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# Positive Allosteric Modulators of Glycine Receptors and Their Potential Use in Pain Therapies

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**Abstract**—Glycine receptors are ligand-gated ion channels that mediate synaptic inhibition throughout the mammalian spinal cord, brainstem, and higher brain regions. They have recently emerged as promising targets for novel pain therapies due to their ability to produce antinociception by inhibiting nociceptive signals within the dorsal horn of the spinal cord. This has greatly enhanced the interest in developing positive allosteric modulators of glycine receptors. Several pharmaceutical companies and research facilities have attempted to identify new therapeutic leads by conducting large-scale screens of compound libraries, screening new derivatives from natural sources, or synthesizing novel compounds that mimic endogenous compounds with antinociceptive activity. Advances in structural techniques have also led

to the publication of multiple high-resolution structures of the receptor, highlighting novel allosteric binding sites and providing additional information for previously identified binding sites. This has greatly enhanced our understanding of the functional properties of glycine receptors and expanded the structure activity relationships of novel pharmacophores. Despite this, glycine receptors are yet to be used as drug targets due to the difficulties in obtaining potent, selective modulators with favorable pharmacokinetic profiles that are devoid of side effects. This review presents a summary of the structural basis for how current compounds cause positive allosteric modulation of glycine receptors and discusses their therapeutic potential as analgesics.

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**Significance Statement**—Chronic pain is a major cause of disability, and in Western societies, this will only increase as the population ages. Despite the high level of prevalence and enormous socioeconomic burden incurred, treatment of chronic pain remains limited as it

is often refractory to current analgesics, such as opioids. The National Institute for Drug Abuse has set finding effective, safe, nonaddictive strategies to manage chronic pain as their top priority. Positive allosteric modulators of glycine receptors may provide a therapeutic option.

## I. Introduction

Glycine receptors (GlyRs) are anion channels that mediate inhibitory neurotransmission within the spinal cord and brain stem (Baer et al., 2009; Lynch, 2009). They belong to a class of structurally related pentameric ligand-gated ion channels (pLGICs) commonly known as Cys-loop receptors, which also includes the mammalian  $\gamma$ -aminobutyric subtype A receptors (GABA<sub>A</sub>Rs), nicotinic acetylcholine receptors (nAChRs), and serotonin type 3 receptors. It also includes nonmammalian channels, such as the bacterial *Gleobacter* (GLIC) and *Erwinia* (ELIC) channels and the invertebrate glutamate-gated Cl<sup>-</sup> channel (GluCl) (Jaiteh et al., 2016). The Zn<sup>2+</sup>-activated chloride channel is also a Cys-loop receptor; however, it shares <15% amino acid sequence identity with other Cys-loop receptors and is the least understood receptor of this class (Trattig et al., 2016).

Within the mammalian genome, four genes have been identified that encode GlyR  $\alpha$ -subunits ( $\alpha_1$ – $\alpha_4$ , ~48 kDa) and a single gene encoding the  $\beta$ -subunit (58 kDa) (Grudzinska et al., 2005). The  $\alpha$ -subunits have high sequence homology (>90%), with variances occurring mainly within the large intracellular domain (ICD) and transmembrane domain 4 (TM4). These subunits combine to form pentameric homomers comprised of only  $\alpha$ -subunits or heteromers, which also incorporate the  $\beta$ -subunit; however, the stoichiometry of heteromeric receptors remains a contested topic. Previously, a 2 $\alpha$ :3 $\beta$  stoichiometry had been accepted (Grudzinska et al., 2005; Burgos et al., 2016); however, recent structural analysis supports a 4 $\alpha$ :1 $\beta$  stoichiometry and suggests the incorporation of more than one  $\beta$ -subunit would occlude the Cl<sup>-</sup> channel (Yu et al., 2021; Zhu and Gouaux, 2021). Although it is possible for  $\beta$ -subunits to form homomeric receptors (5 $\beta$ ), they are considered nonfunctional due to their extremely low conductance and agonist affinity (Grenningloh et al., 1990; Handford et al., 1996), which is consistent with the recent structural findings. The  $\beta$ -subunit also contains a binding motif that allows it to anchor to the scaffolding protein gephyrin (Meyer et al., 1995). This causes

heteromeric receptors to form synaptic clusters, which are responsible for fast synaptic neurotransmission (Baer et al., 2003), whereas homomeric receptors diffuse into the extrasynaptic space to mediate tonic-inhibitory activity (McCracken et al., 2017) or may be expressed on presynaptic terminals to regulate neurotransmitter release (Jeong et al., 2003).

Each subunit has a distinct expression pattern throughout the nervous system, which governs their physiologic functions. The  $\beta$ -subunit is required for synaptic clustering and is widely expressed throughout the central nervous system (Malosio et al., 1991a; Weltzien et al., 2012), whereas the expression of the  $\alpha$ -subunits is more limited. GlyR $\alpha_2$  are highly expressed during embryonic stages and play a key role in development (Avila et al., 2013); however, their expression levels decline sharply after birth and are replaced with GlyR $\alpha_1$  (Becker et al., 1988; Lynch, 2009). Receptors containing the  $\alpha_1$ -subunit are the predominant adult form, which are expressed widely throughout the nervous system and have critical roles in motor control, somatosensation, and respiration (Baer et al., 2003; Baer et al., 2009; Lynch, 2009; Liu and Wong-Riley, 2013). Alternative splicing of the  $\alpha_1$  subunit has been shown to occur, which results in the insertion of 8-amino acid residues into the ICD ( $\alpha_1^{\text{ins}}$ ). This variant has a more restricted expression within the spinal cord, where it constitutes a large portion of the GlyRs present (Malosio et al., 1991b). GlyR $\alpha_3$  also have a reduced distribution and are primarily located in the retina, auditory brainstem, and the dorsal horn of the spinal cord (Baer et al., 2009; Burgos et al., 2016). Alternative splicing of the  $\alpha_3$  subunit also occurs, which inserts 15-amino acid residues into the ICD ( $\alpha_{3L}$ ) and greatly impacts receptor kinetics (Nikolic et al., 1998; Breitingner et al., 2009). The GlyR $\alpha_4$  is a pseudogene that is not expressed in humans due to a premature stop codon; however, it is suggested to occur in other vertebrates (Harvey et al., 2000; Aguayo et al., 2004; Leacock et al., 2018).

### A. Glycine Receptors and Pain

GlyRs containing the  $\alpha_1$  and  $\alpha_3$  subunits are highly expressed within the dorsal horn of the spinal cord

**ABBREVIATIONS:** 5-HT<sub>3</sub>R, serotonin type 3 receptor; CB1, cannabinoid receptor type 1; CB2, cannabinoid receptor type 2; CBD, cannabidiol; CNS, central nervous system; cryoEM, cryogenic electron microscopy; DD-THC,  $\Delta^9$ -tetrahydrocannabinol analogue with both oxygen groups removed; DH-CBD, cannabidiol with 3' hydroxyl group removed; DSPC, 1, 2-distearoyl-sn-glycero-3-phosphocholine; ECD, extracellular domain; ELIC, *Erwinia* ion channel; GABA<sub>A</sub>R,  $\gamma$ -aminobutyric subtype A receptors; GLIC, *Gleobacter* ion channel; GluCl, glutamate-gated chloride channel; GlyR, glycine receptor; GlyT2, glycine transporter type 2; ICD, intracellular domain; MBN, N-methylated ICS-205, 930; MD, molecular dynamic; nAChR, nicotinic acetylcholine receptor; NAGly, N-arachidonoyl glycine; PAM, positive allosteric modulator; PGE<sub>2</sub>, prostaglandin E2; PKC, protein kinase C; pLGIC, pentamer ligand gated ion channel; POPC, palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine; THC,  $\Delta^9$ -tetrahydrocannabinol; TM4, transmembrane domain 4; Tropicsetron, ICS-205, 930; TRPV1, transient receptor potentiation cation channel subfamily V member 1.

and have been implicated in nociceptive signaling (San Martín et al., 2022). They are expressed on inhibitory interneurons, where they mediate somatosensory signals and prevent overactivation of the nociceptive pathway (Cronin et al., 2004; Baer et al., 2009). However, injury and prolonged inflammation can sensitize these neurons by reducing glycinergic neurotransmission (Zeilhofer and Zeilhofer, 2008) and therefore allow the activation of nociceptive protein kinase C (PKC)- $\gamma$  neurons, which causes allodynia (Miraucourt et al., 2007). Allodynia and other nociceptive pain-related symptoms can also be evoked experimentally by the GlyR antagonist strychnine (Yaksh, 1989), whereas intrathecal injection of glycine reduces nociceptive sensitivity in neuropathic pain models (Simpson et al., 1996). This links the degree of nociceptive sensitivity to GlyR activity within the spinal cord.

Chronic pain symptoms have been associated with reduced GlyR expression within the spinal cord (Simpson and Huang, 1998), which is suggested to occur through inflammatory-mediated mechanisms (Harvey et al., 2004; Chen et al., 2012). Several studies have demonstrated a persistent upregulation of cyclooxygenase enzymes, prostaglandin E<sub>2</sub> (PGE<sub>2</sub>), and PGE receptors in response to nociceptive pain and during chronic pain conditions (Ma and Eisenach, 2003; Ma and Quirion, 2008; Ma et al., 2010). In rodent models, intrathecal injection of PGE<sub>2</sub> produces hypersensitivity in a timeframe that directly correlates to reduced expression of GlyR $\alpha_1$  and GlyR $\alpha_3$  in spinal slices (Wang et al., 2018). This is due to the upregulation of PGE<sub>2</sub> causing excess activation of PGE receptors on postsynaptic lamina II neurons, which induces GlyR $\alpha_3$  phosphorylation, internalization, and degradation (Ahmadi et al., 2002; Harvey et al., 2004; Zeilhofer, 2005; Velázquez-Flores and Salceda, 2011). Intracellular phosphorylation of GlyR $\alpha_3$  also elicits global structural changes, including conformational changes within the agonist binding site (Han et al., 2013), which may be responsible for their decreased conductance (Moraga-Cid et al., 2020). Similarly, GlyR $\alpha_1^{\text{ins}}$  expressed within the spinal cord have been shown to undergo inflammatory-mediated phosphorylation, resulting in endocytosis of the receptor and reduced glycinergic neurotransmission (Huang et al., 2007; Zhang et al., 2019a). Additionally, reversing this process through dephosphorylation has been shown to provide antinociception in inflammatory pain conditions (Diao et al., 2020). Intracellular phosphorylation of GlyRs can also disrupt gephyrin binding (Specht et al., 2011). This prevents GlyRs from forming synaptic clusters and instead causes them to diffuse into the extracellular space (Specht et al., 2011; Cantaut-Belarif et al., 2017), which may contribute to the reduced synaptic GlyR expression and overall reductions in glycinergic neurotransmission.

GlyR $\alpha_2$  are considered to be an embryonic form of GlyR as they are predominantly expressed during

prenatal stages, and their expression levels decline sharply after birth (Becker et al., 1988; Malosio et al., 1991a; Lynch, 2009). They are not usually expressed with the adult spinal cord; however, expression within the dorsal horn of the spinal cord has been observed in rat models of chronic pain (Imlach et al., 2016). GlyR $\alpha_2$  have slower activation kinetics and cannot be activated by rapid neurotransmitter release (Mangin et al., 2003). This makes them unable to participate in nociceptive signaling, and thus, their expression reduces glycinergic input onto lamina II neurons (Imlach et al., 2016). Overall, these findings suggest that a reduction of glycinergic neurotransmission within the spinal cord is a causative factor in chronic pain symptoms. Re-establishing the balance between excitatory and inhibitory signaling within the spinal cord by strengthening neural inhibition may alleviate chronic pain symptoms (Tanabe et al., 2008). One way of achieving this is through positive modulation of GlyRs.

### *B. Structure and Function of Glycine Receptors*

Cys-loop receptors are composed of five pseudo-symmetrically arranged subunits that enclose an aqueous channel pore. Each subunit consists of a large extracellular domain containing a series of flexible loops and twisted  $\beta$ -sheets, followed by four TM domains (TM1–TM4). The TM domains are aliphatic  $\alpha$ -helices that form concentric rings around the channel pore to isolate it from the lipid bilayer (Burgos et al., 2016). The inner ring is lined by TM2 domains that form the pore of the ion channel and determine its ion selectivity (Breitinger and Becker, 2002; Keramidis et al., 2002; Harpole and Grosman, 2019). The TM2 domains are enclosed by a ring of alternating TM1 and TM3 domains, which make minor contacts with the lipid membrane. This is followed by the hydrophobic TM4 domains, which extend outward from the channel and form the predominant interface between the protein and lipid environment (Henault et al., 2015). The TM domains are linked by short, flexible loops, with the exception of the TM3-TM4 loop, which is a large, dynamic intracellular loop that forms the ICD.

The orthosteric binding pocket is located within the center of the extracellular domain (ECD) at the interface between adjacent subunits. The binding cavity is shaped by a series of bulky and aromatic residues from loop B (F159, Y161) and loop C (Y202, F207) of the primary subunit (+) and from loop D (F63) and loop E (L117) of the complementary subunit (-). Functional and structural studies have also highlighted important residues S129(-), R65(-), and T204(+) within these loops that directly bind with the carboxyl group of the glycine molecule (Vandenberg et al., 1992; Breitinger and Becker, 2002; Kumar et al., 2020). This forms five distinct agonist binding pockets on each receptor, although occupation of two or more of these sites is sufficient for receptor activation (Grewer, 1999; Gentet and Clements, 2002). This pocket is able to accommodate the primary agonist glycine and partial agonists

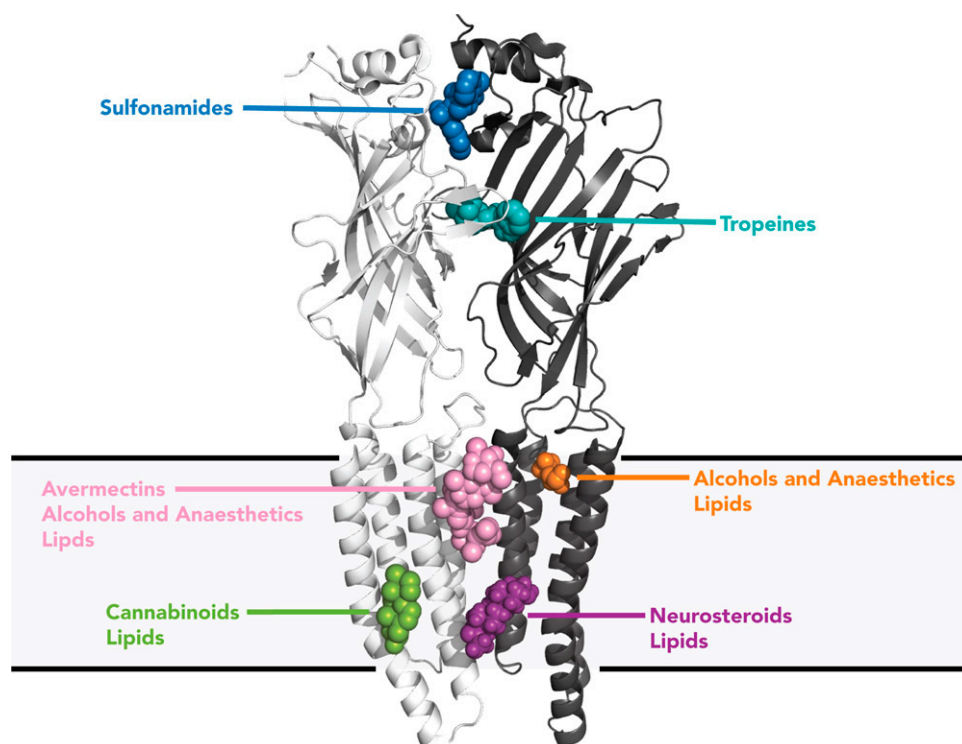
$\beta$ -alanine, taurine, and GABA (Horikoshi et al., 1988; Yu et al., 2021a,b), as well as the GlyR antagonist strychnine (Du et al., 2015). Agonist binding causes a large inward “capping” movement of loop C toward the binding pocket, which induces a reorientation of many ECD loops. In particular, the conserved  $\beta 6$ - $\beta 7$  (cys-loop) and  $\beta 1$ - $\beta 2$  loop at the lower portion of the ECD, which interact with the TM2-TM3 linker to signal agonist binding through to the TM domains (Soh et al., 2017; Yu et al., 2021). This causes TM2 to rotate clockwise about the channel’s axis, which moves the pore lining L261 residues away from the center of the channel and produces an overall expansion of the TM domains (Kumar et al., 2020). This increases the channel radius from 1.4 Å to 4-5 Å, which is sufficient for hydrated and dehydrated Cl<sup>-</sup> ions (3.3 Å and 1.8 Å, respectively) to pass through the channel (Du et al., 2015). Activation of GlyRs cause an influx of Cl<sup>-</sup> that hyperpolarizes the postsynaptic neuron and elicits neural inhibition (Dutertre et al., 2012). After prolonged exposure to high concentrations of agonist, GlyRs will undergo desensitization, where the degree of ionic flux will decay despite the continued presence of the agonist to prevent overactivation (Wang and Lynch, 2011; Kumar et al., 2020). Desensitization of other inhibitory pLGICs has been shown to impact receptor phosphorylation, expression, and the overall efficacy of inhibitory synapses through the induction of long-term potentiation (Field et al., 2021).

Molecular dynamic (MD) simulations, cryogenic electron microscopy (cryoEM), and crystallography techniques

have also identified allosteric binding sites within the ECD, as well as intra- and intersubunit cavities within the TM domains (Fig. 1) (Cerdan et al., 2020; Thompson and Baenziger, 2020). Many analogous studies were originally conducted using the invertebrate GluCl (Hibbs and Gouaux, 2011; Althoff et al., 2014) or the bacterial GLIC (Bocquet et al., 2009; Nury et al., 2011) and ELIC (Henault et al., 2019; Tong et al., 2019) channels; however, recent advances have allowed the use of mammalian channels. These structures have indicated a high degree of conservation of these allosteric binding cavities among cys-loop receptors. In particular, structures of GlyR $\alpha_1$  (Du et al., 2015) and GlyR $\alpha_3$  (Huang et al., 2017) have highlighted the conservation of an intersubunit cavity toward the intracellular portion of the TM domains, which was previously identified in GluCl (Hibbs and Gouaux, 2011; Althoff et al., 2014). Despite the high level of conservation and common binding mechanisms, many of these sites produce diverse effects due to subtle differences in subunit composition.

## II. Positive Allosteric Modulators of Glycine Receptors

Despite GlyRs being highlighted as a promising target for novel nociceptive pain therapeutics, there are no currently approved positive allosteric modulators (PAMs) for this purpose. Chronic pain continues to be treated with medications such as opioids, antidepressants, anticonvulsants, and nonsteroidal anti-inflammatory drugs (Moulin et al., 2014; Cioffi, 2018; Ho et al., 2018; Shaheed et al.,



**Fig. 1.** Binding sites of positive allosteric modulators on the glycine receptor. Sulfonamides (blue) and tropeines (teal) bind within extracellular domain of the glycine receptor between adjacent subunits. The primary subunit is shown in white, and the complementary subunit is shown in black. Within the transmembrane domains there are four cavities that have been shown to bind lipids and lipophilic modulators, including neurosteroids (purple), cannabinoids (green), avermectins (pink), alcohols, and anesthetics (pink and orange). Black lines indicate the lipid membrane.

2020), which are often inadequate for providing pain relief (Dworkin et al., 2010) or have significant side effects and potential for abuse (Hojsted et al., 2010; <https://www2.deloitte.com/au/en/pages/economics/articles/cost-pain-australia.html>). This has enhanced the interest of pharmaceutical companies to identify novel PAMs of GlyRs (Stead et al., 2016; Bregman et al., 2017) and the development of “The Glycine Receptor Allosteric Ligands Library” (Cerdan et al., 2020) to aid in this process.

There are several known classes of modulators for GlyRs; however, many of these are not efficacious *in vivo* due to their nonselective nature (Xiong et al., 2012a; Yang, 2012; Chandler, 2018). It is particularly difficult to obtain selectivity over other cys-loop receptors due to their high degree of structural similarity (Chesnoy-Marchais, 1996; Chesnoy-Marchais et al., 2000). On-target side effects are also predicted to arise due to the widespread distribution of GlyRs throughout the nervous system (Schmid et al., 1991; Baer et al., 2009), requiring further selectivity for specific GlyR subunits, which is difficult to achieve. Additionally, many of these modulators tend to have a poor pharmacokinetic profile and are highly lipophilic (Yang et al., 2008; Gallagher et al., 2020), thus making them unsuitable for pharmaceutical application.

However, the recent advances in structural biology techniques have helped elucidate novel allosteric binding sites and provided additional information for sites previously identified (Huang et al., 2017a,b; Yu et al., 2021a). This has greatly enhanced our understanding of receptor functionality and has opened up new avenues of research, which allow for structure-based optimization of known pharmacophores or the design of new PAMs based on novel binding sites. This review will assess the structure activity relationships developed for known PAMs of GlyRs and evaluate their therapeutic potential as analgesics in light of the new structural and functional information available.

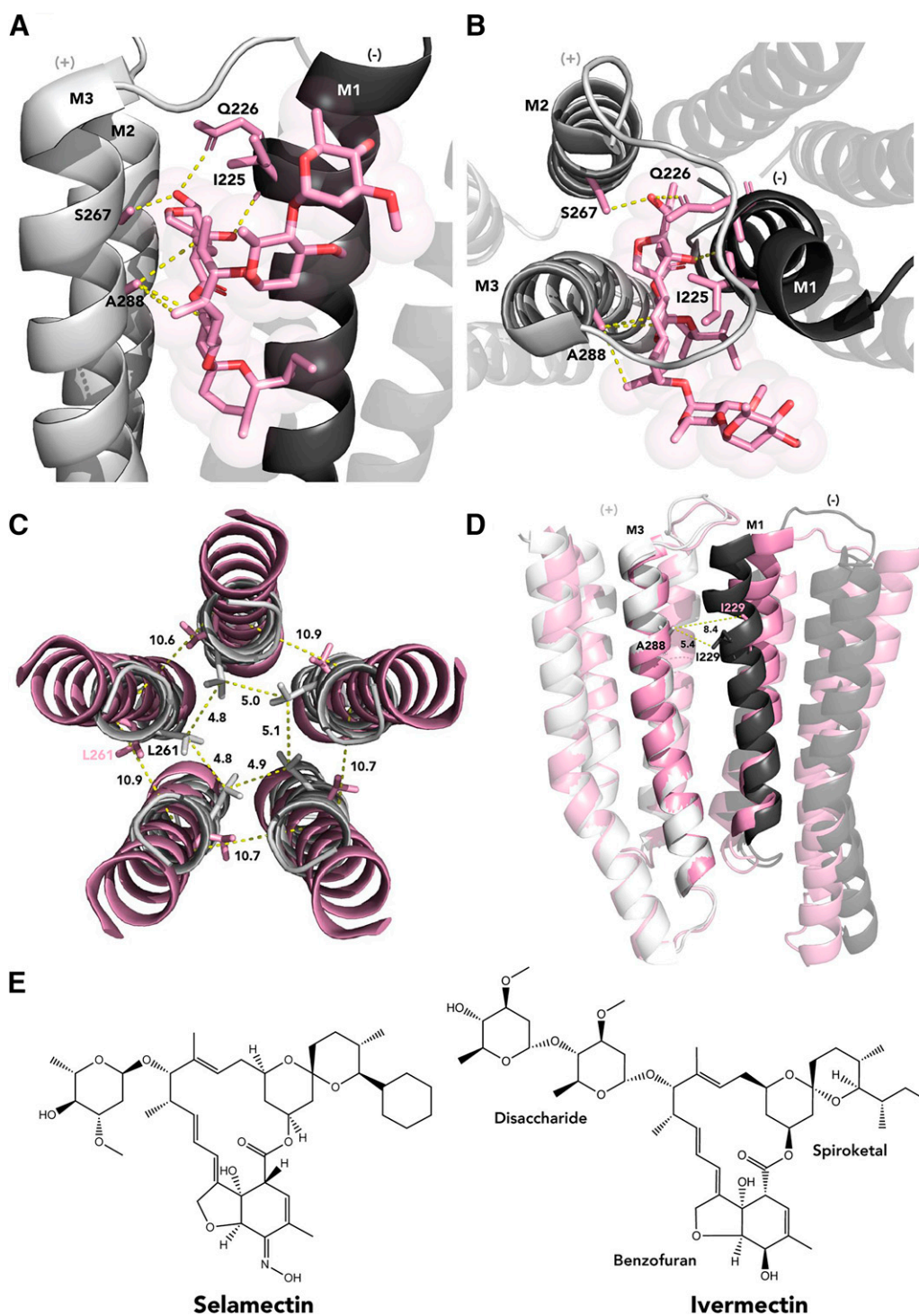
### A. Avermectins

Avermectins are a family of 16-membered macrocyclic lactones synthesized by the soil bacterium *Streptomyces avermitilis*. They were originally isolated and characterized by Merck, leading to the development of several avermectin compounds, which became commercially available due to their anthelmintic, insecticidal, and acaricidal activity (Jansson and Dybas, 1998). Avermectins were found to enhance Cl<sup>-</sup> conductance and were sensitive to picrotoxin, which suggested they act at GABA<sub>A</sub>Rs (Fritz et al., 1979). This was later expanded to other Cl<sup>-</sup>-conducting pLGICs including the GlyR and GluCl (Vassilatis et al., 1997b), which are also sensitive to avermectins (Vassilatis et al., 1997a; Dawson et al., 2000; Shan et al., 2001). Despite their low selectivity, avermectins are relatively safe for commercial use as they have lower potencies at mammalian channels

and are unable to readily cross the blood-brain barrier (Yang, 2012; Chandler, 2018). They are also used therapeutically to treat inflammatory rosacea and neglected topical diseases (Omura and Crump, 2014; Kircik et al., 2016).

One of the most well studied of the family is ivermectin, which is an anthelmintic compound that acts as a potent, allosteric agonist at the GluCl channel (Huang et al., 2017) and is a dual partial allosteric agonist and PAM of GlyRs. At concentrations as low as 30 nM, ivermectin selectively potentiates glycinergic currents evoked by low glycine concentrations (Shan et al., 2001; Lynagh et al., 2011). However, between 0.3 and 30 μM, it exhibits dual functions and additionally acts as a pseudo-irreversible partial allosteric agonist. Ivermectin induces a slow activation of the channel and achieves maximal currents that are approximately 78% of a maximal glycine current (Shan et al., 2001; Lynagh and Lynch, 2010; Lynagh et al., 2011). Ivermectin was suggested to work through a novel mechanism distinct from the glycine binding site as ivermectin-activated currents were not impacted by mutations within the orthosteric binding pocket and could not be inhibited by high levels of zinc or picrotoxin (Shan et al., 2001).

Mutagenesis studies predicted ivermectin binding at the interface between the ECD and the upper region of TM domains, involving residues from the TM2-TM3 loop, the conserved cys-loop ( $\beta 6$ - $\beta 7$  loop), and the  $\beta 1$ - $\beta 2$  loop (Lynagh and Lynch, 2010; Lynagh et al., 2011). Ivermectin's agonist activity correlated to the side-chain volume at position 288 within TM3 (GlyR $\alpha_1$  numbering). This is an alanine in GlyRs and some GABA<sub>A</sub>Rs, which are less sensitive to ivermectin activity, and a glycine residue in GluCl and other highly sensitive channels within parasites and nematodes (Lynagh and Lynch, 2010). Making the reverse mutation in GlyR $\alpha_1$  to reduce steric bulk (A288G) significantly enhances ivermectin sensitivity, whereas mutation to a bulkier phenylalanine (A288F) abolishes ivermectin's agonist activity (Lynagh et al., 2011). The 288 position was predicted to occur at the mouth of the binding cavity, and thus, larger residues would occlude binding. These findings were later confirmed by crystal structures of ivermectin bound to the GluCl channel (Hibbs and Gouaux, 2011) and the human GlyR $\alpha_3$  (Huang et al., 2017) and cryoEM structures of ivermectin bound to the zebrafish GlyR $\alpha_1$  (Du et al., 2015; Kumar et al., 2020). In all three structures, ivermectin binds to an intersubunit cavity in the upper portion of the TM domains (Fig. 2), which has also been shown to bind lipids (Althoff et al., 2014). The benzofuran group of ivermectin is responsible for the majority of binding interactions as it interchelates between TM3(+) and TM1(-) of adjacent subunits and inserts deeply into the cavity, making contacts with the pore lining TM2(+). The spiroketal and the disaccharide groups make some hydrophobic interactions with the TM domains; however, they primarily



**Fig. 2.** Avermectin binding to the glycine receptor. Ivermectin (pink) binding within the upper intersubunit cavity of glycine receptors viewed from (A) the membrane and (B) the top down. The hydroxyl group of the benzofuran moiety hydrogen bonds with S267 from the primary subunit (white) and Q226 and I225 from the complementary subunit (black). A288 makes hydrophobic interactions with the disaccharide and spiroketal groups. (C) Ivermectin binding (pink) rotates the pore-lining L261 residue away from the channel and widens the upper channel pore. (D) Ivermectin binding (pink) wedges apart the upper portions of adjacent TM1(-) and TM3(+) domains by 3Å. (E) Chemical structures of selamectin and ivermectin. Accession codes for PDB files used: 5VDH and 5CFB.

protrude away from the pore and interact with the lipid membrane.

The agonist activity of ivermectin has been attributed to the C5-hydroxyl moiety within the benzofuran group

(Michael et al., 2001). It forms hydrogen bonds with S267 TM2(+) and Q226 TM1(-), which causes TM2 to tilt away from the channel axis and widens the channel pore at 9' L261 (Fig. 2C) (Huang et al., 2017). Altering

the structure of ivermectin to remove this interaction abolishes agonist activity while retaining potentiating capabilities, as seen with the structurally related selamectin (Fig. 2E) (Michael et al., 2001; Lynagh et al., 2011). When comparing the structures of GluCl and GlyR $\alpha_3$ , ivermectin inserts 1 Å deeper into the cavity of GluCl due to the smaller side chain volume of glycine at the 288 TM3(+) position, accounting for its greater sensitivity (Huang et al., 2017). A288 also forms several hydrophobic interactions with both the benzofuran and spiroketal groups, whereas I225 TM1(-) from the neighboring subunit forms a hydrogen bond with the C7-hydroxyl group. Within GlyR $\alpha_3$ , this causes an overall expansion of the upper TM domains, separating TM3(+) and TM1(1) by approximately 3Å (Fig. 2D) (Huang et al., 2017). Ivermectin binding also elicits conformational changes within the extracellular domains, in particular loops C, D, and F (Wang and Lynch, 2012). These changes may facilitate agonist binding or elicit conformational changes that favor the activated state. This not only highlights the importance of these extracellular loops for receptor activation but provides a mechanistic basis for how avermectins potentiate GlyRs (Wang and Lynch, 2012).

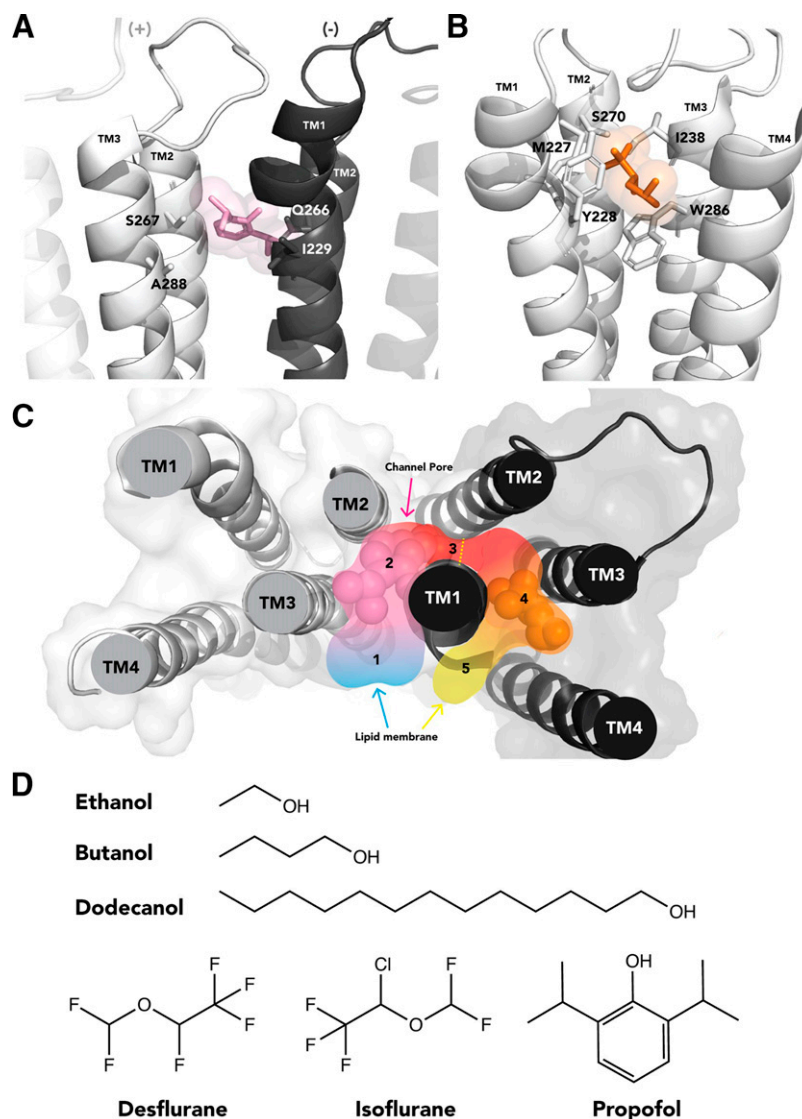
Ivermectin was one of the first PAMs bound to the crystallized GlyR, and its binding cavity remains one of the most well defined across cys-loop receptors. The crystallography and cryoEM structures of ivermectin greatly helped define the intersubunit binding cavity and important binding residues, which have also been shown to interact with lipids (Althoff et al., 2014), steroids (Henin et al., 2014; Alvarez and Pecci, 2019), alcohols, and anesthetics (Crawford et al., 2007; Howard et al., 2011; McCracken et al., 2016), making it a promising cavity to target for further PAM development. However, ivermectin itself produces toxic GABA-mimetic side effects at concentrations that would be required to observe possible antinociceptive activity. These side effects include dizziness, muscle pain, nausea, and hypotension; and can lead to respiratory failure, coma and death at high concentrations (Yang, 2012; Chandler, 2018). Greater optimization that focuses on enhancing selectivity and dampening agonist activity would be required to further the therapeutic potential of avermectin compounds to treat chronic pain conditions. This has caused researchers to instead explore chemogenetic approaches. Two chemogenetic receptors based on the GluCl and GlyR have been developed, which are highly sensitive to ivermectin and silence nociceptive signaling when virally infected into spinal neurons (Islam et al., 2017; Weir et al., 2017). The chemogenetic GluCl channel has been successfully expressed in the spinal sensory neurons of mice and caused ivermectin to produce long-lasting antinociceptive activity in acute and neuropathic pain models, without incurring any motor defects (Weir et al., 2017). This study not only

reinforces that inhibition of nociceptive signaling is a viable approach to treat chronic pain conditions but highlights a novel way to therapeutically use ivermectin's modulatory activity at cys-loop receptors. Chemogenetics remain a controversial topic and undoubtedly requires extensive research before being implemented as a therapeutic approach (Campbell and Marchant, 2018). However, it poses an innovative way to address intractable health issues such as chronic pain and is also being explored for the treatment of epilepsy (Avaliani et al., 2016; Lieb et al., 2019) and Parkinson disease (Pienaar et al., 2015).

### B. Alcohol and Anesthetics

One of the first drug classes found to modulate GlyRs was alcohols. Ethanol is the prototypic alcohol studied and was initially shown in 1988 to increase glycine sensitivity in cultured chick spinal neurons (Celentano et al., 1988), which was suggested to aid in alcohol's sedative effects. This idea continues to be explored, with recent rodent studies showing that mutagenic mouse strains expressing ethanol-insensitive GlyRs recover significantly quicker from the sedative effects of ethanol (Aguayo et al., 2014). They also have modified ethanol consumption levels and altered place preference behaviors in response to ethanol (Munoz et al., 2020). This links the modulatory effect of alcohols on GlyR to sedation and addiction; however, GlyR modulation may also contribute to the high level of antinociception associated with alcohol use (Thompson et al., 2017; Capito et al., 2020).

Primary studies found that ethanol enhances GlyR activity (Celentano et al., 1988), which was more pronounced in GlyR $\alpha_1$  than GlyR $\alpha_2$  due to nonconserved A52 residue in the extracellular  $\beta$ 1- $\beta$ 2 loop (Mascia et al., 1996a). However, longer chain alcohols were found to have similar potencies between GlyRs, which increased with chain length up to tridecanol (12-carbon length), which was inactive (Mascia et al., 1996b). This "cut-off" length was similar to that observed for GABA $_A$ R, which suggested a long, conserved hydrophobic binding pocket. This pocket was also predicted to bind propofol and volatile general anesthetics, which were similarly found to potentiate GlyRs (Hales and Lambert, 1991; Downie et al., 1996; Mascia et al., 1996a,b). A chimeric approach was then used to narrow down possible residues within this binding pocket. Chimeras of the GlyR $\alpha_1$  and GABA $_A$ R $\rho_1$  identified the TM1-TM3 regions, in particular residues S267 (TM2), T264 (TM2), and A288 (TM3) (Mihic et al., 1997). Inverse mutations made in GlyR $\alpha_1$  (S267I and A288W) abolished potentiation by general anesthetics, ethanol, and other primary and tertiary alcohols (Mihic et al., 1997; Krasowski and Harrison, 2000; Ahrens et al., 2008). Mutations at the S267 position also exhibited a strong correlation between residue volume and potentiation effects, with bulky mutations such as S267W



**Fig. 3.** Alcohol and anesthetic binding to the glycine receptor. Structures of anesthetics bound to GLIC were aligned to the glycine receptor. (A) Propofol (pink) binds to the upper intersubunit cavity of glycine receptors. (B) Desflurane (orange) binds to the upper intrasubunit cavity of glycine receptors. (C) Alcohols and anesthetics can enter the intersubunit binding cavity site 2 (pink) from the lipid membrane via site 1 (blue) or from the channel pore between TM2 domains. Alcohols and anesthetics can enter the intrasubunit binding cavity site 4 (orange) from the lipid membrane via site 5 (yellow). Site 2 and site 4 are linked by a small hydrophobic tunnel, site 3 (red), which has a restriction point of approximately 3Å, indicated by a yellow dashed line, allowing the passage of smaller alcohols and anesthetics. (D) Chemical structures of alcohol and anesthetic modulators of glycine receptors. Accession codes for PDB files used: 5MVM, 3P4W, and 5TIO.

and S267Y converting ethanol into an inhibitor (Ye et al., 1998), and abolished the effects of larger general anesthetics such as enflurane (Mihic et al., 1997). Based on the predicted binding site at A52, it was originally suggested that S267 may act as a transduction pathway that stabilizes different conformations of the receptor depending on the volume of the side chain at this position. However, mutations at this site were found to impact the alcohol “cut-off” length (Wick et al., 1998) and the modulation of larger general anesthetics (Ye et al., 1998), suggesting that S267 occurs within the binding site or in close proximity to a binding site whose dimensions are perturbed by S267. This highlighted the possibility of two binding sites—one within the ECD lined by A52 that directly modulates agonist affinity and one within the TM domains that contains S267 and enhances agonist affinity by signaling via the extracellular TM2-TM3 (Dupre et al., 2007) and  $\beta$ 1- $\beta$ 2 loops (Davies et al., 2004; Perkins et al., 2008).

This prompted several studies that aimed to characterize the two sites using both structural and functional

techniques. However, collectively, these studies found the “two” sites actually constitute the upper and lower regions of a singular large, intersubunit cavity constituting the primary binding site and additionally identified a secondary intrasubunit cavity, which is linked to the primary cavity by a hydrophobic tunnel (Crawford et al., 2007; Howard et al., 2011; McCracken et al., 2016).

The primary binding site is an intersubunit cavity that is formed predominantly by TM2(+) and TM3(+) from the principal subunit and TM1(-) from the complementary subunit (Fig. 3A). This cavity can be accessed from the Cl<sup>-</sup> channel via a narrow pore-facing tunnel (Fig. 3C) (Howard et al., 2011), which is the dominant access pathway for smaller hydrophilic molecules such as ethanol (Murail et al., 2011). However, this cavity can also be accessed from the lipid membrane, which was identified using a cysteine crosslinking method. These studies found that when A288 from TM3(+) and I229 from TM1(-) were both mutated to cysteine (A288C/I229C), disulfide bonds were able to form between



adjacent subunits (Lobo et al., 2008) and, when cross-linked, significantly reduced the potentiation of butanol and isoflurane (McCracken et al., 2016). This not only confirmed that these residues act as an entrance gate that permits the access of larger and hydrophobic modulators from the membrane (Murail et al., 2011) but also confirmed that ligands bound to this cavity are responsible for receptor potentiation. The volume of residues lining this access pathway and key residues within the cavity, including S267, correlate well with alcohol cut-off lengths (Murail et al., 2011) and the ability for longer-chain alcohols to produce potentiation (Howard et al., 2011). CryoEM structures of a GLIC-GlyR $\alpha_1$  chimera highlighted conformational changes that occur within the primary binding cavity upon receptor activation, which result in a narrowing of the pocket and a reduction of the cavity's volume (Moraga-Cid et al., 2015). Further analysis of this site using MD simulations found that ethanol binding increased the cavity volume by 50Å<sup>3</sup>, which corresponds to an approximate 10% increase. The expansion of this binding cavity by alcohols and general anesthetics may therefore produce potentiation by facilitating interactions between the TM domains (McCracken et al., 2016) and stabilizes the open conformation by preventing the TM movements required to transition into the closed state (Murail et al., 2011).

Crystal structures of general anesthetics and alcohols bound to the bacterial homolog GLIC (Howard et al., 2011; Nury et al., 2011) further identified an intrasubunit cavity (Nury et al., 2011; Fourati et al., 2018). In structures of GLIC bound to desflurane and propofol (Nury et al., 2011), the anesthetics occupy an intrasubunit cavity that occurs at the upper portion of the TM domains (Fig. 3B) and is accessible from the lipid membrane between TM1 and TM4 (Fig. 3C). Within these structures, propofol sandwiches between TM1 and TM3, forming a hydrogen bond with Y254 (Q227), whereas desflurane buries deeper into the cavity to form hydrophobic interactions with I201, I202 from TM1 (M227, Y228), T255 and I258 from TM3 (I238, W286), and V242 from TM2 (S270). Interestingly, this intrasubunit cavity connects to the primary intersubunit cavity via a narrow <3Å pore that forms between TM1 and TM2 (Fig. 3C). In GLIC, the primary cavity is not accessible from the lipid membrane due to bulky residues obstructing access, whereas GlyRs and GABA<sub>A</sub>R natively have smaller residues, which allows the primary cavity to be membrane accessible (Nury et al., 2011; Fourati et al., 2018). This is responsible for the predominantly potentiating activity of anesthetics in GlyRs compared with their inhibitory activity at GLIC. The acyl chains of membrane lipids have also been shown to enter and obstruct the entrance of the intrasubunit cavity, suggesting that anesthetics may modulate pGLICs by competing with endogenous lipid mediators (Nury et al., 2011).

Fourati et al. (2018) further explored the inter- and intrasubunit binding cavities through extensive mutagenesis, producing 10 structures of GLIC variants in the presence and absence of various general anesthetics. Firstly, when the channel is closed, anesthetics were found to bind within the pore and produce inhibition through allosteric closure and stabilizing the closed conformation. Secondly, bulky mutations made at the bottom of the intrasubunit cavity caused anesthetics to incur bimodal effects and produce potentiation at lower concentrations (Heusser et al., 2013). These mutations reduced the volume of the intrasubunit cavity by up to 40% and produced crystal structures that were in an apparent open conformation, suggesting the intrasubunit cavity may not be wholly inhibitory (Fourati et al., 2018). Lastly, they assessed the primary intersubunit cavity. A single phenylalanine-to-alanine mutation (F238A GLIC numbering, Q266 GlyR numbering) within the primary cavity reduced steric bulk and turned bromoform from an inhibitor to a potent potentiator (Sauguet et al., 2013). Bromoform is a halogenated alkane that acts as a general anesthetic and is often used to explore anesthetic binding cavities in structural studies (Kash et al., 2003; Laurent et al., 2016). An additional N239A mutation, which corresponds to residue S267 in GlyRs, reduced bulk further and allowed propofol to bind within the primary site, enabling GLIC to be potently potentiated by propofol. Within structures of the F238A/N239A GLIC variant, general anesthetics only occupied the intersubunit cavity and were in an open conformation (Fourati et al., 2018). Overall, these findings suggested the pore region and intrasubunit cavity are predominantly inhibitory, whereas the primary intersubunit cavity is responsible for potentiation.

Phosphorylation within the ICD was also found to impact alcohol modulation in GlyRs. Initial studies found that PKC and protein kinase A inhibitors significantly reduce ethanol potentiation of GlyRs, as did the GlyR $\alpha_1$  S391A mutation, which removes a PKC phosphorylation site (Mascia et al., 1998). This was found to impact the effects of ethanol *in vivo* and was linked to ethanol's antinociceptive activity. Rodents that were acutely or chronically exposed to ethanol and then underwent withdrawal would elicit nociceptive pain responses, including mechanical allodynia and thermal hypersensitivity (Gatch, 1999; Gatch and Lal, 1999). This was attributed to alterations in PKC signaling in the spinal cord, identified through immunohistochemical analysis of spinal cord sections (Shumilla et al., 2005), which altered the response of GlyRs to ethanol (Mascia et al., 1998). Further mutagenesis studies of the ICD identified residues K385 and K386 as important for ethanol modulation; however, mutation of these residues was selective for ethanol and did not impact the activity of long-chain alcohols, anesthetics, or other PAMs such as neurosteroids and zinc (Yevenes et al., 2008; Castro et al., 2012). These lysine residues had previously been shown to

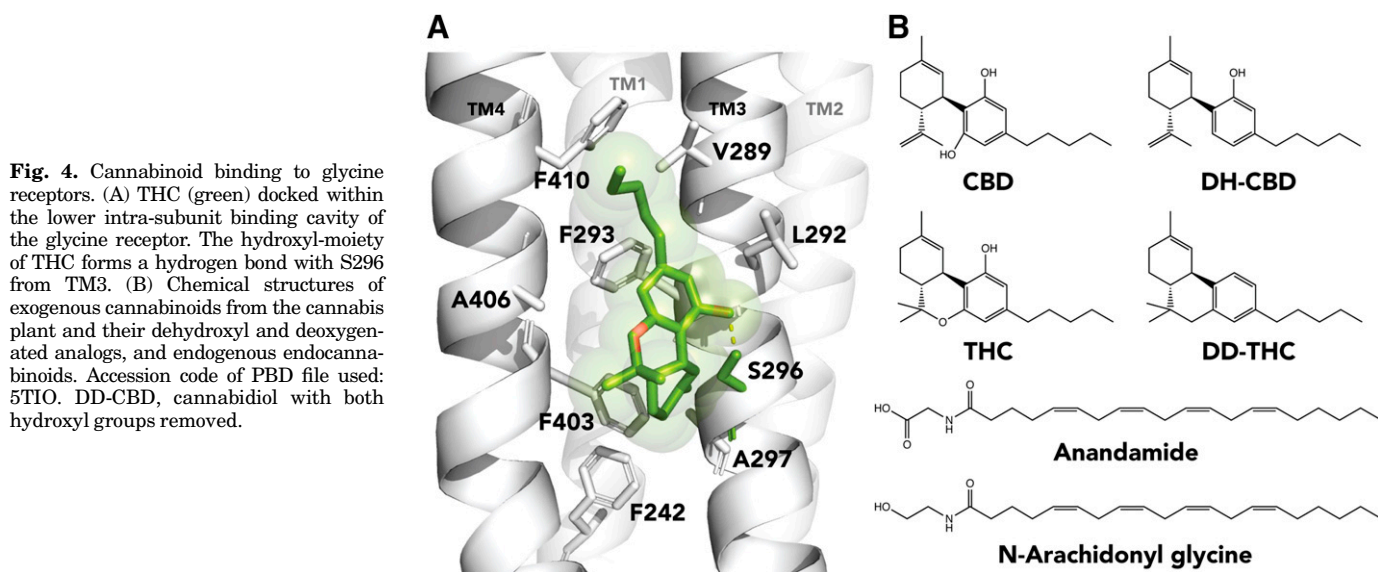
interact with the  $G\beta\gamma$  intracellular protein, which potentiates GlyRs (Yevenes et al., 2003; Yevenes et al., 2006). This suggested that low concentrations of ethanol may indirectly potentiate GlyRs by inducing  $G\beta\gamma$ -GlyR interactions. Using protein scavengers or peptides that inhibit  $G\beta\gamma$  indeed attenuated ethanol potentiation at low concentrations (Yevenes et al., 2008; San Martin et al., 2012). However, GlyR $\alpha_2$  and GlyR $\alpha_3$  are not potentiated by similar ethanol concentrations despite containing the identified lysine residues (Yevenes et al., 2010; Sanchez et al., 2015). A chimeric approach was taken to further elucidate this interaction and suggested that regions other than the ICD and TM4 domains were important for ethanol- $G\beta\gamma$  modulation, in particular, residues A52, G254, and S286, which occur in the ECD, TM2, and TM3, respectively (Yevenes et al., 2010). These results suggest that  $G\beta\gamma$  binding is dependent on residues within the ICD; however, the modulatory effects arise from conformational changes along a complex transduction pathway that includes all receptor domains. A knock-in mouse model containing the double K385A/K386A mutation in GlyR $\alpha_1$  was also developed to further explore the impact of  $G\beta\gamma$  modulation in vivo. Spinal cord slices from the mutant mouse strain had normal GlyR expression within the spinal cord and glycinergic neurotransmission indistinguishable from wild-type mice. However, mutant GlyRs were functionally insensitive to ethanol potentiation, and behavioral studies found that mutant mice were significantly less impacted by the sedative effects of ethanol (Aguayo et al., 2014).

Although alcohols and anesthetics are promiscuous compounds that are unlikely to be therapeutically viable due to significant off-target side effects, they remain important tools for exploring the functional properties of GlyRs. The study of ethanol and propofol modulation in particular has given insight into the multiple hydrophobic binding cavities, identified important intracellular interactions, and linked GlyR activity to nociceptive pathways.

Ethanol is still commonly used to compare the activity of novel PAMs or to assess the impact of mutations within GlyRs (Chesnoy-Marchais, 1999; Xiong et al., 2011; Yao et al., 2020). This has also led to the development of GlyRs that are ultrasensitive to ethanol, which contain mutations in the  $\beta 1$ - $\beta 2$  loop and are potentiated by ethanol in the low nanomolar range (Naito et al., 2014; Naito et al., 2015). These receptors are not only being used to enhance our understanding of GlyR modulation but are also used as a tool to better understand the neurologic impacts of alcohol in brain research (Naito et al., 2014).

### C. Cannabinoids

Cannabinoids are a group of compounds that are produced by the cannabis plant and synthetic analogs or derivatives. Cannabis has been used to treat nociceptive pain and inflammation since ~1500 BC, originating in ancient China (Maione et al., 2013); however, the active constituents responsible for its antinociceptive effects were not identified until the 20th century. The first cannabinoids isolated from the cannabis plant were a series of lipophilic terpenophenolic compounds, including cannabinol, which was isolated in 1940 (Adams et al., 2002), followed by cannabidiol (CBD) and  $\Delta 9$ -tetrahydrocannabinol (THC) in 1964 (Gaoni and Mechoulam, 1964). Their general structure contains a series of oxygenated cyclic moieties conjugated to a short acyl tail (Fig. 4B). These cannabinoids were found to act directly through 2 orphan G protein-coupled receptors, which were later termed the cannabinoid receptor type 1 (CB1) (Matsuda et al., 1990) and type 2 (CB2) (Munro et al., 1993; Piscitelli and Di Marzo, 2021). Activation of these receptors within the medulla modulates descending nociceptive pathways and produces antinociception in inflammatory pain conditions (Bouchet and Ingram, 2020). Their discovery also led to the identification of several endogenous ligands for CB1 and CB2 receptors, which were termed endocannabinoids (Devane et al., 1992; Di Marzo and Fontana, 1995). These



compounds did not contain cyclic moieties but were instead comprised of simplified amide or amino acid groups conjugated to long, unsaturated acyl tails (Fig. 4B).

Endocannabinoids are lipophilic eicosanoids that are synthesized *de novo* from membrane phospholipids (Di Marzo, 2008). Their synthesis is significantly enhanced in chronic pain states (Petrosino et al., 2007) and can be triggered by stress and nociceptive stimuli (Hohmann et al., 2005; Drew et al., 2009). This led to the hypothesis that the endocannabinoid system has evolved specifically to modulate nociceptive pain and inflammation, making it an ideal target for pain therapies. The first endocannabinoids identified were arachidonoyl-ethanolamide (anandamide) (Devane et al., 1992) and 2-arachidonoyl glycerol (Mechoulam et al., 1995), which were found to produce antinociceptive and psychotropic effects similar to THC and CBD (Fride and Mechoulam, 1993; Smith et al., 1994; Di Marzo and Fontana, 1995). Several arachidonoyl amino acids were later identified, including *N*-arachidonoyl glycine (NAGly), which is synthesized in high concentrations within the spinal cord and also produces antinociceptive activity in neuropathic and inflammatory pain models, without incurring motor deficits (Burstein et al., 2000; Huang et al., 2001; Succar et al., 2007; Vuong et al., 2008). However, the antinociceptive activity of these endocannabinoids are not completely reversed by CB1 and CB2 antagonists (Adams et al., 1998; Succar et al., 2007; Vuong et al., 2008), suggesting their antinociceptive activity is partly mediated through alternate pathways. This was initially suggested to be the GlyR, due to its high degree of homology with CB1 and CB2 receptors in regions where cannabinoids were predicted to bind (Lozovaya et al., 2005). Anandamide was found to inhibit glycinergic currents in hippocampal pyramidal neurons (Lozovaya et al., 2005) but caused potentiation of GlyR $\alpha_1$  expressed in HEK293 cells (Yang et al., 2008) and *Xenopus laevis* oocytes (Hejazi et al., 2006). Anandamide also potentiates glycine responses mediated by GlyRs in rodent midbrain neurons (Hejazi et al., 2006) and cultured spinal neurons (Xiong et al., 2012b). Similarly, NAGly was found to modulate glycinergic activity within the dorsal horn of the spinal cord (Jeong et al., 2010) and cause subunit-specific modulatory effects at GlyRs expressed in *X. laevis* oocytes (Gallagher et al., 2020) and HEK293 cells (Yang et al., 2008; Yevenes and Zeilhofer, 2011). Endocannabinoids were predominantly found to potentiate GlyR $\alpha_1$  and were mostly inactive or modestly inhibitory at GlyR $\alpha_2$  and GlyR $\alpha_3$  (Yang et al., 2008; Yevenes and Zeilhofer, 2011; Xiong et al., 2012b; Gallagher et al., 2020).

Exogenous cannabinoids have also been shown to significantly modulate GlyRs, which likely contributes to the antinociception induced by the cannabis plant. THC significantly potentiates GlyR $\alpha_1$  and GlyR $\alpha_3$  when expressed in *X. laevis* oocytes (Hejazi et al., 2006), HEK293 cells, and cultured spinal neurons (Xiong et al., 2011;

Xiong et al., 2012b). Immunoblotting assays confirmed these effects are not due to alterations in GlyR expression or receptor trafficking but instead through direct binding interactions (Xiong et al., 2011). In *X. laevis* oocytes, THC was found to have an EC<sub>50</sub> in the nanomolar range and was highly selective for GlyRs over GABA<sub>A</sub>Rs (Hejazi et al., 2006). CBD also potentiates homomeric and heteromeric GlyRs in HEK293 cells with an EC<sub>50</sub> in the low micromolar range and produces modest agonist activity at high micromolar concentrations (Ahrens et al., 2009). To further explore the structure activity relationships of cannabinoids and aid in identifying their binding sites on GlyRs, several synthetic cannabinoid analogs have also been synthesized. Two examples of this are ajulemic acid and HU-210, which also significantly modulate GlyRs (Yang et al., 2008; Foadi et al., 2010).

Cannabinoids were initially predicted to bind within the alcohol binding site proximal to S267; however, S267 mutations that abolish ethanol potentiation had no effect on THC modulation (Hejazi et al., 2006). One exception to this was S267I, which was found to reduce the potentiating effects of CBD and HU-210; however, this mutation also disrupted normal GlyR functionality (Foadi et al., 2010). When looking for other possible binding sites, Xiong et al. (2011) noted the S296 residue that was conserved between the  $\alpha_1$  and  $\alpha_3$  subunits, whereas the corresponding residue in  $\alpha_2$  is an alanine (A303). The S296A mutation significantly reduced THC potentiation of GlyR $\alpha_1$  and GlyR $\alpha_3$  without impacting glycine sensitivity or the modulatory activity of other PAMs such as alcohol and anesthetics (Xiong et al., 2011). The S296A mutation also significantly reduced anandamide, CBD, and HU-210 potentiation in GlyR $\alpha_1$  and GlyR $\alpha_3$ , whereas the reverse A303S mutation in GlyR $\alpha_2$  enhanced all cannabinoid potentiation (Xiong et al., 2012b), suggesting a novel intrasubunit cannabinoid binding site. MD simulations of anandamide and THC predicted cannabinoid binding between TM4 and TM3 of a single subunit and proposed hydrogen bond formation with S296 via their oxygen or hydroxyl groups (Fig. 4A) (Xiong et al., 2012b). Docking studies conducted with a homology model of GABA<sub>A</sub>R also predicted 2-arachidonoyl glycerol to bind within this cavity (Baur et al., 2013). Removing the oxygen and hydroxyl groups from anandamide (Xiong et al., 2012b), THC (Xiong et al., 2011), and CBD (Xiong et al., 2012b) significantly reduces their potentiating activity, supporting the initial MD findings. A THC analog with both oxygen groups removed (DD-THC) is inactive at GlyRs but prevents the potentiating effects of THC when coapplied. This suggests that deoxygenated cannabinoids are still able to bind within the cavity but cannot elicit potentiation. Yet, this response does not occur when DD-THC is coapplied with propofol, suggesting the binding cavity is cannabinoid specific. Similarly, CBD with both hydroxyl

groups removed has significantly reduced activity at GlyR $\alpha_1$  but competes with CBD for the cannabinoid binding site (Xiong et al., 2012b). However, removing only one hydroxyl group from the 3' position of CBD while retaining the 1' hydroxyl (DH-CBD) significantly enhances potentiation compared with CBD. Removal of the 3' hydroxyl group likely reduces steric bulk and allows the remaining hydroxyl to better interact with the S296 residue. Potentiation of GlyRs by endocannabinoids such as NAGly are also impacted by the S296A mutation. However, endocannabinoids are also affected by a range of mutations within the ECD, TM2, and the ICD, depending on polarity of the endocannabinoid head group (Yevenes and Zeilhofer, 2011). This indicates that the modulatory effects of endocannabinoids at GlyRs are more complex and involve multiple regions of the receptor.

THC, CBD, and other cannabinoid analogs induce strong antinociception in rodent models of nociceptive pain, which are not significantly reduced by CB1 antagonists. However, their effects can be significantly reduced by strychnine or coinjection with inactive deoxygenated analogs (Hejazi et al., 2006; Xiong et al., 2011; Xiong et al., 2012a). THC-induced antinociception is almost completely abolished in GlyR $\alpha_3$  knockout mice but remains in GlyR $\alpha_2$ , CB1, and CB2 knockout mice (Xiong et al., 2012a). The small retention in antinociceptive activity in GlyR $\alpha_3$  knockout mice is likely due to GlyR $\alpha_1$  in the spinal cord, which is also potentiated by THC. Mice carrying the GlyR $\alpha_1$  S296A mutation are also significantly less sensitive to cannabinoid-induced antinociception, highlighting that both GlyR $\alpha_1$  and GlyR $\alpha_3$  mediate cannabinoid induced antinociception (Lu et al., 2018).

Cannabinoid modulation of GlyRs was also shown to be sensitive to cholesterol concentrations. Lowering the cholesterol content of HEK293 cells with methyl- $\beta$ -cyclodextrin was found to significantly reduce the potentiating effects of THC, anandamide, and CBD in cells expressing GlyRs, without impacting the activity of other modulators such as alcohols and anesthetics (Yao et al., 2020). To help elucidate these cannabinoid-specific effects, MD simulations of THC binding to GlyR $\alpha_1$  were conducted in a model membrane with or without cholesterol. Cholesterol was found to lower the free energy for S296-THC binding and cause a lateral and radial tilt of the TM4 domain toward the pore, which alters the proposed THC binding pocket (Yao et al., 2020). Furthermore, this interaction was found to impact cannabinoid antinociception in vivo. Simvastatin is a lipid-lowering drug that is often prescribed to those suffering with high cholesterol (Pedersen and Tobert, 2004). Mice injected with simvastatin were found to have an approximate 20% reduction in spinal cord cholesterol, which directly correlated to a reduction of GlyR potentiation by THC and DH-CBD when recorded

from spinal cord slices (Yao et al., 2020a). The antinociceptive activity of DH-CBD in rodent models of acute and inflammatory pain is also significantly reduced in simvastatin-treated mice (Yao et al., 2020b).

Despite the significant antinociception achieved by cannabinoids, their psychotropic side effects and propensity for recreational use have previously hindered their legality and therapeutic applications. Only recently have cannabinoid-based therapies been legalized in countries such as Canada, America, and New Zealand. As cannabinoids are generally lipophilic and undergo significant hepatic metabolism, their most effective, non-invasive route of administration is sublingual (Xiong et al., 2012a; Urits et al., 2020). The most prevalent cannabis-based therapy is nabiximol, sold under the name Sativex, which is a 1:1 THC:CBD oromucosal spray that is used to treat multiple sclerosis (Giacoppo et al., 2017; D'hooghe et al., 2021), chronic pain conditions (Nurmikko et al., 2007; Johnson et al., 2013), and mental illnesses including depression and anxiety (Gulbransen et al., 2020). Many clinical trials have highlighted the effectiveness of nabiximol and other cannabinoid-based therapies to improve a variety of nociceptive pain symptoms. They are generally well tolerated and have minimal adverse effects—the most common being dizziness, nausea, dry mouth, and sedation (Johnson et al., 2013; Gulbransen et al., 2020). Notably, these therapeutics may be suitable for chronic use as clinical trials found several patients continued treatment of extended periods of time without requiring increased dosing or additional pain relief (Nurmikko et al., 2007; Gulbransen et al., 2020). Despite this, some patients remain hesitant to use cannabinoids or reduce their use of other pain medications in fear of losing opioid prescriptions and the general uncertainty concerning the noninsured costs and lack of regulation of cannabinoid products (Urits et al., 2020). The stigma associated with cannabis use plagues therapeutic cannabinoids and has prompted studies that aim to target the cannabinoid binding site within GlyRs with noncannabis related compounds. A virtual screen of over 1500 Food and Drug Administration-approved drugs was conducted targeting the S296 binding cavity highlighted by cannabinoid research and identified 7 hits that potentiate GlyR $\alpha_1$  to a greater extent than THC when tested at equivalent concentrations (Wells et al., 2015). Several of these hits are medications that are already used for pain relief despite their mechanisms of antinociception not being fully understood, such as pimozide and sulindac. This not only suggests their antinociceptive activity is in part due to GlyR potentiation but also highlights the ability to target the cannabinoid binding cavity within GlyRs with alternate therapeutically viable compounds.

#### D. Lipid Modulators

Lipids are known to indirectly modulate pLGICs by permeating into the membrane and altering the

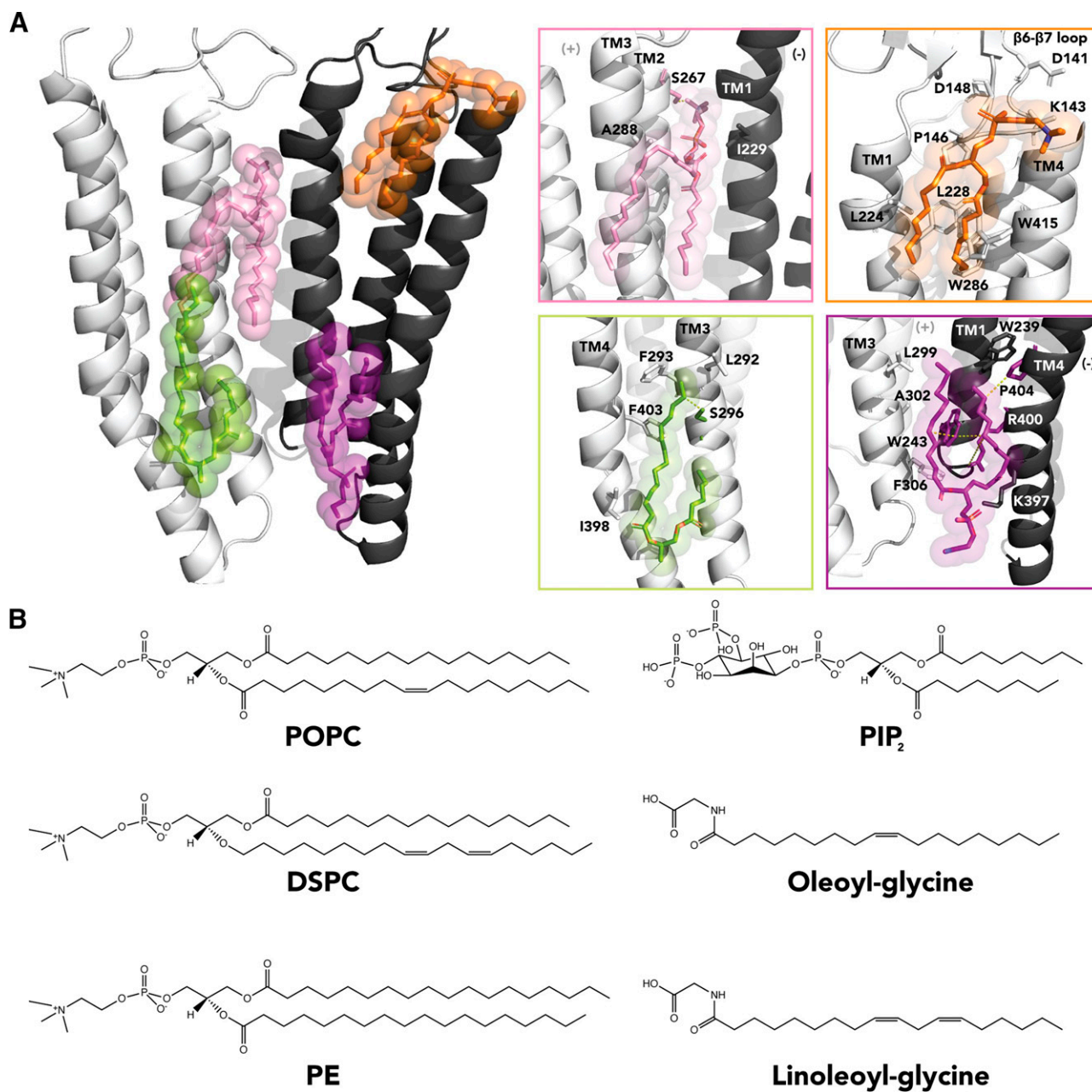
physiochemical properties of the surrounding lipid environment (Sooksawate and Simmonds, 2001; daCosta et al., 2009; Antollini and Barrantes, 2016). This idea was initially based on the observation that nAChRs from the *Torpedo californica* must be purified in the presence of specific lipids to retain functionality (Criado et al., 1982). Extensive research conducted by McNamee and colleagues found that nAChRs conferred a degree of lipid specificity (Andreasen and McNamee, 1977) and that lipid composition impacts the transitional kinetics of these receptors and resulting ion flux, without impacting agonist binding (Ochoa et al., 1983; Criado et al., 1984; Fong and McNamee, 1986). Lipids that optimally match the membrane-exposed regions of the receptor were proposed to enhance functionality by specifically associating within the annular belt. This is the first shell of membrane lipids that occur at the lipid-protein interface and make direct contact with the receptor (Lee, 2011). These lipids can form domains with different fluidity, phase, and composition to the rest of the bulk membrane, which does not directly interact with the receptor (Sunshine and McNamee, 1994; Antollini et al., 2005).

However, additional studies have highlighted specific lipid effects that cannot be accounted for by membrane properties alone. Sunshine and McNamee (1994) found that lipids that incur similar effects on membrane properties produced different modulatory effects. One example of this was squalene, which was able to enhance the functionality of reconstituted nAChRs despite producing membranes with similar fluidity to lipids such as dipalmitoylphosphatidylcholine, which produced low-functioning receptors. This has also been shown recently with vaccenic acid, *cis*-13-octadecenoic acid, and petroselenic acid, which all incur similar effects on membrane fluidity; however, only petroselenic acid modulates nAChRs (Perillo et al., 2012). These studies suggest that lipids not only interact with annular sites at the lipid-protein interface but can also participate in specific binding interactions at nonannular sites, which occur between the  $\alpha$ -helices of the TM domains (Lee, 2011).

Several studies have explored these specific lipid interactions across pLGICs and identified common structure activity relationships that apply to all cys-loop receptors. Overall, these studies conclude that lipid modulators require a double bond in the *cis* conformation and tail lengths between  $\sim$ 10–22 carbon atoms to be active (Witt et al., 1996; Zhang and Xiong, 2009; Antollini and Barrantes, 2016; Perillo et al., 2016). The double bonds induce angularity within the lipid tail that is proposed to perturb the TM at regions, which can disrupt receptor function (Perillo et al., 2012), whereas the increased length of the acyl-chain likely participates in hydrophobic interactions that stabilize lipid binding. Recently, a study that further explored these relationships within GlyRs confirmed that lipids require a *cis* double bond in

the center of the acyl tail to be active at GlyRs and produced the greatest potentiation when occurring in the  $\omega$ 7– $\omega$ 9 positions (Gallagher et al., 2020). This study also found that lipids with small and aliphatic head groups produced greater potentiation than bulkier, aromatic head groups and suggests this may be due to conformationally restrictive binding cavities within the TM domains. Linoleoyl- and oleoyl-glycine (Fig. 5B) were found to significantly potentiate homomeric and heteromeric receptors and were more selective for receptors containing the  $\alpha_1$  and  $\alpha_2$  subunits (Gallagher et al., 2020). Moreover, MD simulations conducted with oleoyl-glycine and structurally related lipids in a model membrane suggest these lipids do not alter the physiochemical properties of the bilayer or general protein structures (Mostyn et al., 2019b; Schumann-Gillett and O'Mara, 2019) and must therefore be potentiating GlyRs through direct binding interactions.

Lipids have also been shown to tightly bind to pLGICs during purification, which further suggests their importance in receptor function and their ability to specifically bind to membrane-exposed regions. Structures of GLIC have shown lipids such as 1,2-distearoyl-sn-glycero-3-phosphocholine (DSPC) and diundecyl phosphatidyl choline can bind in the upper and lower portions of the TM domains (Fig. 5A) (Bocquet et al., 2009; Hu et al., 2018), overlapping with several known binding cavities. DSPC binds to the extracellular portion of the TM domains between TM1 and TM4 of the same subunit. The acyl tails are found to protrude into an intrasubunit cavity shown to bind anesthetics and obstruct the cavities entrance, which may functionally compete for this binding site (Nury et al., 2011). The phosphate backbone of the phosphocholine head group also bridges interactions between F315 (K419) within the post TM4 region and F121 (M147) in the extracellular  $\beta$ 6– $\beta$ 7 loop (Bocquet et al., 2009). Recently, a similar phosphocholine lipid was shown to bridge this interaction in a cryoEM structure of a human GABAR (Lavery et al., 2019). This interaction is important for receptor coupling and communicating agonist binding to the TM domains (Baenziger et al., 2000; daCosta and Baenziger, 2009; daCosta et al., 2009; Dacosta et al., 2013). Although this has not been found in structures of GlyRs, recent MD simulations have shown that numerous phospholipids interact with the GlyR at this region, which occurs more prominently in the active state versus the inactive state (Damgen and Biggin, 2021). The zwitterionic lipid head groups interact with charged residues within the  $\beta$ 6– $\beta$ 7 loop of the principal subunit and the  $\beta$ 8– $\beta$ 9 loop and pre-TM1 region of the complementary subunit. Lipids can also bind in the intersubunit cavity, which binds ivermectin, most notably 1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine (POPC), which is a lipid potentiator of the GluCl (Althoff et al., 2014). Similar to the benzofuran group of ivermectin, the polar phosphocholine head group of POPC wedges between



**Fig. 5.** Lipid binding cavities in the glycine receptor. Structures of lipids bound to GLIC, GluCl, and ELIC were aligned to the glycine receptor: (A) POPC (pink) binds within the upper intersubunit cavity of glycine receptors between adjacent subunits, and the phosphocholine head group interchelates between TM2 domains and interacts with S267. POPC (orange) binds within the upper intrasubunit cavity, and the phosphocholine head group bridges interactions between the post-TM4 region and the  $\beta 6$ - $\beta 7$  loop in the ECD. DSPC (green) binds within the lower intrasubunit cavity with the lipid tails coming within 3.2Å of S296. Phosphatidylethanolamine (PE) (purple) binds within the lower intersubunit cavity and interacts with the conserved P404, W243, and R400 triad. (B) Chemical structures of lipids shown to bind to pLGICs and potentiate glycine receptors. Accession codes for PBD files used: 4TNW, 3EAM, 6HJX, and 5TIO. PIP<sub>2</sub>, Phosphatidylinositol 4,5-bisphosphate.

TM1(-) and TM3(+) and protrudes toward TM2(+) (Fig. 5A). This expands the distance between adjacent TM2 domains and increases the channel radius from 1.4Å to 2.4Å in the POPC-bound structure, thus potentiating the receptor by stabilizing it in a conformation that requires less energy for channel opening. Additional conformational changes in the TM2-TM3 and  $\beta 6$ - $\beta 7$  loops transduce signals to the extracellular domain, which is hypothesized to further strengthen ligand binding (Althoff et al., 2014). The

acyl tails of POPC remain interchelated between TM1(-) and TM3(+) and extend outward, toward the lipid membrane. Although the structures of lipids bound to GlyRs have not been determined, MD simulations have shown a high stability of membrane lipids in close proximity to residues I229 (TM1-) and A288 (TM3+), which are located at the entrance to this cavity (Murail et al., 2011).

Lipids have also been shown to bind within the intracellular portions of the TM domains, overlapping with the proposed cannabinoid and neurosteroid binding site

(Xiong et al., 2012b; Laverty et al., 2017; Miller et al., 2017; Chen et al., 2018). In structures of GLIC, lipids are shown to bind between TM3 and TM4 of the same subunit, within  $<4\text{\AA}$  of V268 (Fig. 5A) (Bocquet et al., 2009), which corresponds to S296 in GlyRs, a key residue for cannabinoid potentiation (Xiong et al., 2011; Xiong et al., 2012b). Phosphatidylinositol 4,5-bisphosphate has also been shown to occupy this site in GABARs (Laverty et al., 2019). Additionally, lipids have been shown to bind within the intracellular intersubunit binding cavity of ELIC (Henault et al., 2019) and GLIC (Bocquet et al., 2009; Hu et al., 2018). Phosphatidylethanolamine binds to ELIC and interacts with a tryptophan-proline-arginine triad that is conserved among anion-selective pLGICs, corresponding to W243 (TM1), R400 (TM4), and P404 (TM4) in GlyRs (Fig. 5A). This triad creates a characteristic kink at the intracellular end of the TM4 and, when mutated, significantly enhances desensitization kinetics without impacting receptor activation (Henault et al., 2019). This is because the extracellular region of TM4 that proceeds the proline kink is highly flexible and dynamic. When the proline kink is removed, the  $\alpha$ -helix straightens and causes TM4 to extend toward the adjacent subunit. This disrupts intrasubunit interactions that are important for receptor activation. When lipids bind within this region, they stabilize TM4 in a kinked conformation, which allows for more efficient receptor activation and slower desensitization rates (Henault et al., 2019), thus potentiating the receptor.

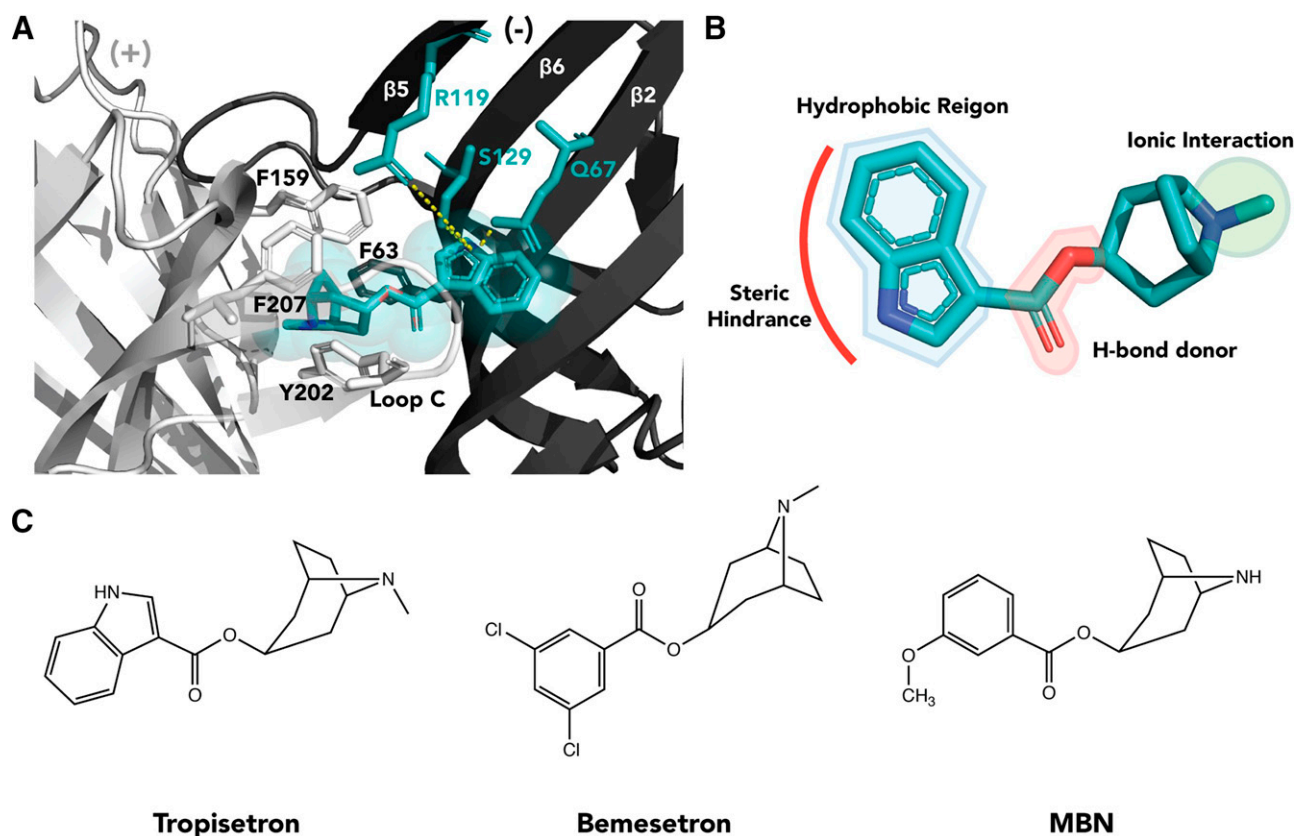
The tryptophan-proline-arginine triad is one of the key components that highlight evolutionary differences between cationic and anionic pLGICs, which may have evolved to modify lipid sensitivity. The proline kink allows TM4 to angle back toward TM1 and TM3, allowing the post-TM4 region to effectively interact with the  $\beta 6$ - $\beta 7$  loop, which communicates agonist binding to the TM domains (Henault et al., 2019). Without this, TM4 would extend outward from the channel pore to compensate for the hydrophobic mismatch and become uncoupled, as seen with nAChRs (Antollini et al., 2005; daCosta and Baenziger, 2009; Dacosta et al., 2013). The second component is a phylogenetically conserved network of aromatic residues that line TM1, TM3, and TM4 in eukaryotic anionic channels such as GABA and GlyRs, whereas cationic channels like nAChRs have much lower aromaticity within this region (Haeger et al., 2010; Carswell et al., 2015). Within the GlyR, there are 16 aromatic residues within the TM1, TM3, and TM4 domains. Homology modeling of the GlyR revealed that three aromatic residues on TM4 (Y406, W407, Y410) face into the membrane and interact with phospholipids to stabilize the receptor (Haeger et al., 2010). The remaining form two clusters of aromatic residues, which form  $\pi$ - $\pi$  interactions. One in the upper portion of the TM domains includes F402 and F405 from TM4, Y228 from TM1, and W286 and

F293 from TM3 and another in the lower portion of the TM domains between F399 and F395 from TM4 and W293 and F242 from TM1 (Haeger et al., 2010; Tang and Lummis, 2018). In combination, these two components make GlyRs less sensitive to the lipid membrane and less dependent on the membrane thickness for receptor activation. However, the residues involved in these processes occur within annular and nonannular sites of receptor and line lipophilic cavities that participate in specific lipid interactions. Although lipids are yet to be resolved in structures of GlyRs, functional studies (Gallagher et al., 2020) and MD simulations (Murail et al., 2011; Damgen and Biggin, 2021) show specific lipid interactions that could be further enhanced through lipid drug design. Greater optimization of lipid PAMs for GlyRs and further structural analysis may allow for lipophilic-based drugs that target allosteric sites within the TM domains of GlyR to treat pain conditions. The main limitation for these compounds, in terms of potential therapeutic applications, are their poor pharmacokinetic profiles, which will be discussed further in section III.C.

### E. Tropeines

Tropeines are alkaloids derived from atropine that act as potent serotonin type 3 receptor (5-HT<sub>3</sub>R) antagonists. They have commonly been used for their antiemetic effects, in particular ICS-205,930 (tropisetron), which is a well tolerated first-line therapy for acute nausea (Simpson et al., 2000) and is also being explored as an analgesic for fibromyalgia (Haus et al., 2000; Papadopoulos et al., 2000). Tropeines have also been shown to positively modulate GlyRs in the femtomolar range (Yang et al., 2007), and novel tropeine analogs have been synthesized in an attempt to achieve GlyR-specific PAMs.

5-Hydroxytryptamine is a primary agonist for serotonin receptors but was serendipitously found to also act as an inhibitor of glycinergic currents in rat spinal neurons (Chesnoy-Marchais and Barthe, 1996). This prompted studies that assessed the activity of various 5-hydroxytryptamine analogs and 5-HT<sub>3</sub>R antagonists at the GlyR. Many had only modest activity, except for the antagonists LY-278,584, MDL-72222, and tropisetron, which incurred biphasic activity, potentiating GlyRs at low concentrations and causing inhibition at higher concentrations (Chesnoy-Marchais, 1996). All potentiating tropeines contained a tropanyl group which was linked to a phenyl or indole group via an ester bond and could be converted to inhibitors by extending either the tropane ring or ester bond (Chesnoy-Marchais, 1996; Maksay, 1998; Chesnoy-Marchais et al., 2000). Around the same time as these discoveries, several tropeines were found to produce antinociceptive effects, including tropisetron and MDL-72222, which elicited antinociceptive effects in rats at concentrations sufficient to saturate the potentiated effects on GlyRs (Glaum et al., 1990; Maksay, 1998; Scapecci et al., 1998).



**Fig. 6.** Tropeine binding in glycine receptors. A structure of tropisetron bound to the mouse serotonin type 3 receptor was aligned to the glycine receptor. (A) Tropisetron (teal) binds within an intersubunit cavity of the ECD, closely aligning with the agonist binding cavity. The tropane moiety sits within an aromatic vestibule formed predominantly by the primary subunit (white), whereas the amide group extends toward the complementary subunit (black) to interact with R119, S129 and Q67. Loop C from the primary subunit closes in on tropisetron, a movement required for receptor activation. (B) Schematic view of the structure activity relationships developed for tropeine activity at glycine receptors. (C) Chemical structures of tropeines with modulatory activity at glycine receptors. Accession codes for PDB files used: 6HIS and 5TIO.

This suggests that tropeines may be eliciting antinociceptive effects through potentiation of GlyRs.

The potentiating effects of tropisetron occurred in the presence of both glycine and taurine (Chesnoy-Marchais, 1996) and were not impacted by coapplication with zinc, ethanol, or propofol, which suggested a novel binding site and modulatory mechanism (Chesnoy-Marchais, 1999). Heteromeric GlyR $\alpha_1\beta$  was more sensitive to potentiation than GlyR $\alpha_1$ , and inclusion of the  $\beta$ -subunit induced potentiation in GlyR $\alpha_2\beta$ , compared with GlyR $\alpha_2$ , which is insensitive (Supplisson and Chesnoy-Marchais, 2000). Conversely, GlyR $\alpha_2$  was found to be more sensitive to the inhibitory effects of tropisetron and atropine compared with GlyR $\alpha_1$ , and inhibition was more prominent in homomeric receptors compared with heteromeric GlyRs (Maksay et al., 1999). Structure activity relationships were further developed by screening a range of tropeine analogs. The results from these studies predicted that the phenyl ring bound within a hydrophobic pocket, which is sterically hindered toward the paraposition, whereas the ester group is likely to interact with a hydrogen-bond donor (Maksay et al., 2004). The tropane ring has the most structurally distinctive interactions, with most

substitutions significantly impacting activity. Significantly, demethylation of the nitrogen within the tropane group significantly enhanced potency at GlyRs while reducing activity at 5-HT $_3$ R, opening an avenue for selective GlyR drug development. *n*-Methylation of the indole ring (MBN) was also found to attenuate inhibitory effects without impacting GlyR potentiation and produced a greater selectivity for GlyRs over 5-HT $_3$ R (Maksay et al., 2009).

Early mutagenesis studies suggested that tropeines bind within the ECD, involving residues T112 (Maksay et al., 1999) and E103 (Chesnoy-Marchais et al., 2000), and were unlikely to interact with the TM2 domain (Supplisson and Chesnoy-Marchais, 2000). Several mutations around the orthosteric binding pocket were found to abolish or reduce inhibitory effects (Maksay et al., 2009), including the N102A mutation, which completely abolishes inhibitory activity without impacting potentiation (Yang et al., 2007). The asparagine residue was predicted to make hydrogen bonds with the nitrogen group within the tropane ring, similar to its docking position in 5-HT $_3$ R. Homology modeling and docking studies using MBN also suggested distinct binding interactions for inhibitory

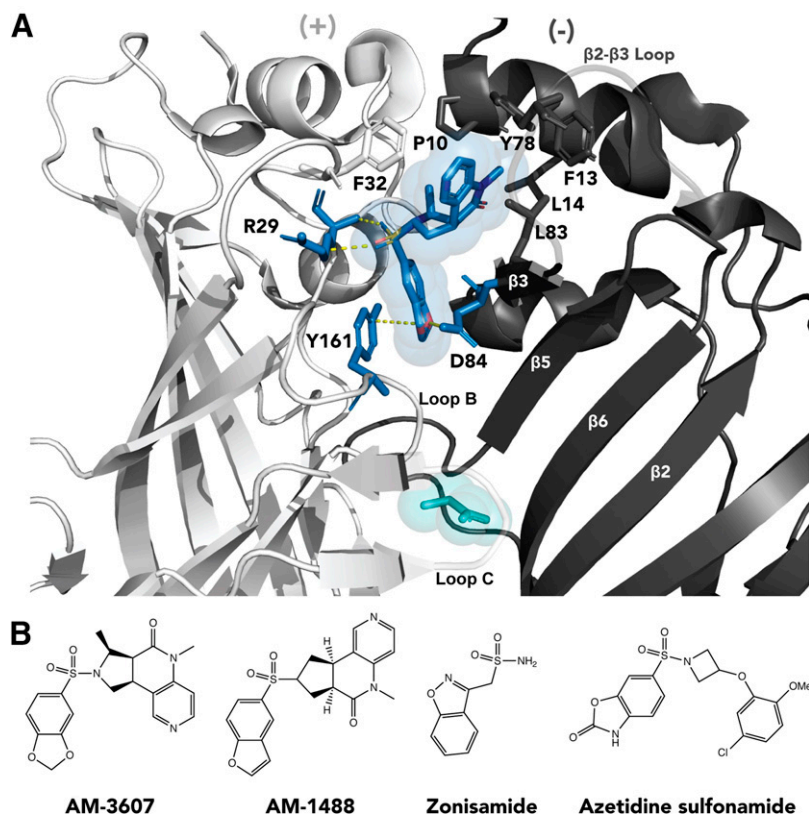


and potentiating tropeines that occur at adjacent binding sites in the ECD, proximal to the orthosteric binding pocket (Maksay et al., 2009). Within the inhibitory site, MBN penetrates deeply below loop C and stabilizes it in an outwardly, half-open conformation, thus hindering the full closure required to elicit channel gating. The tropane moiety binds within a hydrophobic vestibule, with its aromatic region intercalated between F63(-) and F159(+) and the secondary amino group forming hydrogen bonds with N102(+) and N46(-), whereas the carbonyloxy moiety bonds with R131(-) (Maksay et al., 2009). The potentiating binding pocket is more superficial. The tropane ring remains buried within a hydrophobic cleft formed by F63(-) and F159(+); however, it is rotated and extends upwards to include Y202(+) and F207(+) (Fig. 6A). The amide group now forms interactions with Q67(-), R119(-), and S129(-). In this conformation, MBN stabilizes loop C in a closed conformation that mimics that of the agonist-bound receptor. This likely produces potentiation by facilitating channel opening (Maksay et al., 2009).

An interesting aspect of tropeine modulation is the ability to achieve such high affinity at the GlyR $\alpha_1$  (Yang et al., 2007) and GlyR $\alpha_1\beta$  (Supplisson and Chesnoy-Marchais, 2000) with compounds that are already clinically approved, orally available, and shown to have antinociceptive effects in fibromyalgia (Haus et al., 2000; Papadopoulos et al., 2000) and inflammatory and neuropathic pain (Stratz and Müller, 2000; Stratz and Müller,

2004; Nasirinezhad et al., 2016). Many of the antinociceptive effects have been attributed to serotonergic modulation; however, it is likely that positive modulation of GlyRs may also play a role in their antinociceptive activity. Further optimization of lead tropeine compounds that enhance their potentiating activity at GlyRs may therefore produce compounds with superior antinociceptive effects. As tropeines have desirable pharmacokinetic profiles and several are already clinically approved, this makes tropeines an advantageous stepping stone for further GlyR PAM development as potential pain therapies.

However, one major drawback is the lack of potentiation at GlyR $\alpha_3$ , despite the putative binding site being conserved between GlyRs (San Martín et al., 2019). It was suggested that the allosteric transduction pathway linking the ECD to channel gating may differ for GlyR $\alpha_3$  and thus makes GlyR $\alpha_3$ -selective tropeines unobtainable. Nevertheless, with the increasing number of structures refined for mammalian GlyRs and enhanced MD capabilities, further development of the tropeine pharmacophore could be developed to confer greater selectivity for the potentiating effects and attempt to resolve the lack of GlyR $\alpha_3$  potentiation. It also remains questionable whether GlyR $\alpha_3$  potentiation is required for antinociceptive activity, and the ability for tropeines to produce antinociceptive effects, which are likely mediated by GlyR $\alpha_1$ , supports this argument.



**Fig. 7.** Sulfonamide binding in glycine receptors. (A) AM-3607 (blue) binds within an intersubunit cavity of the ECD approximately 10Å above the agonist binding cavity (teal). The benzodioxole moiety interacts with Y161 from the primary subunit (white) and D84 from the complementary subunit (black). The sulfonamide group is coordinated by R29 from the  $\alpha 1$ - $\beta 1$  loop, and the pyrrolidine moiety buries within a hydrophobic cavity formed by the  $\alpha 1$ -helix (+) and the  $\beta 2$ - $\beta 3$  loop (-). (B) Chemical structures of sulfonamides with modulatory activity at glycine receptors. Accession code of PDB file used: 5VDH.

### F. Sulfonamides

The pharmaceutical companies Pfizer and Amgen have both conducted large-scale screens of compound libraries in an attempt to identify novel PAMs of GlyRs. The screens from both companies identified a range of sulfonamides, which are a class of compounds that contain a common  $\text{SO}_2\text{NH}_2$  moiety. They are commonly known as bacteriostatic antibiotics that have been used to treat bacterial infections and allergies; however, the sulfonamide moiety has previously been incorporated into therapeutics to treat epilepsy, hypertension, and glaucoma (Mujumdar and Poulsen, 2015; Davies et al., 2020).

The initial screen was conducted by Pfizer and used a fluorescence-based membrane potential assay in CHO cells expressing GlyR $\alpha_1$ , GlyR $\alpha_3$ , and GlyR $\alpha_3\beta$  (Stead et al., 2016). Of the 56,558 compounds tested, 147 were primary hits. These were then screened using an automated electrophysiology IonFlux HT assay yielding seven true hits—five benzoic acids and two novel benzene-sulfonamides. The most efficacious of the sulfonamides was 4-Fluoro-N-(2-(quinolin-8-yloxy)ethyl)-benzenesulfonamide, which potentiated both GlyR $\alpha_1$  and GlyR $\alpha_3$  and showed no activity at GABA $_A$ Rs (Stead et al., 2016). Soon after, Amgen published a similar screen that used a membrane potential dye assay in HEK293 cells expressing GlyR $\alpha_3\beta$  to identify hits, which were further characterized using Schild shift assays (Bregman et al., 2017). The four hits from this screen were all tricyclic sulfonamides with a benzodioxole moiety. The major metabolic pathways of these hits were through oxidation of the quinolinone core, pyrrolidine ring, and benzodioxole moiety, and thus, modifications were made to reduce oxidation. Incorporating a nitrogen into the quinolinone ring enhanced the sulfonamides potency and achieved high passive permeability, good solubility, and good oral absorption. Removing an oxygen from the sulfonamide moiety to form a benzofuran group (AM-1488) was found to achieve good potency across homomeric and heteromeric  $\alpha_1$  and  $\alpha_3$  GlyRs (Huang et al., 2017). Furthermore, AM-1488 possesses good selectivity over other cys-loop receptors, GCPRs, human *ether-a-go-go*-related gene  $\text{K}^+$  channels, the bile-salt export pump, cytochrome P450s, and the purinergic receptor PXR (Bregman et al., 2017). When tested in a neuropathic pain model in mice, AM-1488 reversed tactile allodynia to levels similar to gabapentin and could be administered orally without incurring any motor side effects (Bregman et al., 2017; Huang et al., 2017).

Modification of the pyrrolidine moiety to incorporate a methyl group at the 2 position (AM-3607) further enhanced potency, achieving a potency two orders of magnitude greater than the initial hits (Bregman et al., 2017; Huang et al., 2017). AM-3607 progressed onto structural studies and was cocrystallized with glycine using a modified human GlyR $\alpha_3$ , in which the ICD was

replaced by a tripeptide linker and the ECD glycosylation site removed (Huang et al., 2017). AM-3607 is bound to a novel intersubunit binding site within the ECD (Fig. 7A). The benzodioxole moiety sits approximately 10Å above the glycine binding site and stacks between Y161(+) from loop B and D84(-) from the  $\beta_3$  strand. The oxygens from the sulfonamide group are coordinated by R29(+), whereas the pyrrolidine moiety buries within a hydrophobic cavity formed by F32(+) and the  $\alpha_1$   $\alpha$ -helix (P10, F13, L14) and the  $\beta_2$ - $\beta_3$  loop (Y78, L83) of the neighboring subunit. Sulfonamide binding is hypothesized to enhance agonist affinity by stabilizing the orthosteric binding pocket. This likely occurs through loop B, which lines both cavities and participates in binding interactions with glycine and AM-3607 simultaneously.

Amgen also conducted further screens of commercial compounds based on the primary leads. These screens used known parameters of the developing pharmacophore and strict pharmacokinetic properties. This yielded compounds with azetidine and methoxy-phenyl groups replacing the tricyclic moiety and compounds containing multiple trifluoro-functional groups (Chakka et al., 2017). These compounds were classed as aminothiazole sulfonamides, which contained a lipophilic core and polar termini and adopt similar conformations to AM-3607 when docked into the identified binding site. Other groups have also identified PAMs of GlyRs that contain sulfonamide moieties, such as zonisamide, which is a therapeutically available anticonvulsant. Zonisamide potentiates GlyR $\alpha_1$  and, to a lesser extent, GlyR $\alpha_3$  (Devenish et al., 2021). It potentiates currents elicited by low glycine and taurine concentrations by over 10-fold, likely due to the benzodioxole group interacting with loop B to enhance agonist affinity, similar to AM-3607. However, it has a significantly lower potency due to the simplified amide group replacing the tricyclic moiety, therefore preventing interactions with the adjacent hydrophobic pocket, that stabilizes binding.

The development of sulfonamide PAMs has focused heavily on metabolism and solubility, ensuring the lead compounds remained drug-like and would be orally available. This makes them one of the most likely candidates to be followed through to clinical trials. However, much like other GlyR PAMs, sulfonamides are unable to achieve a greater selectivity for receptors containing the  $\alpha_3$  subunit over the  $\alpha_1$  subunit (Chakka et al., 2017; Huang et al., 2017). Although compounds that bind in the ECD are more likely to achieve greater solubility, this may limit their ability to target GlyR $\alpha_3$ , which is suggested to have a poor ECD-TMD allosteric transduction pathway (San Martin et al., 2019). The inability to selectively target GlyR $\alpha_3$  does not appear to incur motor deficits or other significant side effects at antinociceptive concentrations in rodent neuropathic models (Chakka et al., 2017; Huang et al., 2017); however, this may produce hesitancy in moving forward to

clinical trials. It is unlikely that further pharmacophore development will achieve GlyR $\alpha_3$  selectivity, and thus, further toxicity screening may be required to determine if sulfonamides will be therapeutically viable.

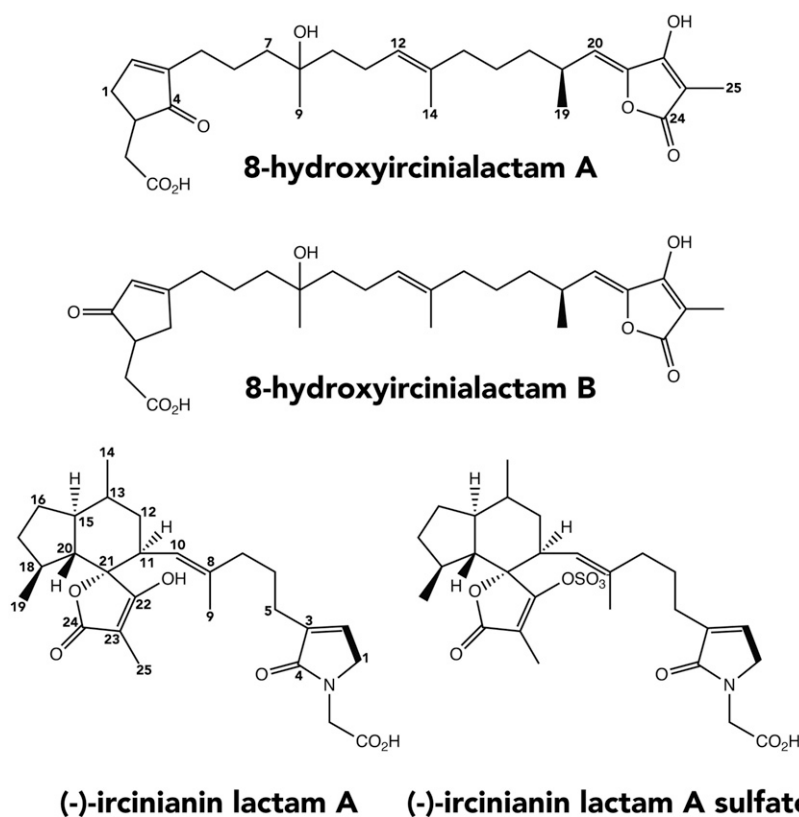
### G. Sesterterpene Glycinyllactams

Sesterterpene glycinyllactams are a class of marine metabolites isolated from sea sponges. They were originally identified in a screen of Australian and Arctic marine invertebrates and algae in an attempt to identify novel PAMs of GlyRs (Balansa et al., 2010). Many of the primary hits from this screen were sesterterpene tetrionic acids, which were later found to have no activity at GlyRs or potentiate GlyR $\alpha_1$  but significantly inhibit GlyR $\alpha_3$ . However, the screen also highlighted glycinyllactam sesterterpenes, which were a rare class of metabolites that had only recently been identified in literature at the time from a Korean sea sponge (Shin et al., 2001; Liu et al., 2003; Wang et al., 2008).

Conjugated tetrionic acid metabolites from the *Irciniidae* sponge family were found to have significant potentiating activity at GlyR $\alpha_1$  if they contained a hydroxyl group at the 8 position (Fig. 8), with all 8-hydroxyl metabolites potentiating glycine currents by over 200% (Balansa et al., 2010). 8-Hydroxyircinialactam B was the first glycinyllactam to be identified that also potentiated GlyR $\alpha_3$  and was the only metabolite where the oxygen within the glycinyllactam moiety was attached in the 1 position. All other metabolites that were inactive or had inhibitory activity at GlyR $\alpha_3$  were not oxygenated

or contained an oxygen attached at the 4 position. This suggested that the 8-hydroxy of the tetrionic acid was important for potentiating activity, whereas the degree of oxygenation and isomerization of the glycinyllactam group conferred subunit selectivity (Balansa et al., 2010). Further screening of metabolites from the *Ianthella* sponge family supported this idea. Structurally similar sesquiterpene metabolites that do not contain a hydroxyl group are devoid of any activity at GlyR, even if they contain an oxygenated glycinyllactam moiety (Balansa et al., 2013b). Several indole alkyls were also identified and significantly inhibited GlyR activity, broadening the scope of this pharmacophore. Ircinianin glycinyllactams were later isolated from *Psammocinia* sponges and also cause modulatory effects. (-)-Ircinianin lactam A contains the 1-oxygenated glycinyllactam moiety, which is now numbered as position 4 (Fig. 8), and selectively potentiates GlyR $\alpha_3$  by 260% (Balansa et al., 2013a). Its sulfonated derivative also potentiates GlyRs, but it is non-selective and less potent, potentiating both GlyR $\alpha_1$  and GlyR $\alpha_3$  by approximately 70%. Several other ircinianin metabolites without the oxygenated glycinyllactam moiety incur modest potentiation of GlyR $\alpha_1$  but were inactive or inhibitory at GlyR $\alpha_3$  (Balansa et al., 2013a), supporting the original hypothesis that the oxygenation and isomerization of the glycinyllactam group confers subunit selectivity (Balansa et al., 2010).

Compounds of this class are promising for therapeutic development due to their ability to selectively potentiate GlyR $\alpha_3$ , which has proven not to be the



**Fig. 8.** Chemical structures of sesterterpene glycinyllactams. Chemical structure of natural sesterterpene glycinyllactams isolated from *Irciniidae* and *Psammocinia* sponge families, which have been shown to modulate glycine receptors. For hydroxyircinialactams, a hydroxyl in the 8 position is important for potentiating activity and an oxygen in the 1 position is required for activity at GlyR $\alpha_3$ . (-)-Ircinianin lactam A derivatives also require a 4-oxygen (corresponding to position 1 in hydroxyircinialactams) for activity at GlyR $\alpha_3$ .

case for other classes of PAM. However, the limited supply of raw material has restricted the ability to study these compounds further. The high number of chiral centers within these compounds makes them difficult to synthesize or modify, therefore relying solely on isolation from natural sources to obtain yields sufficient for functional analysis. This has also prevented the ability to elucidate binding interactions or study their mechanism of action. For these compounds to be considered for therapeutic application, a greater understanding of the pharmacophore would need to be developed by broadening the chemistry of the analogs screened. It has recently been suggested that compounds based on the glycyl-lactam pharmacophore have been synthesized; however, these data are currently unpublished. The newly synthesized derivatives are proposed to maintain the high GlyR selectivity and have favorable physicochemical properties and antinociceptive potency (Lynch et al., 2017). These synthetic analogs may open a new avenue of research for this class of compounds. Importantly, it may allow for production methods that produce sufficient yields for in vivo testing to confirm its potential antinociceptive activity.

### III. Limitations

Despite many known PAMs of GlyRs showing promising antinociceptive activity, there is a hesitancy in developing them for therapeutic application due to their nonselective nature. Additionally, several of the primary candidates are highly lipophilic and bind within the TM domains of the receptor, which can be significantly impacted in vivo by endogenous modulators. Overall, these limitations raise concerns regarding potential on- and off-target side effects and whether these modulators can achieve in vivo efficacy.

#### A. Side Effects and Subunit Selectivity

Glycine neurotransmission is not only involved in nociceptive signaling but also aids in motor and respiratory control, the reward system, and sensory perception (reviewed by Zeilhofer et al., 2018). Therefore, potential target-related adverse effects must be considered when developing PAMs for therapeutic application. A primary concern is GlyR $\alpha_1$  expression throughout the Böttinger complex, which exerts inhibitory control on the respiratory system (Schmid et al., 1991; Zeilhofer et al., 2018). Mice containing hyperekplexic mutations within the  $\alpha_1$  subunit and GlyR $\alpha_1$  knockout mice incur severe motor deficits and respiratory abnormalities, which often results in premature death (Buckwalter et al., 1994; Harvey et al., 2004; Hirzel et al., 2006; McCracken et al., 2013). This has likely deterred pharmaceutical companies from advancing modulators that significantly potentiate receptors containing the  $\alpha_1$  subunit, despite promising antinociceptive activity (Bregman et al., 2017; Huang et al., 2017).

GlyR $\alpha_3$  has also been implicated in respiration; however, GlyR $\alpha_3$  knockout mice survive with no obvious respiratory deficits or only minor abnormalities (Harvey et al., 2004; Manzke et al., 2010). The  $\alpha_3$  subunit also has a more restricted expression within the central nervous system (CNS) (Baer et al., 2009; Burgos et al., 2016). This suggests that PAMs that selectively target GlyR $\alpha_3$  may reduce the potential for on-target adverse effects and be more selective for nociceptive neurotransmission. However, obtaining GlyR $\alpha_3$ -selective potentiators has proven to be difficult. Only the sponge derivative (-)-ircinianin lactam A has been shown to selectively potentiate GlyR $\alpha_3$  (Balansa et al., 2013a); however, its mechanism of action, pharmacokinetic profile, off-target effects, and in vivo activity are yet to be determined. An alternate avenue may be to develop modulators that selectively potentiate the alternatively spliced GlyR $\alpha_1^{\text{ins}}$  and GlyR $\alpha_3^{\text{ins}}$  expressed within the spinal cord (Malosio et al., 1991b). However, this would likely prove difficult due to the high sequence similarity and due to the insert occurring in the ICD, which is the only region of the GlyR yet to be structurally determined.

Despite GlyR involvement in respiration, PAMs that significantly modulate the  $\alpha_1$  subunit have been used without incurring respiratory depression or significant motor deficits. Primary examples of this are tropisetron and Sativex (THC plus CBD). Tropisetron, THC, and CBD have all been shown to significantly potentiate GlyR $\alpha_1$  (Chesnoy-Marchais, 1999; Hejazi et al., 2006; Yang et al., 2007; Ahrens et al., 2009) and are currently used as therapeutics in many countries without incurring severe or intolerable side-effect profiles (Gulbransen et al., 2020; Johnson et al., 2013). Interestingly, both of these drugs are used to treat neuropathic pain or pain-related conditions (Haus et al., 2000; Stratz and Müller, 2000; Stratz and Muller, 2004; Nurmikko et al., 2007; Johnson et al., 2013); however, their nociceptive activities are largely attributed to other proteins. This suggests that the adverse on-target side effects from GlyR $\alpha_1$  may be overstated, and prior suggestions to avoid the receptor for analgesic drug development may be unnecessarily cautious. Further research into the potential toxic side effects and the therapeutic window of GlyR PAMs must be conducted to shed light on this discrepancy and progress this area of research.

#### B. Protein Selectivity

Due to the high degree of sequence and structural similarity between pLGICs, many GlyR modulators also incur modulatory activity at other receptors. This greatly enhances the possibility of off-target side effects and likely reduces the therapeutic window of these compounds. Examples of this include tropeines, which significantly modulate 5-HT $_3$ Rs (Simpson et al., 2000) that are expressed through the CNS and digestive system (Thompson and Lummis, 2006); avermectins, which produce neurotoxic

activity via GABARs (Krůšek and Zemková, 1994; Ménez et al., 2012); and cannabinoids that target the CB1 and CB2 receptors, which causes psychotropic effects (Hejazi et al., 2006; Xiong et al., 2011; Xiong et al., 2012a). Although this makes the current candidates unsuitable for therapeutic application, further insight into their structure-activity relationships could identify distinctive interactions that could be used to enhance GlyR selectivity. Studies that explore alterations within the tropane and indole rings of tropeines have already identified differences between the GlyR and 5-HT<sub>3</sub>Rs and have been used to develop compounds with greater GlyR selectivity (Maksay et al., 2009). Similarly, removing hydroxyl groups from CBD enhances GlyR selectivity over CB1 receptors, which abolishes the psychotropic side effects (Xiong et al., 2012a). Further development of these distinctive interactions could aid in the development of more GlyR-selective compounds and widen the therapeutic window for these drug classes.

Even if complete GlyR selectivity is not obtainable, many of the “off-target” proteins have also been implicated in nociceptive signaling and could be beneficial in achieving multitargeted analgesic compounds. Ongoing research into nociceptive signaling has led to a greater understanding of the complex network involved in nociceptive neurotransmission and has highlighted several targets that may be useful in treating nociceptive pain. This includes GlyRs (Harvey et al., 2004; Miraucourt et al., 2007; Imlach et al., 2016), glycine transporter type 2 (GlyT2) (Dohi et al., 2009; Vandenberg et al., 2014; Zeilhofer et al., 2018), NaV1.7 channels (Dib-Hajj et al., 2017; Hoffmann et al., 2018; Hameed, 2019; Chen et al., 2020), transient receptor potential cation channel subfamily V member 1 (TRPV1) channels (Huang et al., 2006), 5-HT<sub>3</sub>R (Kukushkin and Igon'kina, 2003; Nasirinezhad et al., 2016), and GABA<sub>A</sub>Rs (Enna and McCarson, 2006; Zeilhofer and Zeilhofer, 2008). Traditional drug development has aimed to produce compounds selective for a single nociceptive target; however, this may be insufficient for attenuating sensitization across all signaling pathways and likely activates complex cellular mechanisms in vivo that can circumvent pharmacological effects (Csermely et al., 2005). Primary examples of this are AZD1386 and AMG517, which are both selective TRPV1 antagonists that failed in clinical trials due to lack of efficacy and toxic side effects occurring at concentrations required to produce antinociception (Pang et al., 2012). This indicates that selectively targeting TRPV1 is not a viable way to produce antinociception (Gavva et al., 2008), despite this channel being a prominent protein within the nociceptive signaling pathway and showing promising results in vitro (Huang et al., 2006; Szallasi et al., 2006). Developing multitargeted therapies may achieve greater efficacy in vivo as they are more likely to cause synergetic mechanisms that result in whole-system changes and are less likely to

be impacted by compensatory mechanisms or cause toxicity (Csermely et al., 2005; Pang et al., 2012).

This approach is already being explored with lipid PAMs of GlyRs (Sheipouri et al., 2020). A series of *N*-acyl amino acids that potently inhibit GlyT2 (Mostyn et al., 2017), the transporter responsible for removing glycine from nociceptive synapses (Vandenberg et al., 2014), has recently been screened on GlyRs and found to produce modulatory activity (Gallagher et al., 2020). One of the most efficacious GlyT2 inhibitors has been shown to cause antinociceptive activity in a rodent model of neuropathic pain (Mostyn et al., 2019a); however, a dual-acting lipid has yet to be tested in vivo. This would be expected to achieve even greater antinociceptive activity by synergistically enhancing glycine concentrations and potentiating GlyRs at nociceptive synapses, thus requiring a lower concentration to achieve antinociceptive activity and lowering the chance of adverse side effects. Furthermore, this multitarget mechanism may be responsible for the antinociceptive activity that occurs with tropisetron and cannabinoids that are already clinically available (Haus et al., 2000; Stratz and Müller, 2000; Stratz and Müller, 2004; Nurmikko et al., 2007; Johnson et al., 2013). Despite cannabinoids not currently being considered a first-line pain medication, cannabinoid-containing products have been prescribed to over 84,000 individuals in Australia to treat chronic pain (Henderson et al., 2021). They have also been shown to elicit superior antinociceptive effects and have better long-term outcomes in patients that are refractory to other first-line medications such as opioids (Johnson et al., 2013). This likely occurs due to their multitargeted effects, including their potentiation of GlyRs. Future research into multitargeted antinociceptive drug development may shed a light on why many promising compounds fail during or prior to reaching clinical trials and may aid in the development of analgesics that achieve therapeutic effects in vivo.

### C. Poor Pharmacokinetic Profiles

Many of the current drug leads for GlyR PAMs are lipophilic compounds that bind within the TM domains. Lipophilic compounds are often overlooked for drug development as they do not fit Lipinski's rules for drug likeness (Lipinski et al., 2001) and have poor bioavailability when utilizing desirable administration routes, such as oral administration (Porter et al., 2007). However, even within Lipinski's rules, there are several caveats that open the possibility of lipophilic drug discovery, including lipophilicity rules not holding true for lipids that are substrates for active transporters (Lipinski et al., 2001; Benet et al., 2016). There are several transporters present within the blood-brain barrier that transport lipophilic compounds into the CNS, including the fatty acid transporter protein and fatty acid binding proteins (Mitchell and Hatch, 2011; Mitchell et al., 2011). There is also evidence that

suggests the existence of an endocannabinoid transporter responsible for accumulating lipophilic endocannabinoids such as anandamide (Fowler, 2013). A primary candidate is the sterol carrier protein-2, which is expressed in the brain and has been shown to mediate anandamide translocation (Liedhegner et al., 2014; Hillard et al., 2017). Lipophilic drugs may therefore attain sufficient concentrations within the CNS if they act as substrates at one of the active lipophilic transporters.

Lipid-based drugs indeed already exist. Most notably fingolimod, which is a lipophilic, orally available multiple sclerosis treatment that transverse the blood-brain barrier to act on sphingosine-1-phosphate receptors within the CNS (Brinkmann et al., 2010; Hunter et al., 2016). Alternate pathways of administration are also being explored, including sublingual administration, which is used for lipophilic cannabinoid-based therapies (Xiong et al., 2012a; Urits et al., 2020). This helps bypass first-pass hepatic metabolism and avoid lipid metabolism—another issue for lipid-based drug discovery (Markovic et al., 2020; Piferi et al., 2021). However, intranasal, transdermal, and nanotechnology-based administration methods are also being explored to enhance systemic availability (Bruni et al., 2018).

Many of the lipophilic PAMs of GlyRs are in their initial stages of drug discovery and require further development before they can be considered for therapeutic application. As a greater understanding of their structure-activity relationships are developed, optimization of drug leads can be conducted to enhance drug likeness, reduce metabolic functional groups, or enhance their activity at lipophilic transporters. Despite the traditional understanding of small-molecule drug design, it may be possible to design lipophilic drugs that are still highly effective and bind within the TM domains.

#### D. Impact of Endogenous Mediators

In addition to PAMs that have been developed through drug design, there are several endogenous compounds that can modulate GlyR function in vivo. Many of these have important physiologic functions or are implicated in disease states such as hyperekplexia (Al-Futaisi et al., 2012; Zhou et al., 2013) and inflammatory pain (Harvey et al., 2004). In particular, the ICD is susceptible to many intracellular processes such as phosphorylation (Ahmadi et al., 2002; Han et al., 2013; Moraga-Cid et al., 2020), ubiquitination (Buttner et al., 2001; Zhang et al., 2019b), and protein binding (Kirsch et al., 1991; Yevenes et al., 2003; Yevenes et al., 2006; Breitingner et al., 2020). These processes can alter the expression and functional properties of the receptor, which can be difficult to mimic in vitro. Furthermore, endogenous modulators that produce significant functional and structural changes may disrupt how

exogenous PAMs designed for drug development interact with the receptor in vivo.

The most well studied endogenous mediator of GlyRs is zinc, which is a potent biphasic modulator that potentiates receptor activity between 10 nM and 10  $\mu$ M and inhibits activity at concentration above 100  $\mu$ M (Bloomenthal et al., 1994; Lynch et al., 1998; Harvey et al., 1999; Miller et al., 2005). Zinc is present throughout the nervous system and colocalizes within glycinergic vesicles at nociceptive synapses (Birinyi et al., 2001), where it tonically mediates neuronal excitability (Zhang and Thio, 2007) and nociceptive sensitivity (Jo et al., 2008). The tonic concentration of zinc in the extracellular space is estimated to be in the low nanomolar range (Frederickson et al., 2006); however, it can reach synaptic concentrations of at least 10  $\mu$ M during activation (Zhang et al., 2016). Within this physiologic concentration range, zinc can endogenously modulate both synaptic and nonsynaptic GlyRs and has been shown to act presynaptically to facilitate glycine release (Birinyi et al., 2001).

Zinc has also been shown to synergistically enhance the activity of other PAMs—in particular, enhancing ethanol modulation of homomeric GlyRs (McCracken et al., 2010; McCracken et al., 2013a,b). When tested on GlyRs expressed in *X. laevis* oocytes, the potentiation achieved by the coapplication of zinc and ethanol was greater than the sum of their individual effects, which suggests a synergistic mechanism (McCracken et al., 2010). As zinc is a ubiquitous contaminant in many buffers, purified products, and on common laboratory ware (Kay, 2004; Cornelison and Mihic, 2014), it has been suggested to impact previous functional analyses of GlyRs and has caused overestimations of PAM effectiveness. It is suggested that studies assessing PAMs of GlyR take additional steps to assess their activity in the absence of zinc. Several studies have used metal chelators, including tricine (Kirson et al., 2013; McCracken et al., 2013; Cornelison et al., 2017; Gallagher et al., 2020), EDTA (Kay, 2004; Trombley et al., 2011), and ZX1 (Perez-Rosello et al., 2015; Zhang et al., 2016) in an attempt to remove contaminating zinc from recording solutions; however, these chelators are not completely selective and thus can disrupt functional analysis by chelating other divalent ions in recording solutions such as calcium and magnesium (Ramos Silva et al., 2001; Radford and Lippard, 2013). Some studies have suggested these chelators have minimal impact on baseline controls; however, this does not negate the possibility that chelators may interact with PAMs in solution or with the GlyR itself. Other groups have used zinc-insensitive mutants such as GlyR $\alpha_1$  W170S (Zhou et al., 2013) to screen PAMs (Cornelison et al., 2017). It is important to determine the effectiveness of novel PAMs in the presence and absence of zinc to ensure they are likely

to be effective *in vivo* and to determine possible synergistic effects that may enhance their activity at nociceptive synapses where zinc colocalizes with GlyRs (Birinyi et al., 2001).

Cholesterol has also been shown to modulate GlyR function. Cholesterol is an integral part of cell membranes that can indirectly modulate membrane proteins by altering the physiochemical properties of the lipid bilayer (Cathcart et al., 2015; Subczynski et al., 2017). However, cholesterol can also directly modulate membrane proteins by binding deeply within nonannular sites, thus acting as a PAM (Henin et al., 2014; Damgen and Biggin, 2021). In addition to its direct effects, cholesterol is also a precursor in the synthesis of endogenous neurosteroids (Reddy, 2010), including pregnenolone and dehydroepiandrosterone, which have both been shown to modulate GlyRs (Maksay et al., 2001; Weir et al., 2004). Both cholesterol and neurosteroids have been shown to bind within the TM domains within cavities that overlap with ivermectin, alcohols, anesthetics, and cannabinoids (Henin et al., 2014; Lavery et al., 2017; Miller et al., 2017; Chen et al., 2018; Damgen and Biggin, 2021).

Similar to zinc, cholesterol has also been shown to impact the activity of other PAMs, in particular the cannabinoids THC, anandamide, and CBD (Yao et al., 2020). Cholesterol has been shown to alter the suspected cannabinoid binding cavity within the TM domains, which impacts cannabinoid antinociception *in vivo* (Yao et al., 2020). This could also impact the activity of other PAMs *in vivo* and should be taken into consideration when determining PAM activity. The membrane cholesterol content used for MD simulations can vary greatly and thus impact their results (Yao et al., 2020). Furthermore, the cholesterol content varies between commonly used cells lines such as *X. laevis* oocytes and HEK293 cells (Brannigan, 2017), which both contain less cholesterol than neuronal membranes (Ingólfsson et al., 2017). Cholesterol levels also vary greatly between individuals (Tharu and Tsokos, 2017), and this may be something to consider when developing GlyR mediated analgesics—in particular their use with commonly prescribed cholesterol-lowering drugs like simvastatin.

Recently, glucose has also been shown to modulate glycine receptors at physiologically relevant concentrations (Breitinger et al., 2015; Breitinger and Breitinger, 2016; Breitinger et al., 2016) and produce GlyR-mediated antinociception in rodent models of pain (Yamamoto et al., 2014; Hussein et al., 2019). As glucose is a required supplement for many mammalian-derived cell lines and is often present within cell media, it may be an underlying factor that causes discrepancies between functional studies of GlyRs. Studies conducted using HEK293 cells found that glucose was able to significantly shift the glycine dose response of both homomeric and heteromeric GlyRs and significantly

reduced the variability between experiments (Breitinger et al., 2015; Breitinger and Breitinger, 2016). This is suggested to occur through irreversible glycation of GlyRs within the ECD and TM domains, proximal to the ivermectin binding cavity (Hussein et al., 2020).

Blood glucose levels in healthy individuals vary between 2.2 and 8 mM; however, they can increase to over 15 mM in diabetic patients (Oyibo et al., 2002; Petersmann et al., 2019). As there is a linear correlation between blood glucose levels and glucose concentration in the cerebrospinal fluid, even during hyperglycemia, this permits spinal concentrations to exceed 8 mM (Leen et al., 2012). Within these ranges, glucose can significantly modulate GlyRs (Breitinger et al., 2015; Breitinger and Breitinger, 2016) and likely impacts nociceptive signaling, especially for those with diabetic pain. Indeed, diabetic patients with painful neuropathy were found to have greater glucose flux compared with those without pain (Oyibo et al., 2002). Glucose has also been shown to modify descending inhibitory modulation of the spinal cord to tonically mediate nociceptive signaling (Terry et al., 2016) and can be triggered by nociceptive stimuli (Sim et al., 2012). This not only suggests that glucose can function as an endogenous mediator of nociception but may also be a confounding factor in several *in vivo* studies. If glucose concentrations are not maintained across test groups, this may have significant impacts on baseline nociception levels and on the ability to modulate glycine neurotransmission. Additionally, PAMs that are anticipated to produce antinociception by binding within the same cavity as glucose may be unable to bind and could explain the poor *in vivo* efficacy of many PAMs of GlyRs. Future research may benefit from testing PAMs in the presence of physiologically relevant glucose concentrations to ensure the likelihood of compounds retaining efficacy in endogenous conditions.

#### IV. Conclusion

Positive modulation of GlyRs has been shown to produce antinociceptive effects and may provide a promising avenue for the development of novel pain therapies. The findings summarized in this review outline the development of currently known PAMs of GlyRs and their ability to influence nociceptive signaling. Recent advances in structural techniques have also improved our understanding of the molecular mechanisms underpinning their modulation and have facilitated structure-based design of novel therapeutics. Future studies that explore the limitations of receptor selectivity and adverse effects associated with this approach are also required to ensure these novel therapeutics provide a safer and more effective solution compared with the current first-line pain medications.

### Authorship Contributions

Wrote or contributed to the writing of the manuscript: Gallagher, Ha, Harvey, Vandenberg.

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