased activation of $G_{\alpha}$ proteins remains obscure. Here, we investigate the activation bias in response to ten structurally diverse 5-HT1AR agonists by obtaining their unique profiles of $G_{\alpha}$ protein activation using an optimized cell-based Bioluminescence Resonance Energy Transfer (BRET) assay.

**Materials and Methods:**

**Cell cultures and transfections.** HEK293T/17 cells (RRID:CVCL_1926) were purchased from ATCC and cultured in DMEM (Gibco, 10567-014) supplemented with 10% FBS (Biowest, S1520), non-essential amino acids (Gibco, 11140-050), penicillin 100 units/ml and streptomycin 100 µg/ml (Gibco, 15140-122), and amphotericin B 250 µg/ml (ThermoFisher, 15290-018) at 37°C and 5% CO$_2$. Cells were routinely monitored for possible mycoplasma contamination. Two million cells were seeded in each well of 6-well plates in medium without antibiotics for 4 hours and then transfected with a 1:3 ratio of DNA plasmid (2.5 µg) and polyethylenimine (PEI; 7.5 µl) (VWR, AAA43896). The optimal $G_{\alpha}:G_{\beta\gamma}$ transfection ratio identified for $G_{\alpha_{oA}}$, $G_{\alpha_{oB}}$, $G_{\alpha_{i1}}$, $G_{\alpha_{i2}}$, $G_{\alpha_{i3}}$, and $G_{\alpha_z}$
were 4:1. The empty vector pcDNA3.1 was used to normalize the ratio of transfected plasmids. Transiently transfected cells were incubated for 16 hours before being tested.

**DNA plasmids and chemicals.** The plasmid encoding human 5-HT1AR was obtained from the cDNA Resource Center (www.cdna.org) (HTR01A0000). Gβ1-venus\(^{156-239}\) and Gγ2-venus\(^{1-155}\) were generous gifts from Dr. Nevin A. Lambert (Augusta University, Augusta GA). Go proteins and masGRK3CT-Nluc constructs were generous gifts from Dr. Kirill A. Martemyanov (UF Scripps Biomedical Research, Jupiter, FL). The following 5-HT1AR agonists were purchased from MedChemExpress: vilazodone (HY-14261), vortioxetine (HY-15414A), sumatriptan succinate (HY-B0121), nuciferine (HY-N0049), flibanserin (HY-A0095), aripiprazole (HY-14546), buspirone (HY-B1115), F-15599 (HY-19863), and 8-OH-DPAT (HY-15688). 5-HT hydrochloride was purchased from Tocris (3547/50). All chemicals were resuspended according to manufacturers' instructions, aliquoted, and stored at -20°C until use.

**G protein nanoBRET assay.** The day after transfection, cells were briefly washed with PBS, resuspended in BRET buffer (PBS supplemented with 0.5 mM MgCl\(_2\) and 0.1% glucose), collected in 1.5 ml tubes, and centrifuged for 5 minutes at 500 x g. Pelleted cells were resuspended in 500 µl of BRET buffer and 25 µl of cells were plated in 96-well white microplates (Greiner Bio-One). The nanoluc substrate furimazine (N1120) was purchased from Promega and used according to the manufacturer's instructions. BRET measurements were obtained using a POLARstar Omega microplate reader (BMG Labtech). All measurements were performed at room temperature and BRET
signal was determined by calculating the ratio of the light emitted by Gβ1γ2-venus (collected using the emission filter 535/30) to the light emitted by masGRK3CT-Nluc (475/30). In kinetics assays, the baseline value (basal BRET ratio) was averaged from recordings of the five seconds before agonist injection. In concentration-response experiments, 30 µl of cells per well were plated and mixed with the nanoluc substrate furimazine. Initial readings were performed to establish basal BRET ratio and then agonists at 12 concentrations were added. BRET signal was recorded for 3 minutes. ΔBRET ratios were obtained by subtracting the basal BRET ratio from the maximal amplitude measured.

**Statistical analysis.** Statistical analysis was performed using GraphPad Prism version 9 software (RRID:SCR_002798). Sample size was not predetermined; however, each experiment was performed at least five times before statistical analysis was done. Concentration-response curves were fitted to a sigmoidal four-parameter logistic function (variable slope analysis) to quantify agonist potencies (pEC50) and maximal responses (E_{max}). Importantly, we excluded Hill slope values that did not lie between 0.7 and 1.4 (Winpenny et al., 2016). At least five independent biological replicates were used for each experiment. To obtain the Gα protein bias, we adopted the equation from (Winpenny et al., 2016). Briefly, we first calculated the mean Log(E_{max}/EC50) for each agonist; then, we calculated the ΔLog(E_{max}/EC50) normalized to the reference agonist, in this case 5-HT:

\[
\Delta \text{Log} = \log \left( \frac{E_{\text{max}}}{EC_{50}} \right)_{\text{test}} - \log \left( \frac{E_{\text{max}}}{EC_{50}} \right)_{\text{reference}}
\]
Finally, we calculated the bias factor ($\Delta \Delta \text{Log}$) between different $G\alpha$ proteins using the following equation:

$$\Delta \Delta \text{Log} = \Delta \log \left( \frac{E_{\text{max}}}{E_{\text{C50}}} \right)_{\text{pathway 1}} - \Delta \log \left( \frac{E_{\text{max}}}{E_{\text{C50}}} \right)_{\text{pathway 2}}$$

All of our calculations error were associated with 95% confidence intervals (CI).

Rstudio software was used to visualize the results as a cluster dendrogram in Fig. 3D. Data were grouped into different clusters and the “complete” method was used for hierarchical clustering using distance matrix (Euclidean) dendrogram on R-studio (R Core Team, 2013).

All the data are reported as mean ± S.D. One-way ANOVA was applied to determine statistical differences and p values were reported as follows in the figure: ** **P<0.001, **P<0.01, and *P<0.05. Post hoc tests used and number of replicates are indicated in figure legends. Given the exploratory character of the study, calculated p-values cannot be interpreted as hypothesis-testing but only as descriptive.

**Results**

5-HT1AR uniquely activates heterotrimeric $G_{\text{loo/iz}}$ family members.

To confirm the reported G protein coupling profile of 5-HT1AR, we expressed 5-HT1AR in HEK293 cells together with a representative member of each $G\alpha$ protein family ($G\alpha_{\text{o}}$, $G\alpha_{\text{s}}$, $G\alpha_{\text{q}}$, $G\alpha_{\text{15}}$, and $G\alpha_{\text{13}}$) and we used a G protein nanoBRET assay to measure the coupling efficiency to each G protein in response to 5-HT stimulation (Fig. 1A). Briefly, after activation of the receptor with 5-HT, Gα dissociates from $G\beta\gamma$-venus that is now free to associate with the BRET donor GRK3CT-Nluc and generate a BRET signal (Hollins et al., 2009; Masuho et al., 2015). As expected, 5-HT1AR efficiently activated...
Gαo while we did not observe any activation of Gαs, Gαq, Gα15, and Gα13 (Fig. 1B). With the goal of measuring the activation of each member of the Gαi/o/z family, we then optimized the stoichiometry of each expressed Gα and Gβγ-venus by titrating the amount of Gα subunits against a constant amount of transfected Gβγ-venus. As expected, by increasing the amount of transfected Gα, we observed a reduction in the basal activity, in fact, suboptimal expression of Gα allows free Gβγ-venus to interact with GRK3CT-Nluc increasing the BRET signal detected in the absence of GPCR stimulation. Therefore, optimal Gα:Gβγ ratios were selected based on low basal BRET ratio and high maximal amplitude for each Gαi/o/z protein (Supplemental Fig. 1).

**Gα protein coupling profile of 5-HT1AR stimulated with the endogenous agonist 5-HT.**

According to experimental data available on the GPCR database (https://gproteindb.org/), 5-HT1AR favors Gαo over Gαi and Gαz (Kooistra et al., 2021; Pandy-Szekeres et al., 2022). In order to confirm this ranking order, we applied 100 µM of 5-HT on HEK293 cells transiently transfected with 5-HT1AR and each member of the Gαi/o/z protein family. Then, we quantitatively measured Gα protein activation via the same BRET assay described above as it allows to monitor G protein activation in real time (Hollins et al., 2009; Masuho et al., 2015). We observed that within sixty seconds, GαoA showed the highest amplitude which represents the highest efficacy measured as ΔBRET ratio followed by GαoB, Gαi2, Gαi1, Gαi3, and Gαz (Fig. 2A). For the purpose of evaluating potency and efficacy, we conducted concentration-response studies for each Gα protein in response to increasing concentrations of 5-HT ranging from 2 pM to 100
µM (Fig. 2B). Our analysis of potency and efficacy, measured as maximal ΔBRET ratio, suggest a preferential activation of Ga_o over Ga_i/z (Fig. 2C-D and Supplemental Table 1). However, caveats due to possible differences in individual Ga protein properties such as protein expression levels, endogenous expression of specific regulatory proteins (i.e. RGS proteins), or efficiency in terms of releasing Gβγ-venus do not allow a direct comparison. Later on, we will use the physiological ligand 5-HT as a reference to compare potency and efficacy of 5-HT1AR agonists. Taking in consideration that time to reach an equilibrium could affect maximal amplitude measurements especially at low concentration of agonist, we analyzed each condition over three minutes. We observed that the majority of Ga proteins produced the highest ΔBRET ratio within one minute, with the exception of Ga_z which still reached its highest amplitude within three minutes (Fig. 2E-F and Supplemental Fig. 2).

**Structurally diverse 5-TH1AR agonists produce different Ga protein coupling profiles.**

We hypothesized that structurally diverse 5-HT1AR agonists could elicit a ligand bias at the Ga protein level. To test this hypothesis, we examined nine agonists including clinically approved antidepressant agents and we compared them with the endogenous ligand 5-HT as a reference (Supplemental Fig. 3). Five of these compounds are reported to act as partial agonists on 5-HT1AR while 8-OH-DPAT and sumatriptan are reported to act as full agonists (Alexander et al., 2021). In addition, we included in our study a highly selective 5-HT1AR full agonist, F-15599 (also known as NLX-101) for which biased activity has been reported both *in vitro* and *in vivo* (Depoortere et al.,...
To ensure that the tested agonists do not activate any endogenous receptor, we transfected cells with pcDNA3.1 along with masGRK3CT-Nluc and G\(\beta\)1\(\gamma\)2-venus without 5-HT1AR. As expected, while we could measure in real time the activation of individual G\(\iota\)/o/z protein by 5-HT1AR (Supplemental Fig. 4A), we did not observe any signal in mock-transfected cells (Supplemental Fig. 4B). Similarly, we confirmed activation of each G\(\alpha\) subunit when using high concentrations of each selected agonist in our optimized G protein nanoBRET assay (Supplemental Fig. 4C-K). Next, we generated concentration-response curves, and we calculated efficacy (E\(_{\text{max}}\)) and potency (pEC50) for individual agonists with each of the six G\(\alpha\) proteins (Fig. 3A, Supplemental Fig. 5, and Table 1).

We first observed a wide range of efficacy values, ranging between 0-180% of 5-HT response. As expected, some drugs performed as partial agonists while others can be considered as full agonists. Interestingly, some agonists showed super agonistic properties for certain G proteins compared with the reference ligand. For instance, fibanserin, F-15599, 8-OH-DPAT, and vilazodone showed G\(\alpha\)oB maximum response ranging from 125% to 180% when compared to the endogenous ligand 5-HT. Overall, the application of six independent readouts, one for each G\(\alpha\) protein, revealed a multifaceted response otherwise difficult to appreciate. This data established that the most potent agonists other than 5-HT were vilazodone, F-15599, fibanserin, buspirone, and 8-OH-DPAT across G\(\alpha\) proteins. Interestingly, we also found that some agonists were not able to activate specific G\(\alpha\) proteins: for example, aripiprazole could not activate G\(\alpha\)1 while G\(\alpha\)3 was only activated at very high concentrations (over 100 \(\mu\)M).
Meanwhile, sumatriptan activates $G_\alpha_o$ but it only showed activation to $G_i$ at extremely high concentrations (Fig. 3; Supplemental Fig. 5).

**Ligand-dependent $G_\alpha$ protein signaling bias at 5-HT1AR.**

A formal analysis of signaling bias revealed the existence of two groups of 5-HT1AR agonists. After examining the signaling properties of the different ligands and calculating efficacy and potency (Fig. 3B-C), we evaluated a transduction coefficient as $\log(\frac{E_{\text{max}}}{EC_{50}})$ for each agonist (Fig. 3D). To comprehensively analyze similarities and differences among $G_\alpha$ protein activation patterns elicited by each agonist we applied a cluster analysis (Fig. 3D). Accordingly, our data revealed two groups of agonists: 1) 5-HT, F-15599, vilazodone, buspirone, 8-OH-DPAT, and flibanserin; and 2) vortioxetine, sumatriptan, nuciferine, and aripiprazole. Finally, with a Hill slope proximal to 1, we evaluated the bias factor, expressed as a $\Delta\Delta\log(\frac{E_{\text{max}}}{EC_{50}})$, produced by each agonist across $G_\alpha$ proteins after normalization to the reference 5-HT (Fig. 4). Agonists that did not reach the plateau for certain $G$ proteins were excluded from our bias calculations.

Using these data, we generated paired comparisons that suggest biased activation of a test $G_\alpha$ protein over a reference $G_\alpha$ (positive values), or the opposite (negative values). This set of data revealed for example that vilazodone, 8-OH-DPAT, nuciferine, sumatriptan, and aripiprazole have a bias toward $G_{\alpha_{oA/B}}$ over $G_{\alpha_{i1-3}}$ and $G_\alpha_z$. While, vortioxetine prefers $G_{\alpha_{i/z}}$ activation over $G_\alpha_o$. On the contrary, F-15599 and flibanserin reveal mixed activation between $G_\alpha_o$ and $G_{i/z}$. Both agonists show preference activation toward $G_{oB}$, $G_{i1}$ and $G_{i3}$ over $G_{oA}$, $G_{i2}$, and $G_z$ (Fig. 4). Collectively, we found that individual agonists showed unique $G_\alpha$ protein activation profiles.
**Discussion:**

In the last two decades, a great deal of effort has been put forward to understand ligand bias and functional selectivity between Gα proteins and β-arrestins (Eiger et al., 2022; Rankovic et al., 2016; Smith et al., 2018; Wisler et al., 2018). In fact, ligands that show biased properties hold the promise to be more effective and safer therapeutics (Gurevich and Gurevich, 2020). However, a limited number of studies investigated signaling bias within Gα proteins (Masuho et al., 2015; Von Moo et al., 2022; Voss et al., 2022). In this study, using the physiological ligand 5-HT as a reference, we showed that the action of structurally diverse 5-TH1AR agonists can be biased toward different Gαi/o/z family members. From the concentration-response curves obtained for ten 5-HT1AR agonists we were able to estimate EC50 and E_max for each one of six activated Gα proteins. Analyzing these data, we discovered that some 5-HT1AR ligands perform as super, full, or partial agonists when compared to the endogenous ligand 5-HT in their ability to trigger the release of specific Gα subunits. A striking example is the selective 5-HT1AR agonist F-15599 that acts as a super agonist in the activation of Gαi1, as a full agonist in the activation of GαoA, Gαi2, Gαi3, and Gαz, while it is a partial agonist in the activation of GαoB.

From these data, we calculated a bias factor that was later normalized over 5-HT to compare the relative activation of the six Gα proteins by each agonist (Fig. 4). For each agonist analyzed we generated 15 direct comparisons highlighting their specific preference toward the activation of individual G protein subtypes. This is extremely relevant because even Gα proteins sharing high degree of homology can activate
unique intracellular effectors generating distinct cellular responses. Indeed, studies on individual Gα protein knock out animals frequently revealed a lack of compensating mechanisms, supporting this notion (Jiang and Bajpayee, 2009; Jiang et al., 2001; Leck et al., 2004; Muntean et al., 2021; van den Buuse et al., 2007). More specifically, several studies on 5-HT1AR implicate the activation of such alternative signaling cascades both in vitro and in vivo. For instance, stimulation of 5-HT1AR in rat pituitary GH4C1 cells showed that Gαo, but not Gαi, inhibits calcium channels without affecting adenylyl cyclase (AC) function (Liu et al., 1999; Liu et al., 1994). On the other hand, 5-HT1AR activation in CHO transfected cells showed that Gαi2 and Gαi3 can activate Na+/H+ exchangers while Gαi1, Gαo, and Gαz cannot (Garnovskaya et al., 1997). In another study using antisense knock down of Gα proteins in CHO cells, it was demonstrated a preferential coupling of 5-HT1AR with Gαi3 rather than Gαi2 in suppressing cAMP levels (Rauly-Lestienne et al., 2011). Additionally, in vivo data revealed that treating rats with PTX, which inactivate all Gαi/o family members with the exception of Gαz, followed by treatments with 5-HT1AR agonist 8-OH-DPAT, elevated ACTH and oxytocin levels compared to control rats, while an antisense-induced decrease in hypothalamic Gαz levels dramatically inhibited oxytocin and ACTH responses to 8-OH-DPAT (Serres et al., 2000). Finally, studies on G protein control over individual AC isoforms established unique patterns of inhibition by each Gαi/o/z family member (Ostrom et al., 2022; Sadana and Dessauer, 2009). Altogether, the activation of unique effectors downstream of highly similar Gα proteins could generate signaling bias explaining distinctive cellular responses.
Region- and cell-specific patterns of expression of Gα protein subunits may also lead to differential cellular responses induced by activation of the same receptor. In this context, it has been shown that in the brain 5-HT1A exists as an autoreceptor in serotonergic neurons of the raphe nuclei and as a heteroreceptor in cortical and hippocampal regions (Altieri et al., 2013; You et al., 2016). In ex-vivo experiments, 8-OH-DPAT failed to inhibit forskolin-induced cAMP accumulation in serotonergic neurons in the dorsal raphe nucleus, while buspirone effectively showed a concentration-dependent inhibition of cAMP accumulation (Valdizan et al., 2010) confirming previous reports (Clarke et al., 1996; Johnson et al., 1997). Importantly, while buspirone acts as a full agonist on autoreceptors inhibiting the synthesis of 5-HT and neuronal firing, it behaves as a partial agonist at postsynaptic receptors in cortex and hippocampus (Shireen and Haleem, 2005). On the contrary, it was shown that the compound F-15599 preferentially acts on postsynaptic receptors located in the frontal cortex over somatodendritic 5-HT1A autoreceptors (Llado-Pelfort et al., 2010; Newman-Tancredi et al., 2009). Slope values of concentration-responses curves differed between frontal cortex and raphe nuclei suggesting an underlying mechanism that relies on the preferential activation of selected Gα proteins in different brain regions (Newman-Tancredi et al., 2022; Valdizan et al., 2010). In this context, our data showed that F-15599 is biased to Gαoα, Gαi1, and Gαi3, while buspirone is biased to Gαo and Gαi2 suggesting that these two agonists may mediate distinctive effects at presynaptic and postsynaptic sites because of their intrinsic Gα protein bias. Altogether, these results suggest the existence of a Gα protein-dependent ligand bias at 5-HT1A auto- and hetero-receptors in native brain tissue.
Agonist bias towards selected G protein subfamilies can result in distinguished and unique cellular responses involved in the therapeutic outcome as well as side effects. For instance, it was demonstrated that Gβγ proteins released by Gαo preferentially activate GIRK channels compared to Gαi (Anderson et al., 2020; Sadja and Reuveny, 2009; Zhang et al., 2002). As a consequence, drugs that are biased to Gαo could impact the activation of these channels which could lead to unique physiological or pathological responses. Our data shows that aripiprazole and sumatriptan activation of 5-HT1AR is biased towards Gαo compared to Gαi. This may result in unique properties of these drugs including adverse effects that involve the activation GIRK channels.

Overall, a full understanding of the molecular implications of ligand bias toward Gα protein subtypes will require further investigations at multiple receptors. This information will possibly address conflicting observations obtained both in vitro and in vivo and will guide drug development toward safer and more effective therapeutics.

Data Availability Statement:
All processed data that support the findings of this study are available within the paper and its supplemental data. Raw data are available from the corresponding author upon request.

Author Contributions:
Participated in research design: Alabdali, Franchini, Orlandi
Conducted experiments: Alabdali, Franchini
Contributed new reagents or analytic tools: Alabdali, Franchini
Performed data analysis: Alabdali

Wrote or contributed to the writing of the manuscript: Alabdali, Orlandi
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Footnotes

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Figure Legends

Figure 1. 5-HT1AR stimulation in a BRET-based assay. (A) Cartoon illustration of cell-based BRET assay. GPCR stimulation triggers the dissociation of heterotrimeric G proteins leading to changes in the BRET signal that represents an index of GPCR activation. To limit artifacts due to the modification of Gα proteins, this system was developed by fusing the donor luciferase with an effector of Gβγ (masGRK3-CT-nluc), and a split acceptor, venus, fused with Gβ1 and Gγ2 subunits, allowing the use of wild type Gα subunits. (B) Representative traces obtained by applying 100 µM 5-HT on HEK293 cells transfected with 5-HT1AR and each one of Gs, Gq, G13, G15, and Go proteins. Recording started 10 seconds before agonist application to obtain a basal BRET signal. ΔBRET ratio was calculated by subtraction of the basal BRET at each time point.

Figure 2. Pharmacological characterization of 5-HT1AR. (A) Representative ΔBRET ratio responses after application of 100 µM 5-HT for each Gαi/o/z family member. Basal BRET ratio was measured for 10 seconds before agonist application. (B) Concentration-response curves of different Gα proteins after 5-HT application. Each data point represents the mean ± S.D. (n = 5 independent replicates). (C) Potency (pEC50) obtained from concentration-response curves for each Gα protein. Each bar graph represents the mean ± S.D. (n = 5 independent replicates). (D) Efficacy (E_max) reported as quantified ΔBRET ratio for different Gα proteins. Each bar graph represents the mean ± S.D. (n = 5 independent replicates). (E-F) Representative curves showing the
concentration-dependent increase in ΔBRET ratio over time for Gαo and Gαz recorded over three minutes. Increasing 5-HT concentrations are represented by darker colors ranging from 2 pM (lighter) to 100 µM (darker). ***P<0.001, **P <0.01, and *P<0.05 determined by one-way ANOVA and Tukey post hoc test (n = 5). Color code: red * indicates comparison with GαA; dark blue * indicates comparison with GαB; pink * indicates comparison with Gι2; purple * indicates comparison with Gι3; cyan * indicates comparison with Gz.

Figure 3. Concentration-response curves and activation heatmaps for each Gα protein obtained with different 5-HT1AR agonists. (A) Full concentration-response curves for each of the ten indicated 5-HT1AR agonists with each of the six Gαi/o/z proteins. Each data point represents the mean ± S.D. (n = 5-10 independent replicates). (B) Efficacy values reported as maximal ΔBRET ratio (E_{max}) for each 5-HT1AR agonist using the activation of the six Gα proteins as readout. Colors represents the mean E_{max} value according to the color-coded scale reported to the right (n = 5-10 independent replicates). (C) Potency reported as pEC50 values for each agonist/Gα protein pair. Colors represents the mean pEC50 value according to the color-coded scale reported to the right (n = 5-10 independent replicates). (D) Both values were used to calculate the transduction coefficient as Log(E_{max}/EC50) and to cluster the ten agonists according to their profile of G protein activation. Colors represent the Log(E_{max}/EC50) value according to the color-coded scale reported to the right.
Figure 4. Heatmaps of the bias factor for structurally diverse agonists with different Gα proteins subtypes. For each agonist, the $E_{\text{max}}/EC_{50}$ values were normalized to the $E_{\text{max}}/EC_{50}$ value of the reference ligand 5-HT. Positive values indicate a bias toward the tested Gα protein, while negative values represent a bias toward the reference Gα protein. Each panel represent an individual agonist: (A) 8-OH-DPAT (B) buspirone (C) aripiprazole (D) flibanserin (E) nuciferine (F) sumatriptan (G) vilazodone (H) vortioxetine, and (I) F-15599. Color-coded scale reported to the right of each panel (n = 5-10 independent replicates).
<table>
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<td>GoB</td>
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<td>6.59 ± 0.46</td>
</tr>
<tr>
<td></td>
<td>Gi1</td>
<td>0.045 ± 0.002</td>
<td>6.52 ± 0.07</td>
</tr>
<tr>
<td></td>
<td>Gi2</td>
<td>0.060 ± 0.007</td>
<td>6.86 ± 0.09</td>
</tr>
<tr>
<td></td>
<td>Gi3</td>
<td>0.042 ± 0.005</td>
<td>6.78 ± 0.06</td>
</tr>
<tr>
<td></td>
<td>Gz</td>
<td>0.061 ± 0.006</td>
<td>6.36 ± 0.06</td>
</tr>
<tr>
<td>8-OH-DPAT</td>
<td>GoA</td>
<td>0.084 ± 0.020</td>
<td>7.33 ± 0.20</td>
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<tr>
<td></td>
<td>GoB</td>
<td>0.070 ± 0.008</td>
<td>7.14 ± 0.06</td>
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<tr>
<td></td>
<td>Gi1</td>
<td>0.032 ± 0.002</td>
<td>6.68 ± 0.18</td>
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<tr>
<td></td>
<td>Gi2</td>
<td>0.054 ± 0.016</td>
<td>7.05 ± 0.18</td>
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<tr>
<td></td>
<td>Gi3</td>
<td>0.032 ± 0.003</td>
<td>6.77 ± 0.12</td>
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<tr>
<td></td>
<td>Gz</td>
<td>0.053 ± 0.015</td>
<td>6.70 ± 0.19</td>
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<tr>
<td>Buspirone</td>
<td>GoA</td>
<td>0.050 ± 0.006</td>
<td>6.57 ± 0.10</td>
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<tr>
<td></td>
<td>GoB</td>
<td>0.025 ± 0.004</td>
<td>6.97 ± 0.09</td>
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<td>Gi1</td>
<td>0.011 ± 0.003</td>
<td>7.20 ± 0.20</td>
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<td>0.017 ± 0.005</td>
<td>7.33 ± 0.19</td>
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<tr>
<td></td>
<td>Gi3</td>
<td>0.012 ± 0.007</td>
<td>6.66 ± 0.87</td>
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<tr>
<td></td>
<td>Gz</td>
<td>0.024 ± 0.006</td>
<td>6.85 ± 0.18</td>
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<tr>
<td>Aripiprazole</td>
<td>GoA</td>
<td>0.032 ± 0.009</td>
<td>5.88 ± 0.21</td>
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<td>GoB</td>
<td>0.020 ± 0.005</td>
<td>5.76 ± 0.28</td>
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<tr>
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<td>Gi2</td>
<td>0.013 ± 0.001</td>
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<tr>
<td></td>
<td>Gi3</td>
<td>0.020 ± 0.002</td>
<td></td>
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<tr>
<td>Flibanserin</td>
<td>GoA</td>
<td>0.078 ± 0.019</td>
<td>6.77 ± 0.14</td>
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<tr>
<td></td>
<td>GoB</td>
<td>0.097 ± 0.008</td>
<td>6.93 ± 0.12</td>
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<td>Gi1</td>
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<td>5.96 ± 0.38</td>
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<tr>
<td></td>
<td>Gi2</td>
<td>0.054 ± 0.013</td>
<td>6.13 ± 0.23</td>
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<td>Gi3</td>
<td>0.059 ± 0.010</td>
<td>6.08 ± 0.19</td>
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<td>Gz</td>
<td>0.070 ± 0.008</td>
<td>5.91 ± 0.32</td>
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Table 1. Efficacy and potency values of indicated 5-HT1AR agonists acting on each Goα/β/γ protein. Each value represents the mean ± S.D. of 5-10 independent replicates.
Figure 1

A

5-HT1AR agonists
5-HT

Gα

GRKct

Nuc

Venus

ΔBRET ratio

Time (s)

B

ΔBRET ratio

Time (s)

Gα

Gβ

Gγ

Gq

G13

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Figure 2
Figure 3

A

[B] %BRET ratio (Normalized to 5-HT)

G<sub>G0A</sub>

5-HT
8-OH-DPAT
Buspirone
Aripiprazole
Filbanserin
Nuciferine

G<sub>G0B</sub>

Sumatriptan
Vilazodone
Vortioxetine
F-15599

G<sub>G1</sub>

G<sub>G2</sub>

G<sub>G3</sub>

B

E<sub>max</sub>

SHT
DPAT
Bus
Arip
Flib
Nuci
Suma
Vila
Vort
F-15599

C

pEC50

5-HT
DPAT
Bus
Arip
Flib
Nuci
Suma
Vila
Vort
F-15599

D

Log(E<sub>max</sub>/EC50)

Vila
Suma
Vort
F-15599

F-15599
Figure 4