

Regulation of GABA_AR Signaling and Neuroadaptations in Response to Diazepam

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Despite 50+ years of use as anxiolytics, anti-convulsants, and sedative/hypnotic agents, the mechanisms underlying benzodiazepine (BZD) tolerance are poorly understood. BZDs potentiate the actions of GABA, the primary inhibitory neurotransmitter in the adult brain, through positive allosteric modulation of $\gamma 2$ subunit containing GABA type A receptors (GABA_ARs). Sustained treatment with BZD drugs is intimately associated with the development of tolerance, dependence, withdrawal and addiction. BZD efficacy diminishes after prolonged or high dose acute exposure, with tolerance to the sedative/hypnotic effects forming most quickly. We investigated the adaptive mechanisms occurring during initial exposure to the classical BZD, Diazepam (DZP), and the molecular signature of the mouse brain during established sedative tolerance. We found cultured neurons treated 24 h with DZP presented no change in surface or synaptic levels of $\gamma 2$ -GABA_ARs. In contrast, both $\gamma 2$ and the key inhibitory synaptic scaffolding protein gephyrin levels were decreased after a single DZP treatment *in vitro* and *in vivo*. Live-imaging and label-free quantitative proteomics further revealed alterations in $\gamma 2$ subunit surface trafficking, internalization and lysosomal targeting. In comparison, mice treated seven days with DZP had altered GABA_AR subunit composition, reduced responsiveness to DZP, and tonic inhibition was diminished. Furthermore, DZP increased excitatory NMDA receptor subunit levels and function. State of the art mass spectrometry experiments revealed increased CaMKII subunits, which are positive regulators of NMDA receptors and involved in tolerance to other drugs. Downstream bioinformatics analysis confirmed robust synaptic plasticity after DZP. Together, we describe a time-dependent downregulation of synaptic GABA_AR function after initial DZP exposure

followed by an adaptive increase in excitatory neurotransmission, neuronal remodeling and altered synaptic GABA_AR composition.

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1.0 Introduction

Chapter adapted from:

1) Lorenz-Guertin, J. M. and T. C. Jacob (2017). GABA type a receptor trafficking and the architecture of synaptic inhibition. *Develop Neurobiol*
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1.1 The GABA Type A Receptor

GABA_A receptors (GABA_ARs) are ligand-gated ionotropic chloride (Cl⁻) channels responsible for most fast inhibitory neurotransmission in the mature central nervous system (CNS). Ubiquitous expression supports their central role in regulating most aspects of CNS function. Binding of the neurotransmitter GABA induces GABA_AR ion channel opening, Cl⁻ influx, and subsequent membrane hyperpolarization (**Fig. 1A**). These receptors are heteropentameric structures typically composed of two α (α 1-6), two β (β 1-3), and either a γ (γ 1-3) or a δ subunit (2). Subunits share a common structure consisting of a large N-terminal extracellular domain (ECD) that participates in GABA binding, transmembrane domains (TM) comprised of four α -helical regions (TM1-4) and a small extracellular C-terminus (**Fig. 1C**). The TM regions are connected by a small intracellular loop between TM1-TM2 and a much larger intracellular domain (ICD) between TM3 and TM4 that undergoes extensive post-translational modifications and is key for protein trafficking and function (**Fig. 1C**). The most common GABA_ARs providing fast synaptic inhibition in the mature mammalian cerebral cortex contain α 1 β 2 γ 2 subunits (**Fig. 1B**) (3). As viewed from outside the cell GABA_ARs are arranged in a counterclockwise subunit

configuration of γ - β - α - β - α (**Fig. 1B**) (4, 5). Despite the great diversity of GABA_AR subunits (α 1-6, β 1-3, γ 1-3, δ , ϵ , θ , π , ρ 1-3) and possible configurations, these receptors produce two types of currents: synaptic (phasic) and tonic. Presynaptic terminal release of GABA onto post-synaptically

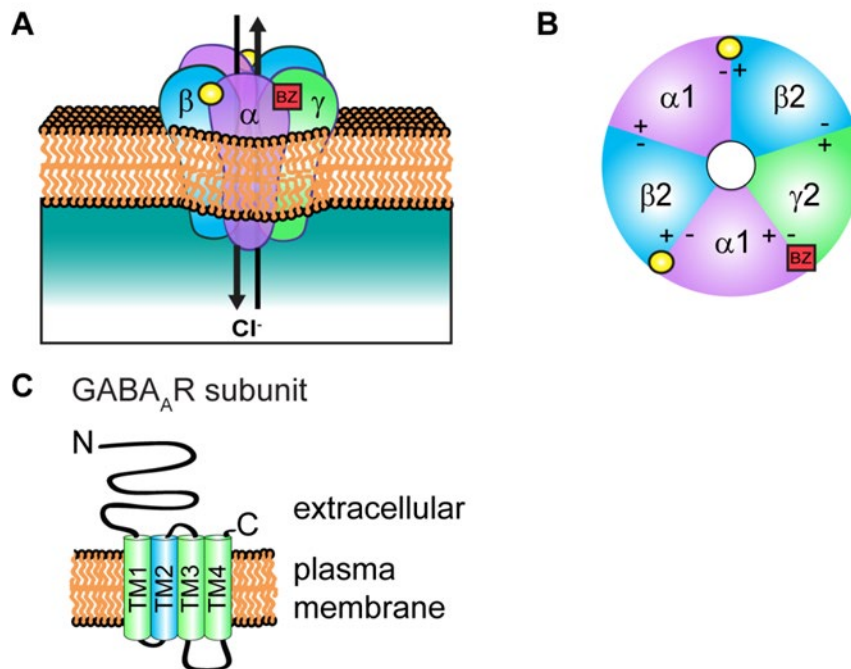


Figure 1. GABA_AR Structure and Subunit Topology.

A) A representation of the heteropentameric GABA_AR composed of $\alpha\beta\gamma$ subunits. Binding of the neurotransmitter GABA (yellow circle) at the $\alpha\beta$ interface triggers ion channel opening and allows the rapid influx of Cl^- and membrane hyper polarization in the mature nervous system. (B) Extracellular representation of the receptor showing all five subunits contributing to the central ion pore and the general binding sites of GABA (yellow circle) and benzodiazepines (BZs) (red square). BZs bind at the interface of an α 1/2/3/5 and γ subunit. (C) All subunits have a common topology including an extracellular N-terminal domain, short C-terminal tail, and four transmembrane domains (TM1–4). GABA_AR subunit TM2 (blue) contributes to formation of the receptor ion channel pore, while the intracellular domain (ICD) between TM3 and TM4 contain sites of phosphorylation and protein interactions that modulate channel function and/or trafficking. Adapted from: Lorenz-Guertin, J. M. and T. C. Jacob (2017). GABA type a receptor trafficking and the architecture of synaptic inhibition. *Develop Neurobiol.*

clustered GABA_ARs triggers fast, transient synaptic currents, while ambient “spill over” GABA generates a persistent tonic current via activation of extrasynaptic receptors. GABA_AR subunit composition therefore determines receptor cell surface localization, electrophysiological properties and drug sensitivities.

In addition to their inhibitory function in the mature CNS, GABA_ARs are of fundamental importance in organization of newly forming circuits by promoting dendritic outgrowth and synaptogenesis. Synapses develop first with the emergence of excitatory GABAergic synaptic signals that drive the subsequent establishment of glutamatergic synapses, before GABA neurotransmission shifts to functioning as an inhibitory signal (6-9). Underlying deficits in GABAergic neurotransmission occur in a wide variety of neurological disorders such as epilepsy, psychiatric disorders (anxiety (10, 11), depression (12, 13), post-traumatic stress disorder (14-17)) and neurodevelopmental disorders including autism (18-21), Fragile X (22, 23) and schizophrenia (24-26). Importantly, pathophysiological events including seizures (27), ischemic stroke (28-30), traumatic brain injury (31) and stress can cause adaptive changes in GABA_AR neurotransmission, compromising GABAergic inhibition and further hampering recovery.

1.2 GABA_AR Pharmacology

1.2.1 GABA_AR Clinical Agents

The ubiquitous expression of GABA_ARs in the CNS makes these receptors key drug targets to enhance inhibition and globally dampen neuronal activity. Multiple clinically recognized agents exert actions at GABA_ARs specifically or non-specifically including barbiturates, benzodiazepines

(BZDs), benzodiazepine-site ligands, barbiturates, intravenous and volatile anesthetics, ethanol and neuroactive steroids (32). In general these drugs induce distinct conformational states of GABA_ARs thereby altering the efficacy of GABA-mediated receptor activation. The site of GABA_AR drug action is highly dependent on GABA_AR subunit composition and binding site interfaces. For example, BZDs bind between the interface of a $\gamma 2$ subunit and a directly adjacent $\alpha 1/2/3/5$ subunit at the ECD (**Fig. 1B**) (33). In contrast, transmembrane domain interactions between non α/γ subunit interfaces mediate binding drugs like etomidate, propofol, barbiturates, volatile anesthetics, octanol, and neuroactive steroids (34). Importantly, a recent surge in high-resolution GABA_AR structural findings (35-40) have dramatically expanded our molecular understanding of drug binding sites and the physical changes in receptor conformation that mediate downstream signaling and clinical effects. GABA_AR structures for the human $\beta 3$ homopentamer bound to benzamidine (35), chimeric $\alpha 5\text{TM}/\beta 3\text{ECD}$ bound to the neurosteroid allopregnanolone (37), human $\alpha 1\beta 2\gamma 2$ heteropentamer bound to the benzodiazepine site antagonist Flumazenil (36), the human $\alpha 1\beta 3\gamma 2$ GABA_AR in a lipid bilayer (38), as well as full-length $\alpha 1\beta 3\gamma 2\text{L}$ bound in different conformations in the presence of a channel-blocker, agonist or competitive antagonist, or the BZDs alprazolam and DZP (39) have all been recently resolved. One notable finding from this work is the physical identification of an additional second low-affinity DZP binding site between the $\beta 3/\alpha 1$ receptor interface (39), consistent with the biphasic response seen in electrophysiology studies using high DZP concentrations (41).

1.2.2 BZD Clinical Use and Tolerance

No GABA_AR drug class has been more heavily utilized clinically or subject to more intensive research efforts than BZDs. The BZD drug class was first introduced in the 1960's by

the company Hoffman-La Roche with the release of the revolutionary drug chlordiazepoxide (Librium) (42). As compared to the widely-used CNS depressant barbiturate agents, chlordiazepoxide demonstrated significantly less dangerous side effects, most notably respiratory depression. By 1963, the second and more potent BZD, diazepam (DZP; Valium), also entered the marketplace. Before long, DZP became one of the top selling drugs in the history of mankind (43). The wide-spread use of these drugs propagated a need to characterize their pharmacological target and mechanism of action, ultimately leading to the discovery of the GABA_AR (also referred to as the “BZD receptor” up until the early 2000s). Clinically, BZDs are used for their sedative, myorelaxant, anticonvulsant and short term memory loss effects. Multiple BZD type drugs exist with differing pharmacokinetic/pharmacodynamics profiles and some selectivity for specific GABA_AR subtypes.

The classical BZD, DZP, belongs to a subclass of non-selective, long-acting BZDs that includes the drug flurazepam (Dalmane). Intermediate-acting BZDs (example: alprazolam; Xanax) have relatively shorter half-lives compared to DZP and flurazepam and their metabolites, where the elimination half-life may take up to 48 h in humans. A subclass of short-acting BZDs with half-lives of 1-4h are also available, namely midazolam (Versed) and triazolam (Halcion). These differences in half-lives, as well as other characteristics including peak onset time and drug administration options, provide clinicians multiple BZD therapy options to suit the preferred therapeutic outcome. This catalog of BZD drugs is heavily utilized in medicine; in 2008 approximately 5.2% of US adults aged 18-80 used BZDs according to one study (44). Additionally, a more recent survey from 2015-2016 found 12.6% of adults reported BZD use in the last year (45). Shockingly, 25.3 million individuals reported taking the drug as prescribed, while 5.3 million were reported to be misusing the drugs.

The chronic use of BZD drugs manifests in a number of behavioral and physical symptoms including tolerance, withdrawal, addiction and dependence. Requiring a higher dose of a drug to achieve the same therapeutic effect overtime is known as tolerance, and is a hallmark of BZD use. At the molecular level, positive allosteric modulation by BZD enhances GABA_AR inhibition by increasing the binding affinity of GABA and increasing ion channel opening frequency (33). This potentiating effect of BZD is lost after prolonged or high dose acute exposure in animal models and humans, characterized first by a loss of sedative/hypnotic activity followed by the anti-convulsant and potentially anxiolytic properties (46). 2-Deoxyglucose quantitative autoradiography in BZD-treated rats suggests that tolerance initiates in the cerebral cortex (47), a region with diverse roles in sensory and motor processing, anxiety (48), memory (49) and sleep (50). The induction of BZD tolerance occurs in part due to the uncoupling of allosteric actions between GABA and BZD, leading to diminished potentiation of BZD on GABA-induced current and a loss in the ability of GABA to potentiate BZD binding (51, 52). Resolving the neuroadaptations that occur after BZD treatment and the molecular mechanisms regulating GABA_AR function and drug responsiveness will provide a critical step in building towards new treatment paradigms that limit the harmful side effects of BZD agents.

1.3 GABA_AR Regulation and Surface Localization

1.3.1 Key GABAergic Synapse Components

The confinement of GABA_ARs at synaptic sites is a key step in tuning the strength of phasic inhibition, receptor function and drug response (53) (**Fig. 2**). The postsynaptic inhibitory

scaffolding protein gephyrin is the main organizer of GABA_AR synaptic localization and density (54), as gephyrin knock out mice exhibit a robust loss of GABA_AR clustering (55), although gephyrin-independent synaptic clustering does occur (56, 57). Gephyrin is a highly conserved 93 kDa protein that is hypothesized to form multimeric complexes which associate with a number of cytoskeletal proteins (58), contributing to its scaffolding function (59). The architecture of gephyrin scaffolding arises from the N-terminal or G-domain of gephyrin participating in dimer-dimer self-associations, while the C-terminal or E-domain forms trimer interactions, likely to create a hexagonal lattice (60, 61). This structure tethers freely-diffusing receptors at synaptic sites through binding GABA_AR α 1, α 2, α 3, α 5, β 2, and β 3 subunits (62-65). The GABA_AR γ 2 subunit also plays an important role in gephyrin-receptor attachment, as γ 2-knockout mice demonstrate diminished clustering of gephyrin and GABA_ARs (66, 67). Importantly, synaptic GABA_AR clustering can occur independent of γ 2 in some cases (68). Functionally, gephyrin acts to confine receptors undergoing diffusion at the cell surface membrane and limit their escape into the extrasynaptic space, a process that is influenced by neuronal activity and GABA_AR specific drugs including DZP (69, 70).

Gephyrin's scaffolding ability is regulated by extensive post-translational modifications. Mass spectrometry studies alone have revealed 22 sites of phosphorylation in gephyrin's C-domain and 1 additional threonine 324 (Thr324) site in the E-domain (71-73). Yet, the exact role of gephyrin phosphorylation is complex and controversial, highlighted by the bidirectional effect of altering gephyrin phosphorylation at the serine (S) 270 site. Initial findings by Tyagarajan et al. (2011) (74) identified phosphorylation of this site by Glycogen Synthase Kinase 3 β (GSK3 β) to negatively modulate gephyrin clustering via enhanced Ca²⁺-dependent protease calpain-1 mediated degradation. Accordingly, overexpression of a phosphodeficient S270A gephyrin mutant

enhanced both the amplitude and frequency of miniature inhibitory postsynaptic currents (mIPSCs), suggesting increased functional GABA_AR clustering. It was later revealed that the S270 site was also a substrate for the proline-directed serine/threonine kinase, cyclin-dependent kinase 5 (CDK5) (72, 75). Gephyrin synaptic clusters were found to be basally phosphorylated at Ser270 in a CDK5-dependent manner (72), with CDK5 knockdown or inhibition leading to loss of phosphorylated gephyrin clusters and postsynaptic γ 2-containing GABA_A receptors (75). To further complicate these findings, S270 is cross-regulated by phosphorylation of a neighboring S268 residue targeted by extracellular signal-regulated kinase 1/2 (ERK1/2) (73) (role for ERK also described in (76)). This study suggested these serine residues control distinct gephyrin clustering dynamics including postsynaptic cluster size and number, again in conjunction with calpain activity. Expanding the role of gephyrin serine site regulation, phosphomutant studies and *in vitro* kinase assays indicate that increased phosphorylation of gephyrin on S305 (mass spectrometry identification by Tyagarajan et al) by the kinase CAMKII is required for activity-dependent inhibitory plasticity (77). Considering the number of additional gephyrin phosphorylation sites identified *in vivo* and the challenges of gephyrin point mutant studies (overexpression concerns), continued multidisciplinary efforts are necessary to resolve the functional relevance of these modifications.

Transsynaptic proteins are also key to GABAergic synapses formation and stability. One of the most well characterized trans-synaptic interactions crucial for GABA_AR synapse development is that of neuroligins and neurexins (78) (**Fig. 2**). Neurexins are found presynaptically and induce differentiation of GABAergic and glutamatergic postsynaptic densities during maturation and plasticity (79, 80), although overexpression of neurexins leads to reduced GABAergic neurotransmission (81). Postsynaptically, different neuroligins (NL1-4) are found at either

glutamatergic or GABAergic synapses and play important scaffolding and receptor recruitment roles. GABAergic synapses primarily rely on NL2 for synapse integrity, and when expressed with recombinant GABA_ARs in HEK cells, NL2 supports formation of functional GABAergic synapses in neuron co-culture systems (82). Moreover, NL2 is critical for GABAergic synapse formation and coding in the retina (83), while enhanced expression of this protein in cerebellar granule cells can accelerate GABA_AR synapse development (84, 85) and strengthen inhibitory synaptic function in hippocampal neurons (86).

Our current overall understanding of the proteins involved in inhibitory synapse stability and clustering remains incomplete, as highlighted by two *in vivo* inhibitory synapse proteomic screenings using α 2-pHluorin (pH-sensitive GFP) tagged subunit knock-in mice (87) or viral expression of inhibitory fusion proteins including gephyrin (88). These mass spectrometry methods revealed 140 (Uezu, et al. 2016) and 149 (Nakamura, et al. 2016) novel protein components of GABA_AR/inhibitory synapses spanning multiple trafficking, stability, and regulatory pathways. Collectively, these studies further validated molecular interactions between GABA_AR intracellular loops and the metabotropic glutamate receptor subunit mGluR5, the Dbl family GEF Ephexin, the metabotropic GABA B receptor (GABA_BR) auxiliary subunit KCTD12, and initiated characterization of a novel inhibitory synaptic regulator inhibitory synaptic protein 1 (InSyn1). Our lab recently found DZP-induced changes in γ 2-GABA_AR using label-free quantitative proteomics (details in Chapter 3), identifying new key interactor proteins and changes in their association by a common clinical agent. Future investigations will need to dissect the exact roles of these identified proteins in GABA_AR regulation and function.

1.3.2 Extrasynaptic GABA_ARs

While synaptic receptors participate in phasic inhibition, extrasynaptic GABA_ARs are responsible for setting the inhibitory tone of a neuron through the generation of a constant tonic current. Receptors composed of $\alpha 4\beta\delta$ or $\alpha 6\beta\delta$ subunits are found extrasynaptically and respond to low concentrations of ambient or “spillover” GABA (89-94) (**Fig. 2**). While hippocampal tonic currents are largely generated by synaptic spillover (95), other GABA sources include astrocytes (96, 97), and neurogliaform cells (98). Furthermore, extrasynaptic GABA_ARs can be spontaneously open in the absence of GABA (99). GABA_ARs incorporating the $\alpha 5$ subunit with $\beta\gamma 2$ also represent a large pool of extrasynaptic GABAergic signaling (100, 101), although this receptor subtype can be found clustered both synaptically (63, 102, 103) and extrasynaptically (104). Scaffolding of $\alpha 5\beta\gamma 2$ GABA_ARs extrasynaptically occurs due to interaction with the ERM (ezrin, radixin, moesin) family protein radixin (104), whereas $\alpha 5$ was recently shown to interact with gephyrin at synaptic sites (63).

It is important to note that GABA_ARs undergo Brownian motion at the surface membrane and are continuously diffusing into and out of the synaptic and extrasynaptic space (105), meaning δ containing GABA_ARs can impact synaptic current, and $\gamma 2$ GABA_ARs participate in extrasynaptic tonic current. GABA_AR subtype specific protein interactions regulate the degree of confinement at a given location and GABA_AR diffusion dynamics and localization are highly influenced by activity-dependent changes and various signaling cascades (Section 1.5). For instance, radixin acts in a phospho-dependent manner to scaffold $\alpha 5\beta\gamma 2$ receptors to the actin cytoskeleton ultimately reducing diffusion rates and concentrating channel activity away from axon terminals (106). Bidirectional control of radixin phosphorylation state by the RhoA GTP- and Rho-kinase (ROCK)

dependent pathway is contingent on GABAergic versus glutamatergic activity (**Fig. 2**). Application of GABA favors radixin phosphorylation and retention of $\alpha 5$ -GABA_ARs extrasynaptically, while AMPA treatment leads to dephosphorylation and increased percentage of $\alpha 5$ -subunit receptors found synaptically (106). Additional GABA_AR subtypes are also subject to synaptic/extrasynaptic exchange following manipulations of the excitatory/inhibitory balance and/or kinase signaling. Gerrow & Triller (2014) identified GABA_BR activity increases $\alpha 2$ -GABA_ARs diffusion from synapses via PKC activity, allowing $\alpha 5$ -GABA_AR synaptic accumulation due to available synaptic binding slots (107). PKC-activation also promotes synaptic accumulation of $\alpha 4$ -containing GABA_ARs (108), while PKA-activation shifts $\alpha 4$ -receptors extrasynaptically (**Fig. 2**) (109). These findings highlight the dynamic nature of GABA_AR synaptic/extrasynaptic exchange and the diverse mechanisms to fine-tune GABAergic neurotransmission.

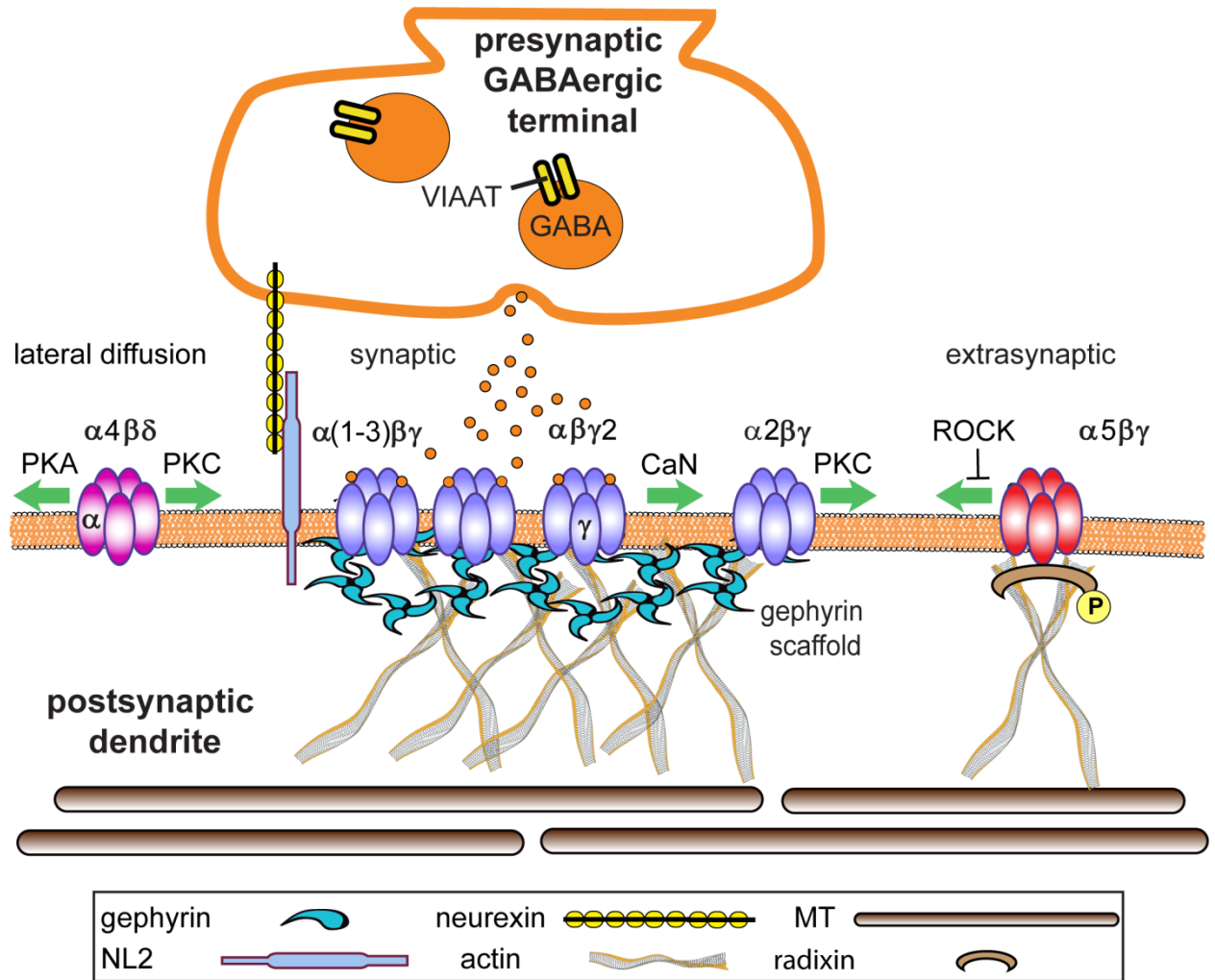


Figure 2. GABA_AR Synapse Structure.

GABA_ARs composed of $\alpha(1-3)\beta\gamma$ subunits are largely synaptically localized via gephyrin interactions and contribute to phasic currents, whereas $\alpha(4/6)\beta\delta$ receptors are extrasynaptic and generate tonic current. $\alpha5\beta\gamma$ receptors are found in both locations due to binding with gephyrin at synapses and radixin extrasynaptically. Proteomics and other modern strategies have significantly enriched the complexity of the inhibitory synapse, however the functions of many new components have yet to be defined. Key synaptic adhesion, scaffold and signaling proteins shown. Adapted from: Lorenz-Guertin, J. M. and T. C. Jacob (2017). GABA type a receptor trafficking and the architecture of synaptic inhibition. *Develop Neurobiol.*

1.4 GABA_AR Intracellular Trafficking

1.4.1 Assembly and Forward Trafficking

GABA_AR biogenesis is controlled via regulated assembly of subunits into heteropentamers within the endoplasmic reticulum (ER). Due to the diversity of receptors generated in recombinant systems during multiple independent subunit transfections, studies on assembly of concatenated subunit constructs have been a major route for determining receptor configuration. GABA_AR studies using heterologous cells show that a β subunit is required for receptor cell surface expression, while the $\alpha\beta$ interface that forms the GABA binding site is required for functional responses. Although unlikely to occur *in vivo*, $\beta 1$ or $\beta 3$ homomeric channels form, while other individual subunit expression leads to ER retention (110, 111). Co-expression of $\gamma 2$ subunits with $\alpha\beta$ leads to preferential assembly of $\alpha\beta\gamma 2$ receptors (112, 113). Receptor complex formation begins with $\alpha\beta$ heterodimer formation, with the N-terminal domains controlling this process. Studies of $\alpha 1\beta 2\gamma 2$ recombinant receptors demonstrate that the N-terminal putative α helical region of the $\alpha 1$ subunit is critical for surface receptor expression, while deletion of the other subunits N-terminal extensions had minimal effects on surface expression (114). Rather, deletion of the $\beta 2$ α -helix decreased GABA sensitivity and receptor desensitization, while $\gamma 2$ N-terminal deletions reduced incorporation of $\gamma 2$ in receptors.

The exit of GABA_ARs from the ER is negatively regulated by constitutive ER-associated degradation (ERAD) (115-117). ERAD recognition of misfolded proteins leads to their dislocation from the ER membrane, ubiquitination via E3 ligases, and proteosomal degradation in the cytoplasm. Chronic neuronal blockade via 24 h tetrodotoxin (TTX) treatment increases $\beta 3$ subunit GABA_AR ubiquitination and ERAD, leading to reduced receptor cell surface expression and

decreased inhibition (117). Conversely, enhanced neuronal activity diminished $\beta 3$ subunit ubiquitination and improved receptor stability. Reduced calcium entry via voltage-gated calcium channels (VGCC) also contributes to ubiquitination and degradation of receptor subunits (118), while enhanced VGCC activity promotes $\beta 3$ S383 phosphorylation and receptor insertion (119), suggesting a mechanistic link to activity-dependent changes. GABA_AR subunit mutations that result in enhanced ERAD contribute to genetically determined epilepsies, or idiopathic generalized epilepsies (IGEs) (120, 121) and altered GABA_AR ERAD is indicated in autism spectrum disorder (ASD) subjects (122)

Once assembled, GABA_ARs undergo transport from the ER to the Golgi apparatus, followed by translocation to the plasma membrane. In the Golgi, the $\gamma 2$ subunit is subject to palmitoylation by the Golgi-specific DHHC zinc finger enzyme (GODZ), a process important for synaptic GABA_AR maintenance and surface expression (123-125). During Golgi forward transport, GABA_ARs are segregated into distinct vesicles from excitatory glutamatergic AMPA receptors, and are subsequently inserted at the cell surface via specialized Rab GTPases and SNARE complexes SNAP23–syntaxin1A/B–VAMP2 and SNAP25–syntaxin1A/B–VAMP2, respectively (126). Proteins contributing to GABA_AR trafficking from the Golgi to the plasma membrane include Big2 (brefeldin A-inhibited GDP/GTP exchange factor 2) (127), GABARAP (GABA receptor-associated protein) (128), GRIP (Glutamate receptor interacting protein) (129, 130), PRIP1/2 (phospholipase C-related catalytically inactive proteins 1 and 2) (131, 132), GRIF-1 (133), Macoco (134), and NSF (135). Vesicular GABA_AR transport from the trans-Golgi network (TGN) to the plasma membrane relies on the microtubule-dependent molecular motor kinesin KIF5 family (KIF5A, KIF5B, KIF5C) (136).

1.4.2 Internalization, Recycling and Lysosomal Degradation

Regulated internalization of cell surface receptors is a universal cellular response to moderate signaling and function. GABA_AR internalization occurs through clathrin-mediated endocytosis dependent on dynamin (the GTPase that is responsible for fission of endocytic vesicles from the plasma membrane) and binding of the adaptor protein AP2 to specific GABA_AR subunits (**Fig. 3**) (137), although clathrin-independent endocytosis occurs in heterologous cells and in *C. elegans* (138, 139). The interaction of AP2 with GABA_ARs is partly regulated by PKA and PKC mediated-phosphorylation of serine residues within a highly basic ten amino acid sequence motif in the intracellular loop of the β subunits (S409 in β 1, S410 in β 2, S408/409 in β 3), with increased phosphorylation reducing AP2 and GABA_AR interaction and endocytosis (**Fig. 3**) (140-144). Two additional motifs in the β -subunit appear important for AP2 interactions: 1) a dileucine motif is critical for receptor internalization in HEK cells (145) and 2) three arginine residues (405RRR407) within the β 3-subunit intracellular domain are important for AP2-stabilization of receptors at dendritic endocytic zones (146). The importance of phosphoregulation of these residues was revealed by S408/409A homozygous mice (the S/A mutation reduces AP2 interaction, mimicking phosphorylation (147)), which exhibit increased phasic but decreased tonic inhibition, and demonstrate the core phenotypes of autism spectrum disorders (148). Moreover, a common model of fragile X syndrome and autism spectrum disorders, the Fmr1 KO mouse, demonstrates enhanced S408/409 phosphorylation, further providing evidence for deregulation of these sites in disease (148). Accordingly, BZD resistance in epileptic mice undergoing sustained seizures is linked to reductions in PKC phosphorylation of β phosphorylation (148). How specific PKC isoforms participate in phosphoregulation of GABA_AR surface levels and internalization is still unclear. For instance, ethanol induced internalization of α 1-containing GABA_ARs is PKC γ dependent (149),

while PKC ϵ reduces GABA $_A$ R sensitivity to ethanol and BZDs by acting at a γ 2 S327 residue (150).

The intracellular loop of the γ 2 subunit also contains two AP2 interaction domains, a 12 basic amino acid region similar to the β -subunits and a YGYECL motif (144). The Tyr 365/367 within the YGYECL motif are targets of Fyn and other Src family kinases (**Fig. 3**) (151, 152), and phosphorylation at these sites reduce AP2 binding (153). Tyrosine to phenylalanine mutations inhibits AP2 binding to the γ 2 subunit, and heterozygous Y365/7F knock-in mice demonstrate surface and synaptic accumulation of GABA $_A$ Rs and spatial memory deficits (154). Importantly, homozygous Y365/7F knock-in mice are developmentally lethal, highlighting the importance of these residues in regulating GABA $_A$ R activity. BDNF-induced phosphorylation of the γ 2 subunit Y365/7 residues was recently implicated as a promoter of receptor surface expression during hippocampal neurogenesis (155). The authors found heterozygous Y365/7F mice demonstrated an antidepressant-like phenotype and enhanced neurogenesis that could not be further enhanced by BDNF.

A number of noxious stimuli trigger GABA $_A$ R endocytosis including seizure models (156-158), oxygen-glucose deprivation (OGD) conditions (159), and prolonged agonist application (160). Protein phosphatases (**Fig. 3**) have an important role in regulating receptor endocytosis under these conditions. For example, inhibition of the calcium-sensitive phosphatase calcineurin (CaN) by FK506 or serine/threonine protein phosphatase 1 (PP1) and 2A (PP2A) by okadaic acid reverses reduction of surface γ 2-subunit containing GABA $_A$ Rs and mIPSC amplitude induced by status epilepticus treatments in slice preparations (161). NMDA receptor mediated calcium entry and CaN activation was further shown to decrease surface α 2-containing receptors during *in vitro* epileptiform activity by live-cell imaging techniques (162). Activation

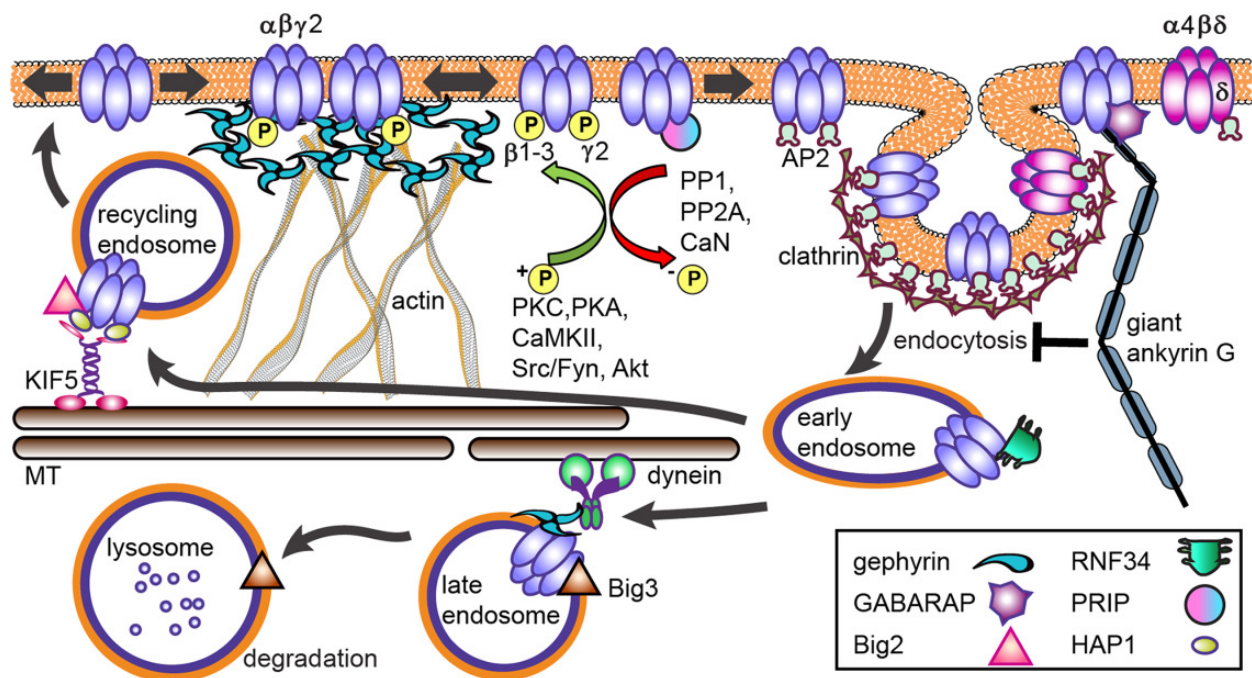


Figure 3. GABA_AR Intracellular Trafficking.

GABA_ARs composed of $\alpha(1-3)\beta\gamma$ subunits are largely synaptically localized via gephyrin interactions and contribute to phasic currents, whereas $\alpha(4 \text{ or } 6)\beta\delta$ receptors are extrasynaptic and generate tonic current. $\alpha 5\beta\gamma$ receptors are found in both locations due to binding with gephyrin at synapses and radixin extrasynaptically. Proteomics and other modern strategies have significantly enriched the complexity of the inhibitory synapse, however the functions of many new components have yet to be defined. Reproduced from: Lorenz-Guertin, J. M. and T. C. Jacob (2017). GABA type a receptor trafficking and the architecture of synaptic inhibition. *Develop Neurobiol.*

of the transient receptor potential cation channel subfamily V member 1 (TRPV1) also appears to cause GABA_AR endocytosis in the dentate gyrus of rodents dependent on calcium influx, CaN, and dynamin-activity (163). In addition, inflammation and release of the proinflammatory cytokine tumor necrosis factor- α (TNF α) stimulates GABA_AR internalization ($\alpha 1/2/5$, $\beta 3$, $\gamma 2$) in a CaN-independent pathway in cultured hippocampal neurons (164). Recent evidence has also recognized

the amyloid β ($A\beta$) peptide, most commonly associated with the pathogenesis of Alzheimer's disease, as a stimulator of GABA_AR endocytosis (165).

Surface biotinylation assays suggest the majority of constitutively-internalized GABA_ARs rapidly recycle back to the cell surface (70% in 1 h), while significant degradation occurs over longer time scales (6 h) (166). The recycling of GABA_ARs is partly mediated by huntingtin associated protein 1 (HAP1) direct association with the β subunits (**Fig. 3**) (136, 166). HAP1 functions as a kinesin adaptor and localizes to early endosomes containing GABA_AR, and thus overexpression of HAP1 promotes receptor surface levels and reverses intracellular accumulation of receptors by constitutive (166) and OGD-induced endocytosis (167). Mutation of the HAP1 protein resulting in polyglutamine expansion, as seen in Huntington's Disease, results in dysregulated transport of GABA_ARs to the cell surface and compromised inhibitory neurotransmission (136). The recycling activity of HAP1 likely arises from its association with the kinesin KIF5 (**Fig. 3**). Purified complexes of β 3-GABA_AR/KIF5 and HAP-1/KIF5 are readily immunoprecipitated from rat brain tissue, while acute blockade of KIF5 reduces GABA_AR synaptic levels and signaling strength (136). The integral membrane protein CAML (calcium-modulating cyclophilin ligand) has also been implicated in GABA_AR forward trafficking and recycling via interaction with the γ 2 subunit cytoplasmic and fourth transmembrane domain regions (168). CAML-deficient neurons have reduced recycling of internalized GABA_ARs and decreased GABAergic neurotransmission in electrophysiological recordings.

GABA_ARs undergoing constitutive internalization from the cell surface may be subjected to lysosomal-mediated degradation (**Fig. 3**), a process blocked by the lysosomal proteolytic inhibitor leupeptin (166). Acute leupeptin treatment also increases the size, number, and strength of GABAergic synapses in cortical slices (159). Certain stimuli can also accelerate degradation of

surface GABA_ARs. For instance, cultured hippocampal neurons undergo enhanced lysosomal-mediated degradation of $\alpha 2$ -containing receptors in response to BZD treatment (169). Ubiquitination of 7 lysine residues within the intracellular loop of the $\gamma 2$ subunit plays a key role in GABA_AR lysosomal targeting (159). Mutation of these lysines to arginine (K7R) reduced colocalization of receptors at late endosomes, made receptors impervious to leupeptin treatment in heterologous cells, and blocked an OGD-induced loss of surface receptor clusters in neurons (159). The ubiquitin E3-ligase, ring finger protein 34 (RNF34), directly interacts with the intracellular loop of $\gamma 2$, co-immunoprecipitates with this subunit from brain extracts, and can be found colocalized at GABAergic synapses (**Fig. 3**) (170). Overexpression of RNF34 enhances the rate of $\gamma 2$ -GABA_AR degradation and reduces GABA_AR synaptic cluster size and strength. Interestingly, expression of the $\gamma 2$ K7R mutant in these experiments did not reverse RNF34-induced degradation of GABA_ARs in co-transfected HEK293 cells, but mutation of additional lysine residues in a K8R, K9R, and K10R mutant did. Moreover, RNF34 mediated ubiquitination appears to contribute to both proteasomal and lysosomal degradation of GABA_ARs in these cells. The ARF GEF, Brefeldin A-inhibited guanine nucleotide-exchange protein 3 (BIG3), may also be important for lysosomal trafficking of GABA_ARs (**Fig. 3**). BIG3 is primarily expressed in pancreatic islets and the brain, and is found colocalized with lysosomes in neurons. BIG3 KO mice demonstrate increased GABA_AR synaptic size and current, suggesting this protein is involved in negative regulation of GABA_AR levels (171). The exact role of specific GABA_AR subunits, associated E3-ligases and ubiquitination patterns, and lysosomal trafficking proteins that regulate the transition of surface receptors to lysosomes is an important area of future research.

1.5 Activity-Dependent Plasticity of GABA_AR Synapses

Synapse plasticity refers to strengthening or weakening of individual synapses in response to changes in stimuli at a local or system level. Two decades of research have uncovered various forms of short and long term plasticity of GABAergic neurotransmission in different brain regions, with underlying cellular and molecular mechanisms being identified both pre- and post-synaptically (172). Persistent changes in synaptic efficacy are generally referred to as long-term potentiation (LTP) and long-term depression (LTD). Traditionally this described excitatory synapse plasticity that produced a respective increase or decrease in synapse strength. However, with growing awareness of GABAergic synapse plasticity, these terms now refer to changes in the gain of either synapse type (for GABAergic synapses, iLTD and iLTP).

GABA_AR postsynaptic plasticity is encompassed by changes in channel function, receptor number or clustering/lateral diffusion, and altered chloride homeostasis (changing the GABA reversal potential/ E_{GABA}). Tonic inhibition generated by extrasynaptic receptors is also dynamic, with acute and chronic stress inducing changes in cell surface trafficking and subunit specific expression (173). Receptor phosphorylation state is a key means for altering channel function or receptor trafficking via activation of protein kinases (including PKC, PKA, CaMKII, and Src) or phosphatases (CaN, PP1, PP2A) (**Fig. 2**) (174). Investigation of GABAergic postsynaptic plasticity has largely focused on excitation driven changes. Early plasticity studies identified that intracellular application of CaMKII (175) and experimental epilepsy kindling models (176) elevated GABA_AR surface levels and potentiated the inhibitory response. Later studies revealed that moderate NMDA activation of hippocampal neurons promote CaMKII α translocation to inhibitory synapses and CaMKII α -dependent insertion of GABA_ARs with concomitant phosphatase-mediated AMPAR (GluR1) removal (177, 178). Aside from NMDAR stimulation,

enhanced VGCC (voltage-gated calcium channel) activity promotes CaMKII phosphorylation of the $\beta 3$ subunit S383 residue and receptor insertion (**Fig. 3**) (119), suggesting multiple routes for calcium signaling to enhance GABA_AR surface levels. In addition, a quantum dot single-particle tracking study showed that NMDA-induced iLTP required CaMKII phosphorylation of $\beta 3$ S383 to reduce GABA_AR lateral diffusion and enhance recruitment of the synaptic scaffold protein gephyrin (179). More recently, this experimental approach revealed additional glutamate- and calcium-evoked plasticity of GABAergic synapses. Low glutamate levels stimulate mGluR-driven calcium store release via PKC and IP3 receptors and stabilization of surface GABA_ARs, while robust NMDAR activation promoted CaN phosphatase activity and destabilization of postsynaptic GABA_AR (180). This is consistent with earlier findings where glutamate application promotes CaMKII α translocation to excitatory synapses, enhanced AMPAR surface levels, and reduced plasma membrane GABA_AR levels (178, 181). Glutamate, high levels of neuronal activity, or strong NMDAR activation also reduces plasma membrane GABA_AR cluster size, stimulates receptor lateral mobility, and decreases mIPSC amplitude via CaN (182) and dephosphorylation of the $\gamma 2$ subunit S327 residue (183). These molecular studies in neuronal culture are consistent with earlier slice and *in vivo* studies showing LTD of GABAergic inhibition via NMDAR activation requires CaN (184) and the $\gamma 2$ subunit (185). Similar mechanisms for iLTD and iLTP that rely on GABA_AR trafficking are supported by studies in other brain regions such as the deep cerebellar nuclei (186, 187). Together these plasticity studies show that glutamate receptor activation and calcium-sensitive signaling pathways can generate either iLTP or iLTD. Moderate or ambient glutamate signaling promotes kinase activity that stabilizes GABA_ARs, while strong stimulation leads to CaN phosphatase activation and receptor diffusion. Ultimately, glutamatergic

activity dictates bidirectional modulation of GABAergic postsynaptic strength and receptor clustering.

Structural reorganization of gephyrin scaffolding is now emerging as a key mechanism of rapid inhibitory synaptic plasticity with changes occurring on a minute timescale (188). Gephyrin post-translational modifications such as phosphorylation and ubiquitination are likely to be central in regulating synapse architecture. A recent organotypic slice culture study of gephyrin dynamics identified that activity patterns promoting NMDAR LTP (carbachol treatment or theta burst stimulation) increase gephyrin cluster size and formation in a CaMKII-dependent manner (77). Furthermore this gephyrin plasticity was associated with enhanced phosphorylation of gephyrin S305, a CaMKII phospho site identified by *in vitro* kinase assay.

On the other spectrum of neuronal activity level, early studies using chronic activity blockade (24 - 48 h TTX treatment) resulted in homeostatic pre- and post-synaptic GABAergic plasticity with decreased GABA_AR synaptic clusters, mIPSC amplitude and frequency (189). *In vivo* chronic sensory deprivation via whisker trimming decreases GABA_AR number and weakens inhibitory synapses (190-192). In contrast, whisker training promotes GABAergic synaptogenesis on dendritic spines, while not on dendritic shafts (193). Analogous findings in the visual cortex (194) indicate that a pool of dynamic GABAergic spine synapses support changes to network activity levels. These chronic *in vivo* protocols reveal how neuronal adaptation operates across a continuum of GABA_AR synaptic plasticity, where reductions in activity lead to loss of inhibition, while learning or heightened neuronal activity strengthens existing GABAergic synapse or initiates new synapse formation. However, some sensory modulation can occur in an inverse fashion, as brief monocular deprivation potentiates iLTP (195), concurrent with increasing gephyrin and GABA_AR perisomatic accumulation (179). Other visual cortex studies indicate that GABA_AR

endocytosis contributes to LTD occurring with repetitive firing, while slow membrane oscillations, comparable to activity during sleep state, promote iLTP via exocytosis (196). Similarly, acquisition of a fear response is accompanied by surface GABA_AR decreases (197) and extinction of fear requires GABA_AR insertion (198). Collectively, GABAergic synapse plasticity and rewiring is fundamental for sensory experience adaptation and behavior, with functional changes in inhibition matching structural changes.

1.6 Advancing our Understanding of Dynamic GABA_AR Trafficking and Regulation

Considerable scientific progress has revealed a network of molecular mechanisms underlying GABAergic plasticity. Yet, advancement of new and existing methods is promoting major inroads for our understanding of GABA_AR signaling and trafficking. Recent proteomic strategies from other labs has vastly expanded the protein repertoire of GABAergic synapses to nearly 200 proteins by targeted purification of GABA_ARs, NL2, or gephyrin and their respective interactomes (87, 88, 199, 200). Microscopy-based approaches encompass the fastest growing means of discovery *in vitro* and *in vivo*, including optogenetically controlled GABA_ARs (201, 202), two-photon based GABA photolysis (203), single-particle-tracking of receptor diffusion (204), quantitative super-resolution imaging of gephyrin (205) and gephyrin recombinant antibody-like proteins (206, 207) or fluorescent super-binding peptides (208). Additionally, proximity ligation assays allow for researchers to detect native protein interactions utilizing widely-available primary antibodies (209, 210), while emerging fluorescence resonance energy transfer methods (FRET) have begun to be applied, as in our recent publication (211). Herein we validate and characterize a new tool to address multiple GABA_AR trafficking questions within a

single assay using a dual fluorescent sensor GABA_AR γ 2 subunit to advance our knowledge of basal receptor trafficking and drug-induced neuroadaptive changes.

2.0 Designing an Optical Tool to Measure Multistage GABA_AR Trafficking

Chapter adapted from: Lorenz-Guertin, J. M., et al. (2017). A versatile optical tool for studying synaptic GABA_A receptor trafficking. *J Cell Sci* 130: 3933-3945; doi: 10.1242/jcs.205286 (212) <https://jcs.biologists.org/content/130/22/3933.long>

JL-G performed the biochemistry, fixed- and live-imaging acquisition and analysis. Madeleine R. Wilcox performed the electrophysiology and Madeleine R. Wilcox and Jon W. Johnson performed electrophysiology data analysis.

2.1 Introduction

The majority of GABA_ARs are composed of two α , two β , and a $\gamma 2$ subunit forming a heteropentamer, but considerable subunit heterogeneity may exist ($\alpha 1-6$, $\beta 1-3$, $\gamma 1-3$, δ , ϵ , θ , π , $\rho 1-3$) (53). The $\gamma 2$ subunit plays a critical role in GABA_AR function, as it is necessary for receptor synaptic targeting and cluster maintenance (67, 213-216), coassembles with nearly all α and β subunits (217), and is the only subunit characterized to undergo ubiquitination leading to lysosomal degradation (159). The degree of $\gamma 2$ -GABA_AR synaptic clustering directly impacts the strength of GABAergic synaptic inhibition and is dynamically regulated by changes in receptor trafficking (53, 218). A number of endogenous and pharmacological agents including GABA, neurosteroids, ethanol, and BZDs are known to influence receptor trafficking (149, 219-226). Despite this knowledge, precise GABA_AR trafficking mechanisms induced by these and other clinically relevant compounds remain underexplored at the molecular level.

Real-time receptor trafficking measurements typically rely on genetically encoded fluorophores to track single protein localization and movement within living cells. In contrast to immunofluorescence based live-cell techniques which require reliable antibodies and are restricted

to measurements of surface proteins (227), fluorescent tags allow for identification of a protein from synthesis through degradation. Despite this advantage, traditional fluorophores still remain limited in their ability to spatially resolve surface from internal populations without the use of total internal reflection fluorescence (TIRF) imaging approaches (228). This issue led to the generation of pH-sensitive fluorescent proteins, such as pHluorin (pHGFP), which exhibit fluorescence in extracellular environments with alkaline pH (pH \sim 7.4), but not in more acidic areas like intracellular vesicles (229). pHGFP is not without limitations, as some discernable signal can be observed in the E.R. where pH can be roughly 7.2 (230). One possible way to resolve protein trafficking occurring at the cell surface from the intracellular space is to use compartment specific high-affinity labeling techniques. We previously described a labeling method utilizing a GABA_AR subunit genetically tagged with an α -bungarotoxin binding site which selectively binds cell-excluded fluorescent bungarotoxin, allowing for selective monitoring of receptor insertion and internalization (231). Unfortunately, the inherent fluorescence of Alexa dye coupled bungarotoxins necessitates extensive washing after labeling to reduce background signal. Furthermore, bungarotoxins were recently shown to function as antagonists of the GABA_AR, further complicating the use of this reagent (232). To overcome these obstacles associated with GABA_AR imaging we have employed an innovative paired optical reporter system where two individually non-fluorescent components become highly fluorescent upon binding: a genetically encoded fluorogen-activating peptide (FAP tag) and exogenously applied malachite green (MG) dyes. FAPs are antibody single chain variable fragments (scFvs) which have been characterized to selectively bind MG synthetic dyes with high specificity and affinity (233). These synthetic dyes are non-fluorescent in solution until bound by their respective FAP and can be modified to have distinct characteristics including cell permeability, pH-sensitivity, and various fluorescence

properties (234-238). The FAP-dye system offers many advantages for live-imaging: (i) the dyes can be added directly to a culture dish and saturate the target FAP in seconds; (ii) a number of distinct dyes can be used for the same genetically encoded FAP; and (iii) the dyes are highly specific for their target FAP. Moreover, high affinity MG-FAP binding forms a stable fluorescent module that allows for measurements of receptors undergoing internalization and recycling (239-241). Measuring drug-induced changes in FAP-tagged receptor trafficking has proven largely successful (234, 236, 241-244) placing this technique at the forefront of pharmacological screening.

In order to design a tool to track synaptic GABA_AR internalization and trafficking, we engineered a $\gamma 2$ subunit encoding a pHGFP and the fluorogen-activating peptide dl5 ($\gamma 2^{\text{pH}}$ FAP) (233, 240, 245, 246). We find that $\gamma 2^{\text{pH}}$ FAP containing GABA_ARs are trafficked to the cell surface in both HEK293 cells and primary neurons, and are localized appropriately at synapses. We further demonstrate how this construct can be combined with malachite green (MG) dye derivatives to measure alterations in surface localization and intracellular trafficking using high-resolution confocal microscopy approaches. Finally, using these FAP based methods we found that an *in vitro* seizure model induced rapid loss of dye-labeled synaptic GABA_ARs concomitant with enhanced targeting of internalized receptors to lysosomal compartments, key results that were not detectable using pHGFP signal alone. We therefore demonstrate an innovative tool to monitor multistage synaptic GABA_AR trafficking.

2.2 Methods and Materials

2.2.1 Cell culture and Transfection

All procedures were approved by the University of Pittsburgh Institutional Animal Care and Use Committee. Cortical neurons were prepared from embryonic day 18 Sprague Dawley rats and nucleofected (Lonza, Switzerland) at plating (54). HEK293 cells were maintained in DMEM with 10% FBS (Life Technologies, Carlsbad, CA) and were transfected by nucleofection.

2.2.2 DNA Constructs and Antibodies

The $\alpha 2$, $\beta 3$, and pH-sensitive GFP tagged $\gamma 2$ subunit ($\gamma 2^{pH}GFP$) plasmids have been previously described (54, 65, 247, 248). The fluoren-activating peptide *dl5* (240) was inserted upstream of *pHGFP* ($\gamma 2^{pH}FAP$) separated by a *G-A-P-P-A* amino acid linker. The *EEA1-GFP* was a gift from Silvia Corvera (Addgene plasmid #42307) (249). All constructs were sequenced to confirm the fidelity of final plasmids. The following primary antibodies were used: mouse anti- β -actin (1:2000, A1978, Sigma); rabbit anti-GFP (1:1000, A11122, Invitrogen); rabbit anti-VGAT (1:1000, 131002, Synaptic Systems); mouse anti-EEA1 (1:1000, 610457, BD Biosciences) and immunofluorescence secondary antibodies: goat anti-rabbit Alexa Fluor 641 (1:1000, A21245, Invitrogen); goat anti-mouse Alexa Fluor 405 (1:1000; A31553, Invitrogen).

2.2.3 MG Dyes

MG dyes were kindly provided by Dr. Alan S. Waggoner, Dr. Ming Zhang, Dr. Marcel P. Bruchez, and Dr. Brigitte F. Schmidt at CMU. The MG dye MG-BTau was synthesized as described in (236, 239) and the MG dye Cy3pH(S/SA)-MG was prepared by the method of (238). The IUPAC name for Cy3pH(S/SA)-MG is 2-((E)-3-((Z)-3,3-dimethyl-5-sulfoindolin-2-ylidene)prop-1-en-1-yl)-1-(6-((3-(4-((4-(dimethylamino)phenyl)(4-(dimethyliminio)cyclohexa-2,5-dien-1-ylidene)methyl)phenoxy)propyl)amino)-6-oxohexyl)-3,3-dimethyl-5-sulfamoyl-3H-indol-1-ium. Structural, synthetic and analytical details for MG-BTau are as described previously (239, 241, 250).

2.2.4 Immunocytochemistry and Confocal Microscopy

Primary cortical neurons grown on glass coverslips were fixed at days *in vitro* (DIV) 13-14. Neurons were permeabilized and stained with anti-VGAT antibody. Images were taken on a Nikon Ti-E A1 Confocal microscope equipped with a motorized Z-stage and perfect focus system (PFS) using a 60x oil immersion objective (NA 1.49) at 3x zoom. Data were analyzed using NIS Elements software (Nikon, NY). Thresholds were set using binary masks to selectively identify brightly fluorescent objects above background (54). Three dendritic 10 μm regions of interest (ROI) were drawn per neuron to measure synaptic colocalization of pHGFP signal with VGAT in $\gamma 2^{\text{pH}}$ FAP characterization studies. $\gamma 2^{\text{pH}}$ GFP control and $\gamma 2^{\text{pH}}$ FAP expressing neuron pixel intensity and sum area of synapses in μm^2 was measured and values were normalized to control mean. Fixed EEA1 early endosome studies utilized a 2 min 100 nM MG-BTau dye pulse-labeling protocol in HBS at room temperature. After live cell MG dye incubation steps, cells were washed 5 times to

remove all unbound dye prior to returning the cells to 10°C or 37°C solution for 30 min followed by fixation and immunostaining. Total pixel intensity of MG-BTau labeled receptors colocalized with EEA1 was measured within a cell body ROI. Laser settings were held constant across experiments. The researcher was blinded during image acquisition and data analysis.

2.2.5 Live-Cell Imaging

Transfected DIV 12-14 cortical neurons or HEK293 cells were plated on MatTek glass-bottom dishes (Ashland, MA). Imaging was performed in HEPES-buffered saline (HBS): 135 mM NaCl, 4.7 mM KCl, 1.2 mM MgCl₂, 10 mM HEPES, 2.5 mM CaCl₂, 11 mM glucose, pH 7.4 (169). Low pH HBS (pH 6.4-6.8) was similarly prepared, while pH 4.8 saline was a MES-buffered saline: (135 mM NaCl, 4.7 mM KCl, 1.2 mM MgCl₂, 10 mM MES, 2.5 mM CaCl₂, 11 mM glucose). All dye pulse-labeling steps were performed in HBS at room temperature. Following dye incubation steps, cells were washed 5 times to remove all unbound dye prior to treatment or imaging. All images were taken at room temperature using a 60x objective at a 3x zoom within 10 min of dye washout. Perfusion assays utilizing different pH saline buffers monitored a single cell per assay, while 2-3 cells were imaged in each experimental dish for all other experiments. Researchers were blinded during data analysis where applicable.

Cy3pH(S/SA)-MG dye was used for neuron constitutive trafficking assays. Neurons were pre-incubated in DMSO vehicle control (t₀, t₃₀) or 80 μM dynasore (2897, Tocris) 30 min prior to pulse-labeling. After dye exposure, neurons were either immediately imaged (t₀) or returned to conditioned media ± the continued presence of dynasore for 30 min at 37°C prior to imaging. Cy3pH(S/SA)-MG dye acquisition was taken sequentially to measure Cy3pH (561 nm excitation) induced MG emission (680 nm) followed by MG (640 nm excitation) induced MG emission (680

nm). Laser settings were then switched to allow for capture of pHGFP (488 nm excitation; 510 nm emission). Individual vesicles were identified using the NIS Elements Spot Detection tool and thresholding analysis. A ROI was drawn around the cell body and binary thresholds were set to selectively capture only pHGFP clusters and MG_{ex640} (MG signal excited by 640 nm) signal above background. Next, spot detection thresholds were set to selectively identify MG_{ex561} (signal excited by 561 nm) fluorescent objects with a minimum circular area of 0.55 μm^2 and signal above threshold. Colocalization of MG_{ex561} spot signal and MG_{ex640} binary signal was considered a $\gamma 2^{\text{pH}}$ FAP positive vesicle. To remove contributions of surface synaptic GABA_ARs from these vesicle measurements, MG_{ex561} and MG_{ex640} signals colocalized with pHGFP signals were subtracted. The values reported reflect the total number of MG_{ex561} and MG_{ex640} positive objects (vesicles) identified and the MG₅₆₁/MG₆₄₀ ratio of each vesicle. Early endosome characterization assays measured colocalization of Cy3-MG objects with EEA1-GFP vesicles to determine the MG₅₆₁/MG₆₄₀ ratio in these compartments, while all non-associated Cy3-MG objects were placed in the “other” category. A ROUT outlier test (Q = 1.0%) was used in this experimental analysis. For surface Cy3pH(S/SA)-MG pH characterization perfusion assays, the ratio of MG₅₆₁/MG₆₄₀ was determined by selectively measuring synaptic clusters of $\gamma 2^{\text{pH}}$ FAP GABA_ARs.

Neuron surface and lysosomal-association assays utilized MG-BTau dye for surface receptor pulse-labeling. For bicuculline-induced seizure assays, neurons were either immediately imaged following 100 nM MG dye incubation (t₀) or returned to conditioned media in the presence of 50 μM (-)-bicuculline methiodide (2503, Tocris) or DMSO vehicle control. To label lysosomes, neurons were incubated at 37°C in 50 nM LysoTracker Blue DND-22 (Life Technologies) in conditioned media 30 min prior to imaging. For image analysis, independent ROIs were drawn to capture the soma, three 10 μM sections of dendrite, and the whole cell. Binary thresholds and

colocalization measurements were performed as above to identify MG-BTau, pHGFP synaptic GABA_AR clusters, and lysosomes. Total surface pHGFP expression was determined by taking the entire cell surface signal following background subtraction.

2.2.6 Western Blot

Transfected and non-transfected DIV 13-14 cortical neurons were lysed using RIPA buffer containing: 50 mM Tris-HCl (pH 8.0), 50 mM NaCl, 1 mM EDTA, 1% Igepal, 0.5% sodium deoxycholate, 0.1% SDS, 10mM NaF, 2 mM sodium orthovanadate, and protease inhibitor cocktail (Sigma, St. Louis, MO), solubilized for 15-30 min at 4°C, and spun at 13,500xg for 15 min to remove the nuclear pellet. BCA protein assay was performed on the supernatant, and equivalent amounts of protein were loaded for SDS-PAGE analysis. After electrophoresis and transfer to nitrocellulose membrane, samples were probed with primary antibody overnight followed by the appropriate HRP-coupled secondary antibody. Blots were visualized using a Biorad Chemicdoc XRS+ following ECL development (Thermo Scientific).

2.2.7 Electrophysiology

Whole-cell voltage-clamp recordings were performed on HEK293 cells 12-48 h after nucleofection with GABA_AR subunits. Cells were transfected with (a) *EGFP:α2:β3:γ2^{pH}GFP* or (b) *EGFP:α2:β3:γ2^{pH}FAP* in a 1:1:1:3 ratio to favor the production of γ2 subunit-containing receptors. Pipettes were pulled from borosilicate capillary tubing (Sutter Instruments) to a resistance of 2 – 5 MΩ on a Sutter Instruments-Flaming Brown P-97 electrode puller and fire polished. Unless otherwise indicated, the extracellular solution contained (in mM): 140 NaCl, 4.7

KCl, 1.2 MgCl₂, 2.5 CaCl₂, 10 HEPES and 11 D-glucose, and was pH adjusted to 7.4 ± 0.05 with NaOH. The intracellular solution contained (in mM): 140 CsCl, 0.1 CaCl₂, 10 HEPES, 1.1 EGTA, 2 MgCl₂, 2.5 phosphocreatine, 2 ATP-Mg and 1 GTP-Na, and was pH adjusted to 7.2 ± 0.05 with CsOH. Recordings were made from cells expressing *EGFP* identified by epifluorescence illumination on an inverted Zeiss Axioscope microscope. Cells were held at a membrane potential (V_m) of -50 mV for all experiments. V_m was corrected for an empirically determined liquid junction potential between the extracellular and intracellular solution of -4 mV. Whole-cell currents were recorded using an Axopatch 200A patch-clamp amplifier (Molecular Devices), low-pass filtered at 5 kHz and sampled at 10 kHz in pClamp10.7 (Molecular Devices). Series resistance was compensated with the prediction and correction circuitry to at least 75% in all experiments. Rapid solution exchange was achieved using an in-house-fabricated 10-barrel fast perfusion system connected to gravity-fed reservoirs similar to the system previously described (251). All experiments were performed at room temperature. Peak currents were measured relative to baseline current prior to agonist application using Clampfit 10.7.

2.2.8 Statistics

Statistical analysis was performed using GraphPad Prism 6 (GraphPad Software, San Diego, CA) or Microsoft Excel. Unpaired Student's t-tests or one way ANOVA with subsequent post hoc Tukey's test were used to determine significance in indicated imaging studies. Significant differences in data distribution for Cy3pH(S/SA)-MG experiments were determined using the Mann-Whitney test. Paired or unpaired two-tailed Student's t-tests were used to determine significance of differences in electrophysiological studies. All data are reported as mean \pm S.E.M. unless otherwise indicated in the text.

2.3 Results

2.3.1 Expression and Function of $\gamma 2^{\text{pH}}$ FAP in HEK293 Cells

We began by introducing the dl5 FAP into a previously characterized N-terminal pHGFP $\gamma 2$ -construct ($\gamma 2^{\text{pH}}$ GFP) that functions comparably to wild-type $\gamma 2$ (54, 183, 247, 252) (**Fig. 4A**). The FAP will selectively bind MG dyes with distinct biophysical and fluorescence properties. For example, the MG derivative (2-((4-[(2,5-dioxopyrrolidin-1-yl)oxy]-4-oxobutanoyl}amino)ethanesulfonate; MG-BTau) is cell impermeant, binds to dl5 FAP with high binding affinity (K_d value less than 0.5 nM), and is non-fluorescent until dl5 FAP binding occurs, which causes activation of fluorescence in the far red spectral region (680 nm) (239-241, 250) (**Fig. 4B**). We first examined if the full length $\gamma 2^{\text{pH}}$ FAP construct was appropriately expressed in HEK293 cells. GABA_AR $\beta 3$ subunits were coexpressed in these experiments as a β subunit is required for trafficking of receptors to the cell surface (253). Western blot analysis of non-transfected, $\gamma 2^{\text{pH}}$ GFP control, and $\gamma 2^{\text{pH}}$ FAP expressing cells reveal $\gamma 2^{\text{pH}}$ FAP is ~25 kDa larger than $\gamma 2^{\text{pH}}$ GFP, consistent with the molecular weight of the dl5 FAP (240) (**Fig. 4C**). Next, we evaluated surface expression and specificity of MG-BTau dye labeling of GABA_ARs in cells transiently transfected with $\beta 3 + \gamma 2^{\text{pH}}$ FAP or $\beta 3 + \gamma 2^{\text{pH}}$ GFP. Addition of MG-BTau to a live-cell culture should swiftly and selectively label surface GABA_ARs containing $\gamma 2^{\text{pH}}$ FAP. To test this dye based labeling approach, living cells plated on glass-bottom Mattek dishes were pulse-labeled with 250 nM MG-BTau in HEPES-buffered saline (HBS) for 1 min at room temperature, washed 5x times with saline, and then immediately imaged by confocal microscopy. We found that HEK293 cells expressing $\gamma 2^{\text{pH}}$ FAP demonstrate selective receptor surface labeling by MG-BTau, while $\gamma 2^{\text{pH}}$ GFP control cells show no cell membrane MG-BTau fluorescence (although occasional low-level

background MG-BTau binding can occur with cellular debris (239)) (**Fig. 4D**). The majority of cells express heteromeric receptors composed of $\beta 3 + \gamma 2$ subunits, although a few cells express the $\gamma 2$ subunit alone, leading to subunit retention in the endoplasmic reticulum (ER) and no MG-BTau signal in $\gamma 2^{\text{pH}}$ FAP cells (**Fig. 4D**, yellow arrowheads). These results highlight key advantages of FAP-fluorogen labeling over pHGFP alone: 1) higher signal-to-noise ratio and 2) the removal of pHGFP intracellular background fluorescence generated by ER localized receptors where pH can be roughly 7.2 (230).

We further investigated the ability of $\gamma 2^{\text{pH}}$ FAP to assemble into functional heteromeric $\alpha 2\beta 3\gamma 2$ GABA_ARs with normal chloride channel activity in response to the endogenous agonist GABA which binds between α and β subunits. Patch clamp recordings were used to determine the GABA dose-response curve for HEK293 cells expressing receptors composed of $\alpha 2\beta 3\gamma 2^{\text{pH}}$ GFP or $\alpha 2\beta 3\gamma 2^{\text{pH}}$ FAP. Concentration-response analysis revealed these receptors exhibit similar GABA EC₅₀ values ($\alpha 2\beta 3\gamma 2^{\text{pH}}$ GFP, $22.0 \pm 6.2 \mu\text{M}$; $\alpha 2\beta 3\gamma 2^{\text{pH}}$ FAP, $14.3 \pm 8.9 \mu\text{M}$; $p > 0.05$) and Hill coefficients ($\alpha 2\beta 3\gamma 2^{\text{pH}}$ GFP, 1.14 ± 0.26 ; $\alpha 2\beta 3\gamma 2^{\text{pH}}$ FAP, 0.90 ± 0.29 ; $p > 0.05$) (**Fig. 5A**). The EC₅₀ values are consistent with previously reported values for receptors containing this subunit composition (254). To directly test if addition of the FAP tag altered drug binding and functional properties of the $\gamma 2$ subunit, we compared the potentiation response induced by the BZD, diazepam (DZ/DZP), a GABA_AR positive allosteric modulator that binds at

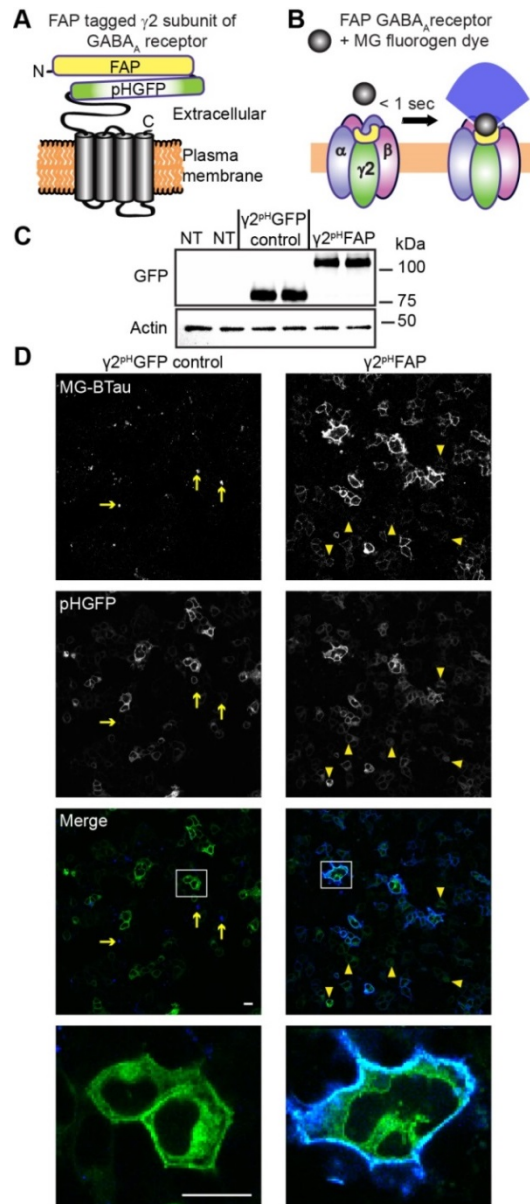


Figure 4. Novel Optical $GABA_A$ R Paired Reporter System.

(A) The fluorogen activating peptide (FAP) dl5 was inserted upstream of an N-terminal pH-sensitive GFP tag (pHGFP) in a $\gamma 2$ -subunit construct. Cartoon schematic of $\gamma 2^{pH}FAP$ subunit. Model not to scale. (B) The MG dye, MG-BTau, is cell impermeant and dark in solution. Fluorescence is generated when MG dye binds to surface receptors containing the $\gamma 2^{pH}FAP$ subunit. (C, D) HEK293 cells were transfected with $\beta 3 + \gamma 2^{pH}GFP$ control or $\beta 3 + \gamma 2^{pH}FAP$ ($\beta 3$ subunits are needed to form surface targeted receptors). (C) Representative western blot from NT (non-transfected), $\beta 3 + \gamma 2^{pH}GFP$ control and $\beta 3 + \gamma 2^{pH}FAP$ expressing cells ($n = 2$ experiments). (D) HEK293 cells

transfected with $\beta 3 + \gamma 2^{pH}GFP$ control or $\beta 3 + \gamma 2^{pH}FAP$ were pulse-labeled with 250 nM MG-BTau dye for 1 min prior to live-cell imaging. pHGFP fluorescence is shown in green and MG-BTau is shown in blue in the Merge panels and boxed areas enlarged below. MG-BTau signal is selectively localized at the cell surface in $\gamma 2^{pH}FAP$ expressing cells and is absent in $\gamma 2^{pH}GFP$ control cells. Note that with double transient transfection ($\beta 3 + \gamma 2^{pH}FAP$), some cells contain the $\gamma 2^{pH}FAP$ subunit alone (yellow arrowheads), leading to intracellular retention and a pHGFP signal (green) but no MG dye labeling (blue). Scale bars = 20 μm .

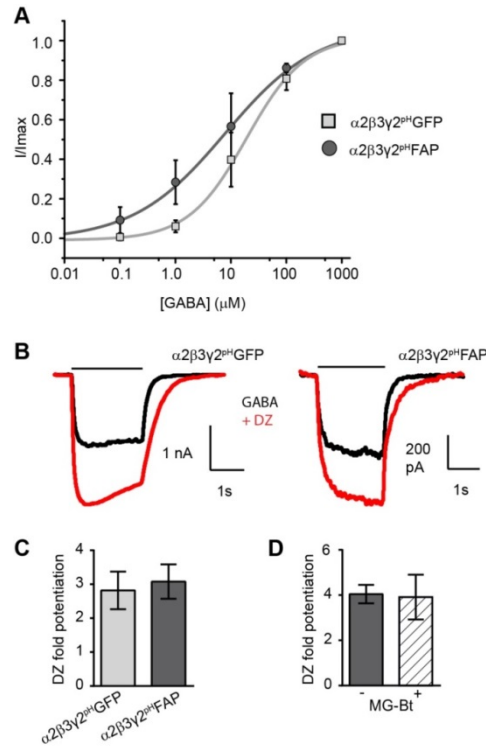


Figure 5. Recombinant GABA_ARs Containing $\gamma 2^{pH}FAP$ Maintain Responsiveness to GABA and the Benzodiazepine Drug Diazepam in HEK293 Cells.

(A) The GABA concentration response curve in $\alpha 2\beta 3\gamma 2^{pH}GFP$ and $\alpha 2\beta 3\gamma 2^{pH}FAP$ expressing cells is equivalent. 1s GABA applications were made at ≥ 120 s intervals and peak response was measured. Curves were fit with the Hill equation, and the EC_{20} was determined. (B) GABA currents are equivalently potentiated by 1 μM DZ (at the GABA EC_{20}). Representative traces show responses to application of GABA (black) and of GABA with DZ (DZP) (red). (C) Quantification of DZ potentiation ($n = 5-8$ cells per treatment). (D) DZ potentiation of the GABA response in $\alpha 2\beta 3\gamma 2^{pH}FAP$ expressing cells is not altered by the presence of 100 nM MG-BTau dye ($n = 4$ cells per treatment). (C,D) Data presented as mean \pm S.E.M., Student's t-tests.

the interface of $\gamma 2$ and specific α subunits ($\alpha 1, 2, 3$ or 5) (**Fig. 5B**) (217). We found no significant difference in the DZ potentiation of the EC₂₀ GABA response between $\alpha 2\beta 3\gamma 2^{\text{pH}}\text{GFP}$ or $\alpha 2\beta 3\gamma 2^{\text{pH}}\text{FAP}$ expressing cells (**Fig. 5C**, Fold DZ potentiation $\alpha 2\beta 3\gamma 2^{\text{pH}}\text{GFP} = 3.1 \pm 0.5$, $\alpha 2\beta 3\gamma 2^{\text{pH}}\text{FAP} = 2.8 \pm 0.6$; $p > 0.05$). Finally, we tested if binding of a MG dye to the $\gamma 2^{\text{pH}}\text{FAP}$ subunit would interfere with receptor function. We compared the DZ potentiation response of $\gamma 2^{\text{pH}}\text{FAP}$ before and after co-application of MG-BTau. Binding of MG-BTau to the receptors did not alter the response to DZ (**Fig. 5D**, Fold DZ potentiation $\gamma 2^{\text{pH}}\text{FAP}$ without dye = 4.0 ± 0.4 , $\gamma 2^{\text{pH}}\text{FAP}$ with dye = 3.9 ± 1.0 ; $p > 0.05$). Taken together these results suggest GABA_ARs incorporating $\gamma 2^{\text{pH}}\text{FAP}$ maintain normal receptor function and responsiveness to GABA and DZ in the presence of MG dye.

2.3.2 $\gamma 2^{\text{pH}}\text{FAP}$ is Clustered at Synapses in Neurons and Can be Used to Monitor

Multistage Receptor Trafficking

To confirm that $\gamma 2^{\text{pH}}\text{FAP}$ is fully expressed in cultured neurons, we compared non-transfected rat cortical neurons to those transfected with $\gamma 2^{\text{pH}}\text{FAP}$ or $\gamma 2^{\text{pH}}\text{GFP}$ control at plating (**Fig. 6**). Neurons were lysed 14 days after transfection and subsequently immunoblotted with anti-GFP antibody (**Fig. 6A**), revealing robust expression of $\gamma 2^{\text{pH}}\text{FAP}$ and $\gamma 2^{\text{pH}}\text{GFP}$ as seen in HEK293 cells (**Fig. 4C**). We then tested if neurons with $\gamma 2^{\text{pH}}\text{FAP}$ GABA_ARs could selectively bind and activate MG-BTau dye fluorescence. Days *in vitro* (DIV) 12 cortical neurons expressing $\gamma 2^{\text{pH}}\text{GFP}$ or $\gamma 2^{\text{pH}}\text{FAP}$ were pulse-labeled with 250 nM MG-BTau dye for 1 min at room temperature, then immediately washed and used for live-cell imaging. Only $\gamma 2^{\text{pH}}\text{FAP}$ expressing neurons demonstrate dye activation and colocalization with pHGFP surface synaptic clusters (**Fig. 6B**). Furthermore, it is evident that MG-BTau labeling in neurons also has a higher signal-to-noise ratio

than pHGFP due to 1) the continually generated pHGFP signal of diffuse newly inserted extrasynaptic $\gamma 2^{\text{pH}}$ FAP receptors that are not yet clustered at synapses, which contrasts with the small MG-BTau pulse-labeled extrasynaptic population (if the MG dye was continually present rather than being washed away, its extrasynaptic signal would be more similar to pHGFP) and 2) the low but observable pHGFP background from ER resident $\gamma 2^{\text{pH}}$ FAP subunits, whereas there is no ER signal from MG-BTau labeling. These data establish MG dyes as a selective label for synaptic $\gamma 2^{\text{pH}}$ FAP containing GABA_AR populations in living primary cortical neurons.

Synapse formation and receptor clustering are critical for neuronal development and regulation of inhibitory neurotransmission. To determine if $\gamma 2^{\text{pH}}$ FAP clusters normally at GABAergic synapses in mature neurons, we transfected cortical neurons at DIV 0 with $\gamma 2^{\text{pH}}$ GFP control or $\gamma 2^{\text{pH}}$ FAP and fixed the cells for immunofluorescence studies at DIV 15. We assessed receptor synaptic localization by measuring colocalization of the pHGFP tagged receptors with the vesicular GABA transporter (VGAT), a presynaptic marker of GABAergic synapses (**Fig. 6C**). Expression of $\gamma 2^{\text{pH}}$ FAP did not alter presynaptic GABAergic input as indicated by unchanged VGAT levels (intensity) and area compared to control (**Fig. 6D**). Additionally, the size of postsynaptic GABAergic synapses was not significantly different between constructs, although the mean intensity of $\gamma 2^{\text{pH}}$ GFP synapses was 20.7% (95% confidence interval) greater than $\gamma 2^{\text{pH}}$ FAP, likely due to higher overall expression of the control subunit. These results indicate that the full length $\gamma 2^{\text{pH}}$ FAP construct is expressed, assembles with endogenous subunits into receptors, traffics to synapses, and does not disturb neuronal development.

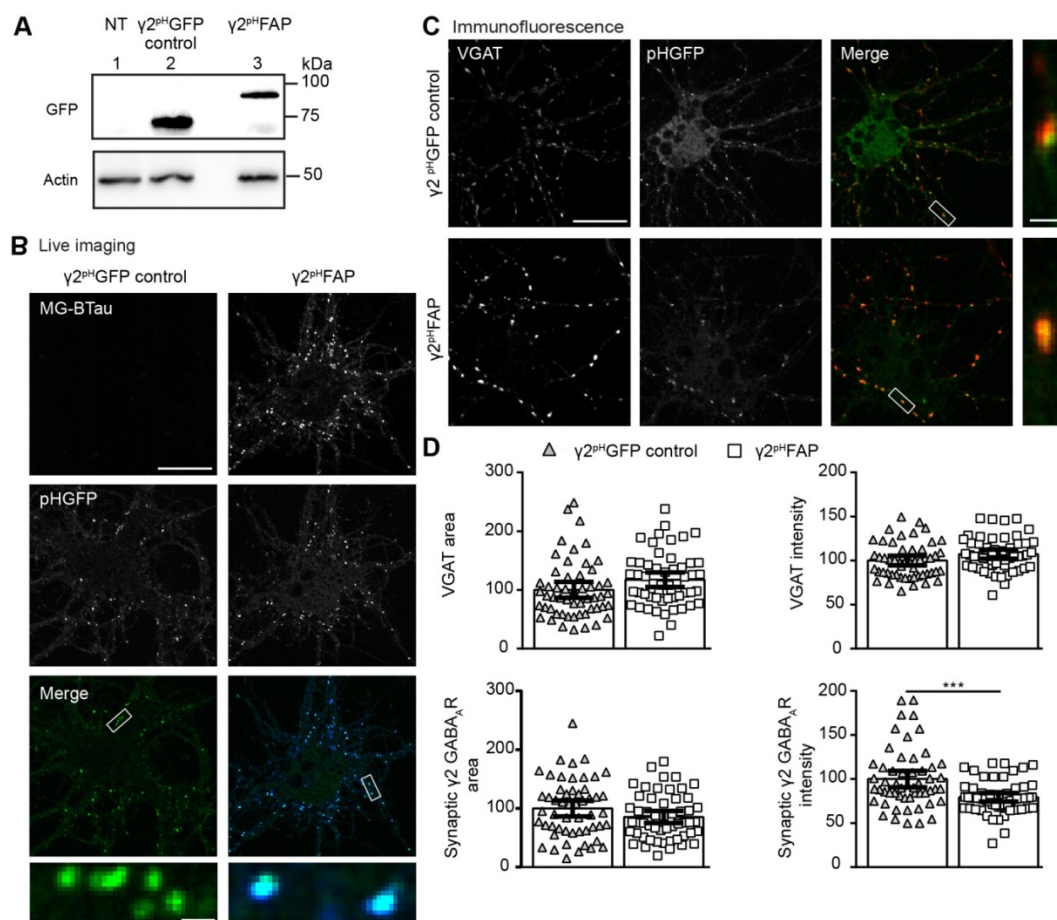


Figure 6. $\gamma 2^{\text{PH}}$ FAP is Fully Expressed in Neurons and Appropriately Clustered at GABAergic Synapses.

(A) Detection of $\gamma 2^{\text{PH}}$ GFP control and $\gamma 2^{\text{PH}}$ FAP receptors via western blot in cortical neurons 14 days post-transfection. NT = non-transfected. ($n = 3$ neuronal cultures). (B) DIV 12 neurons expressing $\gamma 2^{\text{PH}}$ GFP control or $\gamma 2^{\text{PH}}$ FAP were pulse-labeled with 250 nM MG-BTau dye for 1 min prior to live-cell imaging. Surface GABA_ARs are selectively labeled in $\gamma 2^{\text{PH}}$ FAP neurons as evidenced by extensive colocalization of the pHGFP signal (green, Merge) and MG-BTau signal (blue, Merge). Note that in $\gamma 2^{\text{PH}}$ GFP control neurons, surface GABA_ARs are not labeled by MG-BTau dye. Boxed areas enlarged below. (C) Confocal fixed immunofluorescence images of $\gamma 2^{\text{PH}}$ GFP control and $\gamma 2^{\text{PH}}$ FAP expressing neurons with presynaptic GABAergic terminals labeled with VGAT antibody. pHGFP fluorescence (green in Merge) shows intracellular $\gamma 2$ subunit and synaptically localized receptors on dendrites that are colocalized with VGAT (red in Merge). Boxed areas enlarged below. (D) VGAT and surface $\gamma 2$ containing receptor synaptic clusters were quantified. Scatter plot graphs showing mean area and mean fluorescence intensity in neurons transfected with $\gamma 2^{\text{PH}}$ GFP control or $\gamma 2^{\text{PH}}$ FAP. No changes were observed in GABAergic presynaptic terminals as

measured by VGAT area and intensity. Synaptic $\gamma 2$ GABA_AR measurements were determined from pHGFP signal colocalized with VGAT: synaptic $\gamma 2$ GABA_AR fluorescence area was equivalent, while the intensity was slightly lower in $\gamma 2^{\text{pH}}$ FAP neurons (** $p < 0.001$, Student's t-test; $n = 54$ -57 neurons from 3 cultures for each condition; error bars represent \pm 95% confidence interval). Scale bars: main panels = 20 μm , enlargements = 1 μm .

Having validated and established the application of FAP technology to generate a synaptic GABA_AR reporter system, we first explored the experimental flexibility afforded by the distinct characteristics of available MG dyes to study receptor trafficking. First we examined if MG-BTau labeled surface receptors could be identified in endosomal pathways following internalization. DIV 12-13 $\gamma 2^{\text{pH}}$ FAP neurons were pulse-labeled with 100 nM MG-BTau, transferred to 10°C or 37°C HBS for 30 min, and then fixed and immunostained with the early endosome marker EEA1 (**Fig. 7A**). Neurons maintained at 37°C demonstrated greater mean intensity and area of MG-BTau colocalized at EEA1 vesicles compared to those kept at 10°C to inhibit internalization, indicating MG-BTau labeling can also be used to track GABA_AR internalized pools (**Fig. 7B**).

We next investigated the adaptability of $\gamma 2^{\text{pH}}$ FAP with other MG dye applications in live-imaging intracellular trafficking assays. The Cy3pH(S/SA)-MG dye is a dichromophore consisting of a pH-sensitive forester-resonance energy transfer (FRET) donor Cy3pH molecule and an acceptor MG (**Fig. 8A**) (238). Excitation of Cy3pH (561 nm excitation) results in highly efficient FRET to MG and emission is observed at 680 nm, while direct stimulation of MG (640 nm excitation) also results in 680 nm emission, allowing calculation of an emission ratio of $\text{MG}_{561}/\text{MG}_{640}$ (**Fig. 8A**). Increasingly acidic environments such as endosomes and lysosomes lead to protonation of Cy3pH and increased fluorescence intensity, enhancing FRET, and the ratio of $\text{MG}_{561}/\text{MG}_{640}$ (236, 238, 255, 256) The pH sensor dye is cell impermeant like MG-BTau and thus allows for selective labeling of surface $\gamma 2$ -containing GABA_ARs. To characterize the pH-

sensitivity of Cy3pH(S/SA)-MG in our $\gamma 2^{\text{pH}}$ FAP neuronal system, we first performed live-cell imaging perfusion experiments using different pH solutions to simulate receptor progression through an increasingly acidic endolysosomal pathway, as similarly performed in other cell culture methods using Cy3pH(S/SA)-MG (238). Neurons were pulse-labeled with pH sensor dye and then first imaged with pH 7.4 physiological saline, followed by pH 6.8 and pH 4.8 solutions, demonstrating a clear shift in the ratio of $\text{MG}_{561}/\text{MG}_{640}$ across treatments (**Fig. 8B**). Quantification of $\text{MG}_{561}/\text{MG}_{640}$ mean ratios at surface synaptic cluster sites revealed pH 7.4 (0.58 ± 0.01), pH 6.8 (0.69 ± 0.01), and pH 4.8 (0.99 ± 0.02) conditions were significantly different from one another (**Fig. 8C**). Therefore, Cy3pH(S/SA)-MG labeled $\gamma 2^{\text{pH}}$ FAP receptors can be readily identified in environments of different acidities using the $\text{MG}_{561}/\text{MG}_{640}$ ratio.

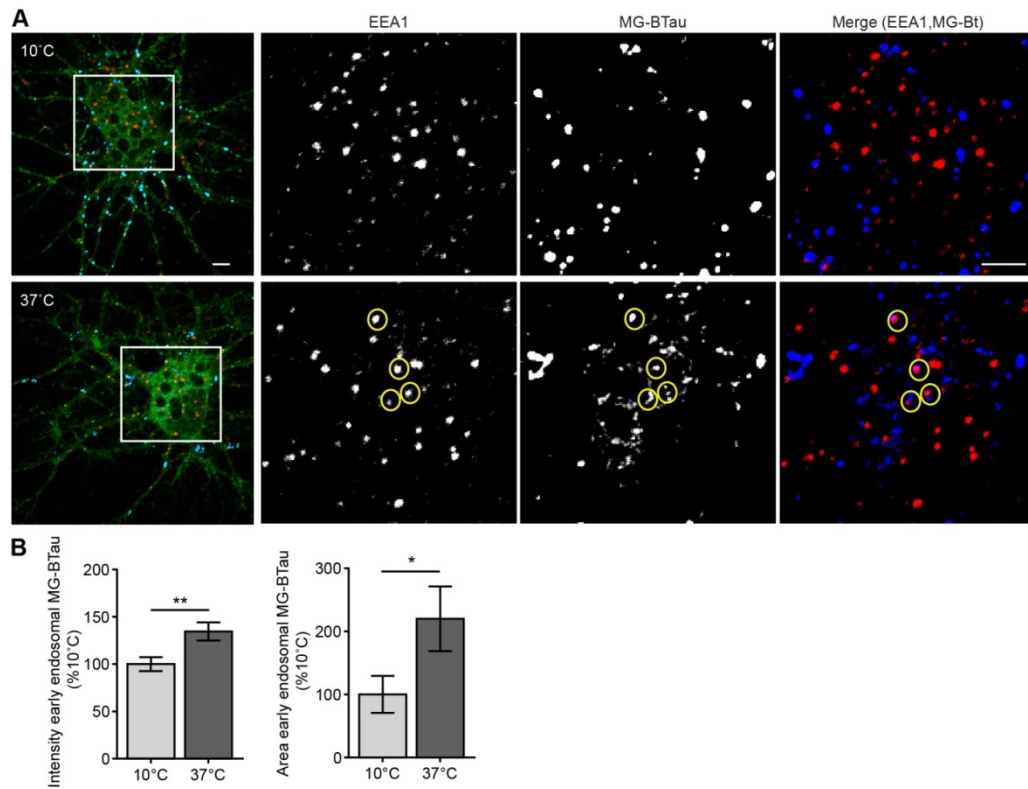


Figure 7. MG-BTau Dye Signal Shows Trafficking of $\gamma 2^{\text{pH}}$ FAP GABA_ARs to Early Endosomes.

(A) DIV 12 $\gamma 2^{\text{pH}}$ FAP expressing neurons were pulse labeled with 100 nM MG-BTau dye for 2 min, then incubated in HBS at 37°C or 10°C for 30 min prior to fixation. MG-BTau (blue) labeled neurons were permeabilized and stained with early endosome marker EEA1 antibody (red). pHGFP (green) is visible throughout the cell after fixation. Boxed area is enlarged to the right with EEA1 (red), MG-BTau (blue), and Merge panels. Yellow circles show colocalized EEA1 and MG-BTau signal. (B) The intensity and area of MG-BTau labeled receptors colocalized with EEA1-positive intracellular vesicles is increased when endocytosis is not inhibited by 10°C. (* $p \leq 0.05$, ** $p < 0.01$, Student's t-test; $n = 25$ neurons from 3 cultures each condition; error bars represent \pm S.E.M.). Scale bars = 5 μm .

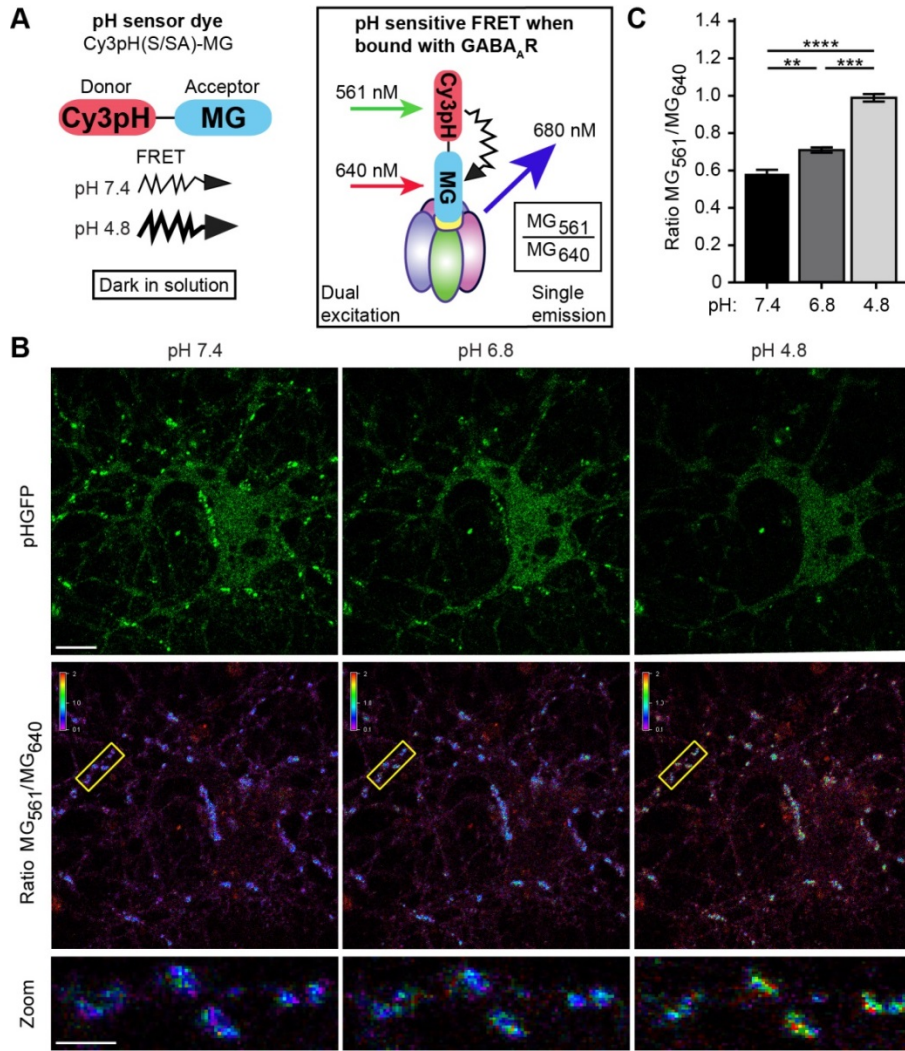


Figure 8. Cy3pH(S/SA)-MG Dye Bound to Surface $\gamma 2^{\text{pH}}$ FAP Receptors Displays a pH-Sensitive FRET Signal.

(A) pH sensor dye Cy3pH(S/SA)-MG is a fluorogen FRET sensor. Increasingly acidic environment enhances Cy3pH fluorescence intensity and FRET. A higher MG₅₆₁/MG₆₄₀ ratio indicates lower pH. (B) DIV 12-13 $\gamma 2^{\text{pH}}$ FAP expressing neurons were pulse labeled with 100nM pH sensor dye Cy3pH(S/SA)-MG for 2 mins, then were immediately used for live-imaging. Cells were first perfused with pH 7.4 HBS, then pH 6.8 HBS, and finally MES-buffered saline pH 4.8. Zoomed dendrite images below highlight MG₅₆₁/MG₆₄₀ ratios at surface synaptic clusters across different acidities. All ratiometric images are on a scale from 0.1 to 2. Scale bars: whole image = 10 μm ; zoom image = 2.5 μm . (C) The MG₅₆₁/MG₆₄₀ ratio of individual surface $\gamma 2^{\text{pH}}$ FAP GABA_AR synaptic clusters were quantified at each pH (**** $p \leq 0.0001$, one way ANOVA followed by post hoc Tukey's test; $n = 41$ synaptic clusters from 4 cells; error bars represent \pm S.E.M.

Following pH characterization of Cy3pH(S/SA)-MG, we then utilized this dye to identify localization of internalized $\gamma 2^{\text{pH}}$ FAP receptors in the endosomal-lysosomal system. Acidity increases as intracellular receptors undergo transition from early endosomal/recycling pathways to late endosomal/lysosomal pools (**Fig. 9A**). We therefore anticipated differences in mean $\text{MG}_{561}/\text{MG}_{640}$ ratios between these vesicular populations. To examine this effect, we cotransfected $\gamma 2^{\text{pH}}$ FAP neurons with the early endosome marker EEA1-GFP for live-imaging experiments. At DIV 12-13, 10 nM Cy3pH(S/SA)-MG was added directly to the cell culture media and neurons were incubated for 30 min at 37°C prior to imaging. Cells were first perfused with pH 7.4 HBS to acquire $\text{MG}_{561}/\text{MG}_{640}$ data, then with pH 6.4 solution to eliminate surface $\gamma 2^{\text{pH}}$ FAP (pHGFP) signal (orange stars; **Fig. 9B**) to isolate intracellular EEA1-GFP for image analysis. Cy3pH(S/SA)-MG vesicles colocalized with EEA1-GFP (yellow arrows; **Fig. 9B**) demonstrated a mean $\text{MG}_{561}/\text{MG}_{640}$ ratio of 0.824 ± 0.012 , while all other identified vesicles not-associated with EEA1-GFP (white triangles; **Fig. 9B**) displayed a significantly higher ratio of 0.918 ± 0.016 (Other; **Fig. 9C**). The Cy3pH(S/SA)-MG found in non-EEA1 intracellular sites typically displayed the lowest pH and was in comparably larger vesicular bodies, suggesting lysosomal compartments. These results indicate Cy3pH(S/SA)-MG labeled $\gamma 2^{\text{pH}}$ FAP receptors can be used to decipher the localization of internalized GABA_AR pools along the endosome-lysosome axis.

Next we wanted to elucidate if Cy3pH(S/SA)-MG could be used to monitor the constitutive endolysosomal trafficking of GABA_ARs by using conditions that limit internalization. We compared $\gamma 2^{\text{pH}}$ FAP neurons pulse-labeled with 100 nM Cy3pH(S/SA)-MG dye either immediately after washing (t_0) or 30 min later \pm the dynamin inhibitor, dynasore (80 μM) at 37°C. Importantly, GABA_ARs have been previously characterized to undergo constitutive dynamin-dependent clathrin mediated endocytosis (137, 257). Images of neurons allowed 30 min of trafficking show

enhanced dye-labeled GABA_AR accumulation within the cell body compared to t0 and to t30 + dynasore (**Fig. 9D**). The number of GABA_AR-positive vesicles inside the neuronal cell body was measured using the spot detection feature in NIS Elements. Quantification confirmed that the total number of vesicles identified at t30 is $78.7 \pm 20\%$ greater than at t0 and that vesicle internalization is blocked by dynasore co-treatment (**Fig. 9E**). To better understand the receptor population distribution along the endosomal-lysosomal trafficking axis, we examined each measured vesicle's respective MG₅₆₁/MG₆₄₀ ratio using a histogram plot (**Fig. 9F**). This analysis revealed that the increase in vesicles found at t30 were primarily at lower MG₅₆₁/MG₆₄₀ ratios, suggesting early endosomal trafficking. Moreover, the vesicle median MG₅₆₁/MG₆₄₀ ratios were significantly different between all conditions: t0 = 1.31; t30 = 0.767; and t30 + dynasore = 0.826. Interestingly, we found that while dynasore reduced the number of internalized receptors detected back to t0 levels, dynasore treated neurons demonstrated a unique vesicular MG₅₆₁/MG₆₄₀ ratio profile (**Fig. 9E**). Dynasore inhibition of clathrin-coated pit formation and endocytosis generates half formed “U” and “O” shaped pits/vesicles associated with the plasma membrane (258). The few vesicles present in t30 + dynasore treated neurons (**Fig. 9D**) are likely to be these structures undergoing partial acidification during the 30 minute experimental period. In summary, $\gamma 2^{\text{pH}}$ FAP and the Cy3pH(S/SA)-MG dye reveal significant constitutive clathrin-dependent endocytosis of GABA_ARs that favors early endosomal pathways.

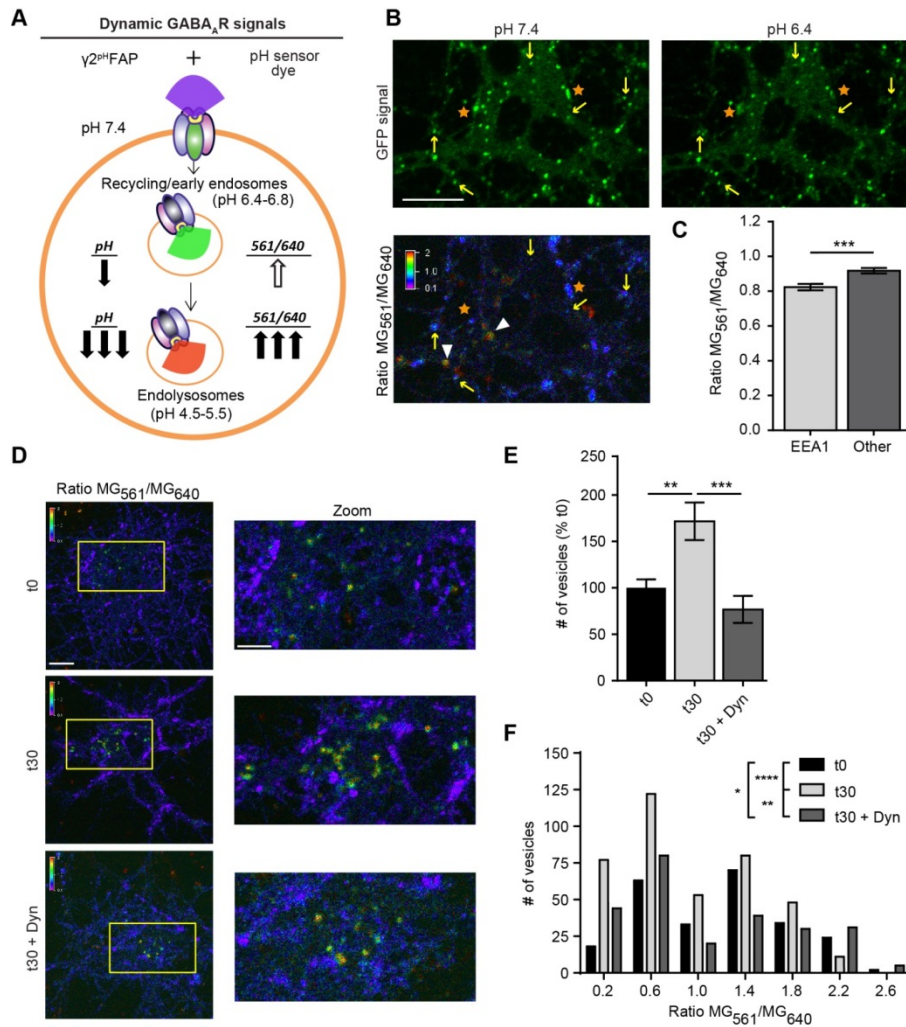


Figure 9. Constitutive Endolysosomal Trafficking of GABA_ARs can be Measured using the pH-Sensitive Dye Cy3pH(S/SA)-MG and $\gamma 2^{pH}FAP$.

(A) Application of pH sensor dye to visualize and distinguish intracellular vesicle targeting of internalized GABA_AR. Once internalized, the pHGFP signal is immediately quenched, and the increasingly acidic environment enhances Cy3pH fluorescence intensity and FRET. A higher MG₅₆₁/MG₆₄₀ ratio indicates vesicular acidification. Recycling/early endosomal vesicle signal represented as green, late endosome/lysosomes as red to match the MG₅₆₁/MG₆₄₀ ratio heatmap in images. (B) Neurons transfected with $\gamma 2^{pH}FAP$ and *EEA1-GFP* were incubated in the continuous presence of 10nM Cy3pH(S/SA)-MG dye for 30 min in conditioned media at 37°C and then washed and rapidly imaged. After initial images were taken at pH 7.4, pH 6.4 HBS was perfused onto cells to quench surface pHGFP signal of $\gamma 2^{pH}FAP$ and selectively identify EEA1-GFP positive vesicles. Yellow arrows indicate vesicles where EEA1-GFP is colocalized with Cy3pH(S/SA)-MG; white triangles indicate larger Cy3pH(S/SA)-MG vesicular

structures not colocalized with EEA1-GFP (Other); orange stars represent $\gamma 2^{\text{pH}}$ FAP pHGFP surface signal that is eliminated after pH 6.4 saline perfusion. Scale bar = 10 μm . (C) Quantification of individual intracellular vesicles MG₅₆₁/MG₆₄₀ ratio at either EEA1-GFP positive sites or other internal compartments ($n = 243$ EEA1-GFP; 511 Other from 9 cells and 2 neuronal cultures; Student's t-test; error bars represent error bars represent \pm S.E.M.). (D) Confocal images of pH sensor dye-labeled GABA_ARs at t0, t30 and t30 + dynasore (Dyn, 80 μM), with cell body indicated by yellow outlined region of interest (ROI). Zoomed images of timepoints are shown to right. Scale bars: whole image = 10 μm ; zoom image = 5 μm . (E) More intracellular vesicles are quantified at t30 than t0 or t30 + dynasore (one way ANOVA followed by post hoc Tukey's test; error bars represent \pm S.E.M.). (F) Histogram analysis reveals most t30 vesicles had lower MG₅₆₁/MG₆₄₀ ratios and the median values between all conditions were significantly different (Mann-Whitney test) ($n = 14$ neurons per treatment from 3 independent cultures). All ratiometric images are on a scale from 0.1 to 2. p values for (C,E,F): * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$, and **** $p \leq 0.0001$

2.3.3 $\gamma 2^{\text{pH}}$ FAP Reveals Enhanced GABA_AR Synaptic Turnover in an *In Vitro*

Bicuculline Seizure Paradigm

We last set out to investigate if the $\gamma 2^{\text{pH}}$ FAP-dye system could be used to measure pharmacologically-induced changes in GABA_AR trafficking in living neurons. Prolonged exposure of the GABA_AR antagonist bicuculline is proconvulsant due to sustained dampening of network inhibition, leading to seizure-type activity *in vitro* and *in vivo* (259-262). Multiple hyperexcitable neuronal states have previously been reported to enhance $\gamma 2$ -containing GABA_AR internalization and reduce total surface levels at 1 h post induction (156-158, 263). We investigated if the $\gamma 2^{\text{pH}}$ FAP construct could be used to simultaneously examine multiple stages of receptor trafficking including receptor surface, synaptic, and lysosomal levels following a bicuculline-induced seizure paradigm. At DIV 12-14 $\gamma 2^{\text{pH}}$ FAP neurons were pulse-labeled with MG-BTau dye and then returned to conditioned media +/- 50 μM bicuculline at 37°C for 1 h. 50 nM LysoTracker was added 30 min prior to the end of treatment to identify association of receptors with lysosomes.

Representative images indicate MG-BTau labels synaptic GABA_AR clusters on the surface of dendrites as seen by colocalization of MG-BTau (blue) and pHGFP (green) (**Fig. 10A,B**). MG-BTau also reveals internalized receptors within the cell body in lysosomes (**Fig. 10C**, LysoTracker in red). These data demonstrate that the binding of MG-BTau to $\gamma 2^{\text{pH}}$ FAP GABA_ARs and its resulting fluorescence is stable even in very low pH environments such as lysosomes, consistent with previous findings using different FAP-tagged receptors colocalized with LysoTracker in cell culture (236). Image analysis uncovered no significant difference in total surface expression of $\gamma 2^{\text{pH}}$ FAP between DMSO control and bicuculline treated cells when measuring pHGFP signal (**Fig. 10D**). There was a trend towards a decrease in synaptic levels of $\gamma 2^{\text{pH}}$ FAP in bicuculline treated neurons ($75 \pm 13\%$ of control), determined by pHGFP cluster fluorescence, but this was not significant. In contrast, (**Fig. 10E**) shows bicuculline treatment reduced total and synaptic MG-BTau signal by $41 \pm 10\%$ and $67 \pm 8\%$, respectively, indicating the population of pulse-labeled $\gamma 2^{\text{pH}}$ FAP receptors had decreased. In support of enhanced receptor turnover, we found that bicuculline treatment increased association of labeled receptors with lysosomes by $107 \pm 41\%$ compared to control. These findings suggest that bicuculline-induced seizure activity leads to augmented GABA_AR synaptic turnover, lysosomal targeting, and a compensatory increase in new, non-recycled GABA_AR insertion to

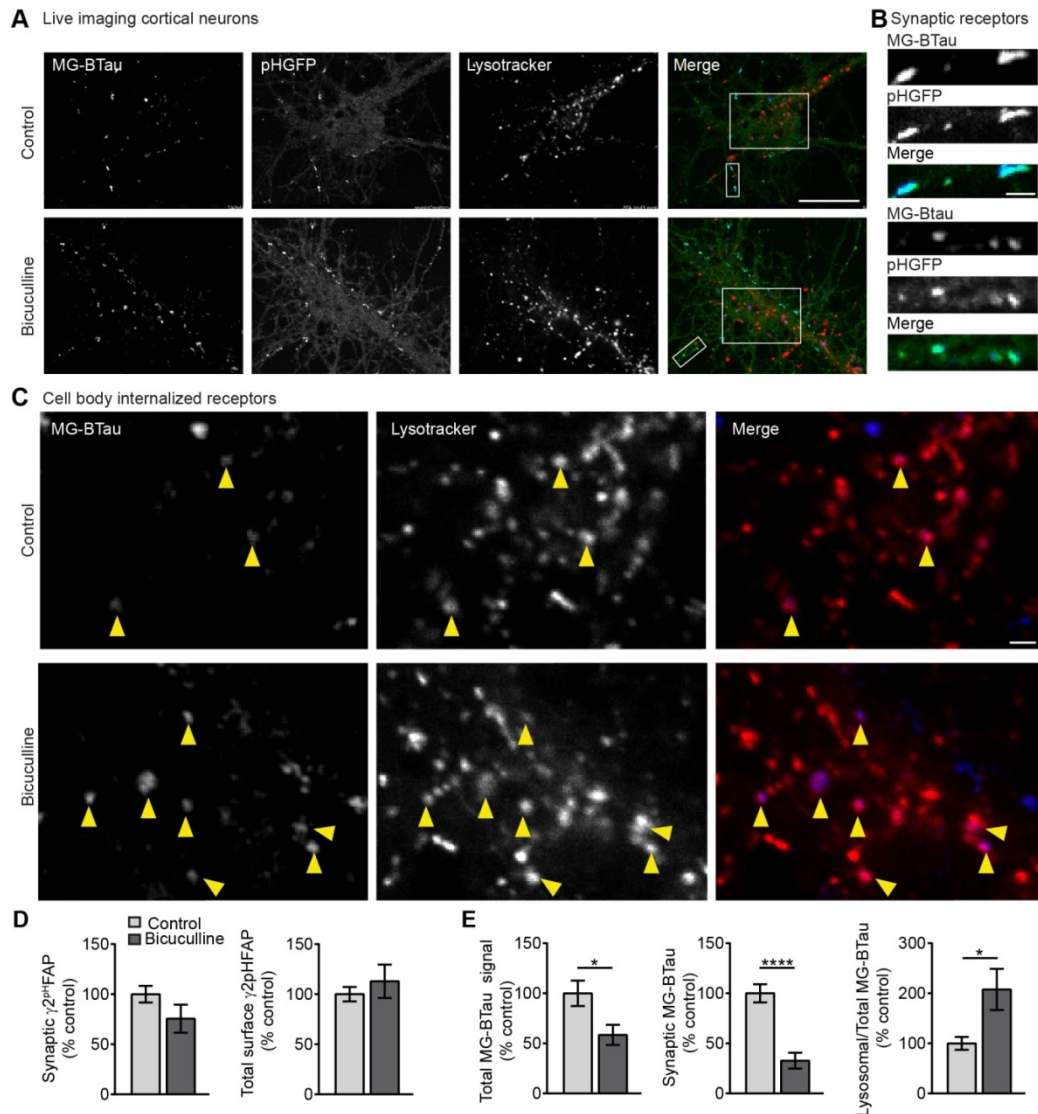


Figure 10. $\gamma 2^{pH}FAP$ Imaging Reveals Increased Internalization and Enhanced GABAAR Turnover Rates Following a Bicuculline-Induced Seizure Paradigm.

(A) $\gamma 2^{pH}FAP$ neurons were pulse-labeled with 100 nM MG-BTau for 2 min then returned to 37°C conditioned media +/- 50 μM bicuculline for 1 h. LysoTracker (50 nM) was added directly to the media after 30 min to label lysosomes. pHGFP fluorescence is shown in green, LysoTracker in red, and MG-BTau in blue in the Merge panels. Smaller boxed areas in Merge panel identify surface synaptic receptors (enlarged in B). Larger boxed area identifies internalized receptors present in endosomes and lysosomes in cell body of neuron (enlarged in C). (B) Surface synaptic receptors on dendrites are seen with colocalization of MG-BTau and pHGFP signals. (C) Enlargements of cell body area show colocalization of internalized MG-BTau labeled GABA_ARs and lysosomes. (D) Quantification of pHGFP signal showed synaptic and total surface levels were not changed following bicuculline treatment. (E) In contrast,

quantification of MG-BTau signal revealed reductions in total and synaptic receptor levels after the bicuculline seizure paradigm. Bicuculline treatment also enhanced the ratio of MG-BTau labeled receptors associated with lysosomes over total MG-BTau signal. (* $p < 0.05$, **** $p < 0.0001$, Student's t-test; synaptic measurements performed on three 10 μm regions located on dendrites; $n = 13$ neurons per treatment from 3 independent cultures; error bars represent \pm S.E.M.). Scale bars: 20 μm in A and 2 μm in B,C.

mitigate this response. These results robustly demonstrate the versatility of the $\gamma 2^{\text{pH}}$ FAP-dye system and its ability to measure numerous trafficking events to address complex questions.

2.4 Discussion

Live-cell receptor tracking approaches offer critical information by revealing real-time alterations in protein trafficking. Here we describe a flexible paired GABA_AR $\gamma 2$ -subunit optical reporter system that can be used to monitor multi-stage receptor trafficking. Compared to previously available methods that require reliable antibodies, conventional fluorophore tagging, or fluorescent α -bungarotoxin labeling, the $\gamma 2^{\text{pH}}$ FAP-dye system can allow for simultaneous monitoring of surface, synaptic, and intracellularly trafficking GABA_ARs in real-time. The strength of this method lies in the ability to simply alternate FAP-compatible MG dyes to address the specific experimental question of interest.

We applied the pH sensor dye, Cy3pH(S/SA)-MG, to monitor internalization and constitutive endosomal and lysosomal trafficking of GABA_ARs in neurons. We found that Cy3pH(S/SA)-MG labeled surface $\gamma 2^{\text{pH}}$ FAP receptors can be tracked to small EEA1-positive early endosomes (MG-BTau labeled receptors also identified at EEA1 endosomes; **Fig. 7**) and also to larger vesicular structures with low pH (likely lysosomes), generating high MG₅₆₁/MG₆₄₀ ratios (**Fig. 9B,C**). Synaptic GABA_AR endocytosis occurs primarily in a dynamin-dependent manner

(257) and can be identified within 30 minutes using an antibody feeding approach (137). Our results in **Fig. 9** demonstrate rapid internalization of receptors in endosomal/lysosomal pathways on this same time scale, a process reduced by the dynamin-inhibitor dynasore. As a result of the vesicle-level pH-sensitive measurement afforded by this tool, we were able to further generate a histogram plot identifying differences in the trafficking stages of $\gamma 2^{\text{pH}}$ FAP-positive vesicles. These analyses suggest internalized receptors favor early endosomal pathways, a finding supported by a previous study that determined over 70% of internalized GABA_ARs are recycled back to the cell surface within 1 h (143). Furthermore, dynasore treated neurons displayed vesicles with a distinct MG ratio profile, possibly resulting from acidification of endocytic pits/vesicles not released from the plasma membrane, non-dynamin dependent endocytosis of receptors, or dynasore off-target effects. GABA_ARs undergo both clathrin-dependent and -independent endocytosis pathways in heterologous cells (138), with both mechanisms being recently identified in neurons for glutamateric AMPA receptors (264, 265). Dynasore has also been shown to disrupt lysosomal fission by inhibiting dynamin-2 (266) as well as have other non-specific, dynamin independent effects (267, 268) that could result in different vesicle MG₅₆₁/MG₆₄₀ ratio profiles. Further studies investigating additional time points are necessary to identify the rate, equilibrium, and overall population dynamics of constitutive GABA_AR internalization.

To test the utility of $\gamma 2^{\text{pH}}$ FAP in detecting pharmacologically-induced changes in GABA_AR trafficking, we exposed neurons to a bicuculline-induced seizure paradigm following a MG-BTau pulse-labeling protocol (**Fig. 10**). This unique dye labeling approach readily detected enhanced synaptic receptor turnover rates and lysosomal targeting that were not detectable by pHGFP fluorescence alone. Previous work has shown that more aggressive seizure protocols relying on

depolarization via high external potassium and/or agonist application targeting highly calcium permeable NMDA receptors reduces total surface GABA_ARs in cultured neurons (157). It is likely that the mild seizure paradigm used here does not affect total surface receptor levels, but instead enhances surface turnover that is offset by increased receptor insertion rates. In support of this argument, another recent study (160) found that 1 h treatment with GABA_AR antagonists did not lead to a reduction in surface GABA_AR levels.

This paper lays the groundwork for future investigations of GABA_AR trafficking using the $\gamma 2^{\text{pH}}$ FAP sensor. Importantly, this technique can be further extended toward pharmacology focused efforts in high throughput screenings (234, 244), assay development based on flow cytometry (235, 243) or high resolution 96-well plate assays (250), and for *in vivo* protein labeling (237, 269). In summary, our $\gamma 2^{\text{pH}}$ FAP is the first protein-FAP conjugate characterized in primary neurons, providing a unique tool to monitor multistage GABA_AR trafficking in living cells with relevance both for basic science research and applied pharmacology.

3.0 Early Diazepam Exposure Alters GABA_AR Intracellular Trafficking and Accelerates Synaptic Exchange

Chapter adapted from: Lorenz-Guertin, J. M., et al. (2019). Diazepam Accelerates GABA_AR Synaptic Exchange and Alters Intracellular Trafficking. *Front Cell Neurosci* (270) <https://doi.org/10.3389/fncel.2019.00163>

JL-G performed the biochemistry, immunoprecipitation, bioinformatics analysis and fixed and live imaging acquisition and analysis. Matthew J. Bambino performed the FRET imaging and analysis. Joshua Lorenz-Guertin, Tija C. Jacob and Susan T. Weintraub designed the Mass spectrometry experiments. The Weintraub lab performed mass spectrometry and data was analyzed by Joshua Lorenz-Guertin, Tija C. Jacob and Susan T. Weintraub.

3.1 Introduction

The most prevalent synaptic GABA_AR subtype is composed of two α , two β , and a $\gamma 2$ subunit forming a heteropentamer (32). BZDs are a widely used clinical sedative-hypnotic drug class that selectively bind between the interface of a GABA_AR $\gamma 2$ subunit and either an $\alpha 1/2/3/5$ subunit (33). Receptors containing these α subunits are considered to be primarily synaptic, with the exception of $\alpha 5$, which is localized both synaptically and extrasynaptically (63). Positive allosteric modulation by BZD enhances GABA_AR inhibition by increasing the binding affinity of GABA and increasing channel opening frequency (32). It is known that the potentiating effect of BZDs are lost after prolonged or high dose acute exposure (271, 272), characterized first by a loss of sedative/hypnotic activity followed by the anti-convulsant properties behaviorally (46, 273-275). The induction of BZD tolerance occurs in part due to the uncoupling of allosteric actions between GABA and BZD (276, 277), a process that appears to rely on GABA_AR receptor internalization (278, 279). We have previously shown that 24 h BZD treatment leads to decreased

surface and total levels of the $\alpha 2$ subunit in cultured hippocampal neurons that was dependent on lysosomal-mediated degradation (169); however, the process by which the $\alpha 2$ subunit is selectively targeted to lysosomes is still unknown. GABA_AR subunit ubiquitination and subsequent degradation at proteasomes or lysosomes modulates cell surface expression of receptors (117, 159, 170, 280, 281). Ubiquitination of the $\gamma 2$ subunit is the only currently known mechanism identified to target internalized surface GABA_ARs to lysosomes (159).

Another major regulator of GABA_AR efficacy is postsynaptic scaffolding. Confinement at synaptic sites maintains receptors at GABA axonal release sites for activation. Furthermore, this limits receptor diffusion into the extrasynaptic space where internalization occurs (282, 283). The scaffolding protein gephyrin is the main organizer of GABA_AR synaptic localization and density, as gephyrin knock-down and knock-out models show dramatic reductions in $\gamma 2$ - and $\alpha 2$ -GABA_AR clustering (54, 55). Evidence suggests gephyrin interacts directly with GABA_AR $\alpha 1$, $\alpha 2$, $\alpha 3$, $\alpha 5$, $\beta 2$, and $\beta 3$ subunits (62, 63, 65, 284-286). Gephyrin recruitment is involved in inhibitory long term potentiation (iLTP) (77, 287), while its dispersal coincides with GABA_AR diffusion away from synapses (54, 182). Extensive post-translational modifications influence gephyrin function (288, 289). Accordingly, expression of gephyrin phosphorylation site mutants revealed complex effects on GABA_AR diffusion and gephyrin ultrastructure and scaffolding (289, 290). Phosphorylation at the gephyrin serine 270 (Ser270) site has been particularly characterized to negatively modulate scaffold clustering and density, in part by enhancing calpain-1 protease mediated degradation of gephyrin (73). Given the well-established interdependent relationship between gephyrin and the $\gamma 2$ subunit in maintaining receptor synaptic integrity (54, 55, 67, 215, 291, 292), impaired postsynaptic scaffolding should affect both pre-existing and newly inserted GABA_AR clustering

and ultimately the efficacy of inhibitory neurotransmission. Thus a central unanswered question is if BZD exposure causes changes in gephyrin phosphorylation or protein levels.

Here we demonstrate that 12-24 h treatment with the BZD diazepam (DZP) leads to a reduction in total $\gamma 2$ subunit and full-length gephyrin levels *in vitro* and *in vivo*. This reduction occurred coincident with enhanced $\gamma 2$ subunit ubiquitination, but resulted in no significant change in overall $\gamma 2$ surface levels. Using our recently published dual fluorescent BZD-sensitive GABA_AR reporter ($\gamma 2^{\text{pH}}$ FAP), we further show that cell surface $\gamma 2$ -GABA_ARs are more frequently targeted to lysosomes after DZP exposure. Forester resonance energy transfer (FRET) experiments further confirmed specific loss of synaptic $\alpha 2/\gamma 2$ GABA_AR levels following DZP treatment. The scaffolding protein gephyrin also demonstrated augmented phosphorylation at Ser270, increased cleavage and was significantly decreased in membrane and cytosolic compartments. Fluorescence recovery after photobleaching (FRAP) assays identified that DZP treatment increased the simultaneous recovery of $\gamma 2$ -GABA_AR and gephyrin at synaptic sites, indicating reduced receptor confinement and accelerated exchange between the synaptic and extrasynaptic GABA_AR pool. This process was reversed by the BZD site antagonist Ro 15-1788. Lastly, co-immunoprecipitation, quantitative mass spectrometry and bioinformatics analysis revealed shifts in the $\gamma 2$ -GABA_AR interactome towards trafficking pathways *in vivo*. Together, these data suggest that DZP exposure causes a compensatory decrease in inhibitory neurotransmission by reducing BZD-sensitive GABA_AR and gephyrin confinement at synapses and via ubiquitination and lysosomal targeting of $\gamma 2$ by reducing BZD-sensitive GABA_AR and gephyrin confinement at synapses, and via ubiquitination and lysosomal targeting of $\gamma 2$.

3.2 Methods and Materials

3.2.1 Cell Culture, Transfection, Expression Constructs and Mice

Cortical neurons were prepared from embryonic day 18 Sprague Dawley rats and nucleofected with constructs at plating (Amaxa). The $\gamma 2^{\text{pH}}$ FAP construct was characterized in (212) and RFP-gephyrin was described in (63). The $\gamma 2^{\text{RFP}}$ construct was generated by PCR cloning and fully sequenced: the red fluorescent protein *mCherry* replaced *pHluorin* in the previously published $\gamma 2^{\text{pHGFP}}$ construct (54). *GFP-ubiquitin* was a gift from Nico Dantuma (Addgene plasmid # 11928) (293). 8-10 week old male C57BL/6J mice (Jackson Laboratory) were maintained on a reverse 12 h dark/light schedule. Mouse cortical brain tissue was collected and flash frozen 12 h after I.P. injection with either vehicle or diazepam (in 40% PEG, 10% EtOH, 5% Na Benzoate, 1.5 % Benzyl alcohol (Hospira)). All procedures were approved by the University of Pittsburgh Institutional Animal Care and Use Committee.

3.2.2 Reagents, Antibodies, and MG Dye

Diazepam (cell culture, Sigma; injections, Hospira); Ro 15-1788 (Tocris Bioscience); calpain-1 inhibitor MDL-28170 (Santa Cruz); L-glutamic acid (Tocris Bioscience). Primary antibodies: rabbit GAPDH (WB) (14C10, Cell Signaling); guinea pig GAD-65 (IF) (198104, Synaptic Systems); rabbit $\gamma 2$ GABA_AR subunit (IF, WB, IP) (224003, Synaptic Systems); rabbit gephyrin (WB) (sc-14003, Santa Cruz); rabbit gephyrin (IF, total) (147002, Synaptic Systems); mouse gephyrin mAb7a (IF, phospho) (147011, Synaptic Systems); chicken GFP (WB) (GFP-1020, Aves); rabbit (P)ERK (WB) (4370, Cell Signaling); mouse ERK (WB) (9107, Cell

Signaling); rabbit (P)GSK3 β (WB) (9322, Cell Signaling); rabbit GSK3 β (WB) (9315, Cell Signaling); rabbit CDK5 (WB) (2506, Cell Signaling). MG-BTau dye prepared as in (212).

3.2.3 Fixed and Live-Imaging

Measurements were made on days *in vitro* (DIV) 15–19 cortical neurons. Live-imaging performed in Hepes-buffered saline (HBS), containing the following (in mM): 135 NaCl, 4.7 KCl, 10 Hepes, 11 glucose, 1.2 MgCl₂, and 2.5 CaCl₂ (adjusted to pH 7.4 with NaOH). Images were acquired using a Nikon A1 confocal microscope with a 60 \times oil objective (N.A., 1.49) at 3 \times zoom. Data were analyzed in NIS Elements software (Nikon, N.Y.). Measurements were taken from whole cell or averaged from three dendritic 10 μ m regions of interest (ROI) per cell. For fixed imaging, media was quickly removed and coverslips were washed twice with Dulbecco's Phosphate Buffered Saline (DPBS) and immediately fixed with 4% paraformaldehyde and then blocked in PBS containing 10% fetal bovine serum and 0.5% bovine serum albumin. Surface antibody staining was performed under non-permeabilized conditions overnight at 4°C. Intracellular staining was performed overnight at 4°C following 0.2% Triton-X permeabilization for 10 min in blocking solution. Synaptic sites were determined during analysis by binary thresholds and colocalization with GAD-65. Extrasynaptic intensity was measured by taking the total dendrite ROI sum intensity minus background and synaptic fluorescence intensity. Dendritic fluorescence was measured using binary thresholds. Experimental conditions were blinded during image acquisition and analysis. The ROUT test (Q=1%) or Grubbs' Test (α =0.05) was used to remove a single outlier from a data set.

3.2.4 Lysosomal Targeting Assay

Neuron surface and lysosomal-association assays utilized MG-BTau dye for surface receptor pulse-labeling. DIV 15-16 neurons were treated with vehicle or DZP for 8-12 h, then pulse labeled with 100 nM MG-BTau for 2 min at room temperature in HBS. Neurons were then washed 5x times with HBS and returned to conditioned media +/- DZP for 1 h. To identify lysosomal targeting, 50 nM LysoTracker Blue DND-22 (Life Technologies) and the lysosomal inhibitor, Leupeptin (200 μ M Amresco), was added 30 min prior to imaging. Following incubation, neurons were washed and imaged in 4°C HBS. Two-three neurons were immediately imaged per culture dish within 10 min of washing. For image analysis, independent ROIs were drawn to capture the soma, three 10 μ m sections of dendrite and the whole cell. Binary thresholds and colocalization measurements were performed to identify MG-BTau, pHGFP synaptic GABA_AR clusters and lysosomes. Total surface pHGFP expression was determined by taking the entire cell surface signal following background subtraction.

3.2.5 NH₄Cl Intracellular Imaging

DIV 15-16 neurons were washed and continuously perfused with HBS + treatment at room temperature. Multiposition acquisition was used to image 2-3 neurons per dish. An initial image was taken to identify surface γ 2^{pH}FAP GABA_ARs. Neurons were then perfused with NH₄Cl solution to collapse the cellular pH gradient and were reimaged. NH₄Cl solution (in mM): 50 NH₄Cl, 85 NaCl, 4.7 KCl, 10 Hepes, 11 glucose, 1.2 MgCl₂, and 2.5 CaCl₂ (adjusted to pH 7.4 with NaOH). pHGFP intensity was measured following background subtraction and smoothing. Surface/total levels were determined by dividing the first image (surface only) from the second

image (total). The spot detection tool in Nikon Elements was used to selectively count larger intracellular vesicles positive for $\gamma 2^{\text{pH}}$ FAP. A stringent threshold was set to identify brightly fluorescent circular objects with a circumference of approximately 0.75 μm . Values reflect new vesicle objects that were only seen after NH_4Cl perfusion (second image – first image).

3.2.6 Intermolecular FRET Imaging, Characterization and Analysis

The $\alpha 2^{\text{pH}}$ construct was previously published (65) and the $\gamma 2^{\text{RFP}}$ construct was generated by PCR cloning and fully sequenced. DIV 15-16 neurons were treated with Veh or DZP for 20-28 h, then washed and continuously perfused with HBS at room temperature. Images were acquired with a 60x objective at 2x zoom. For each cell, an initial image was acquired containing two channels to identify surface $\alpha 2^{\text{pH}}$ (excited by 488 laser, emission band pass filter 500-550) and $\gamma 2^{\text{RFP}}$ participating in FRET (excited 488 FRET, emission band pass filter 575–625 nm, FRET channel). A second, single channel image was taken immediately following with only 561 nm excitation to reveal total $\gamma 2^{\text{RFP}}$ levels (excited by 561 laser, emission band pass filter 575–625 nm). For synaptic quantifications, binary thresholding based on intensity was applied with smoothing and size exclusion (0-3 μm) factors. FRET and 561 channel binaries shared identical minimum and maximum binary threshold ranges. Individual synaptic ROIs were created to precisely target and measure synaptic clusters containing both $\alpha 2^{\text{pH}}$ and $\gamma 2^{\text{RFP}}$. Manual trimming and single pixel removal were used to remove signal not meeting the criteria of a receptor cluster. Restriction criteria were applied in the following order: 1) at least 15 synapses measured per cell, 2) FRET $\gamma 2^{\text{RFP}}$: raw $\gamma 2^{\text{RFP}}$ sum intensity ratio must be less than one, 3) synaptic $\alpha 2^{\text{pH}}$ mean intensity of at least 500, and 4) $\alpha 2^{\text{pH}}$ sum intensity limit of 300% of average sum intensity. ROI data was then

normalized to vehicle control as percent change. The percentage of RFP participating in FRET was also calculated using FRET RFP:Total RFP ratio.

FRET activity was directly assessed by acceptor ($\gamma 2^{\text{RFP}}$) photobleaching. Photobleaching ROIs were implemented on 2 synapses per cell. Pre-bleaching images were acquired every 5 seconds, followed by a $\gamma 2^{\text{RFP}}$ photobleaching event using 80% 561 nm laser power. After photobleaching, image capturing resumed without delay using pre-bleach laser power settings for 2 minutes. Image analysis incorporated background subtraction and the measurement of percent change in $\alpha 2^{\text{pH}}$ /FRET $\gamma 2^{\text{RFP}}$ ratio over the time course. FRET efficacy measurements compared directly adjacent $\alpha 2^{\text{pH}}$ and $\gamma 2^{\text{RFP}}$ subunits in a GABA_AR complex. Live-imaging with perfusion of pH 6.0 extracellular imaging saline solution (MES) was used to quench the pH-dependent GFP fluorescence from the $\alpha 2^{\text{pH}}$ donor fluorophores and show the dependence of FRET on surface $\alpha 2^{\text{pH}}$ fluorescence. Acidic extracellular saline solution, MES solution pH 6.0 (in mM): 10 MES, 135 NaCl, 4.7 KCl, 11 glucose, 1.2 MgCl₂, and 2.5 CaCl₂ (adjusted to pH 7.4 with NaOH). Images were collected under HBS conditions for 1 minute at 20 second intervals, and then followed by a 2 minute MES wash with the same imaging interval to quench donor emissions. FRET RFP mean intensity was measured under both conditions and normalized to HBS. Percent or fold change in FRET RFP emissions were reported. We confirmed loss of $\alpha 2^{\text{pH}}$ donor lead to 90% loss of FRET $\gamma 2^{\text{RFP}}$ emissions. $\gamma 2^{\text{RFP}}$ emission from 488 laser excitation in the absence of donor was not tested. Measurements did not correct for channel bleed through.

3.2.7 Synaptic Exchange Rate FRAP Imaging

Neurons were washed and media was replaced with HBS + treatment. Imaging was performed in an enclosed chamber at 37°C. An initial image was taken for baseline

standardization. Photobleaching was performed by creating a stimulation ROI box encompassing two or more dendrites. This stimulation region was photobleached using the 488 and 561 lasers at 25% power for 1 minute. The same stimulation ROI was used for every cell in an experiment. Immediately following photobleaching, 10 nM MG-Tau dye was added to the cell culture dish to re-identify surface synaptic GABA_AR clusters. Time-lapse imaging was then started every 2 min for 60 min. During image analysis, objects were only considered synaptic if they demonstrated colocalization with γ 2^{pH}FAP pHGFP signal, RFP-gephyrin signal and had obvious surface MG-BTau fluorescence. ROIs were drawn measuring the rate of fluorescence recovery at 4-8 synaptic sites and one extrasynaptic site (10 μ m long region; Bezier tool) per cell. For data analysis, synapse post-bleach fluorescence intensity time point data was first normalized to pre-bleach fluorescence intensity (post-bleach/pre-bleach). Normalized synapse post-bleach data was then calculated as percent change from t0 ($(tx/t_0)*100$, where x = min). Individual synapses were then averaged to calculate fluorescence recovery and statistically significant changes across time points.

3.2.8 Quantitative PCR

RNA was extracted from primary cultured neurons purified using a RNeasy mini kit (Qiagen). RNA concentration and purity were assessed using a Nanodrop spectrophotometer (Thermo Scientific). cDNA was synthesized from 320 ng of total RNA per reaction using the High Capacity cDNA Reverse Transcription Kit (Applied Biosystems). The Quantitative Polymerase Chain Reaction (qPCR) was performed using SYBR Green and the 7300 RealTimePCR system (Applied Biosystems Corp.), starting with 50°C for 2 min and 95°C for 10 min, followed by 40 cycles at 95°C for 15 s and 60°C for 1 min, and concluding with 15 s at 95°C, 60°C for 1 min and 95°C for 15 s to ensure a single product on melting curves; 1 μ l of cDNA was used per well. All

data were analyzed using the $\Delta\Delta C_t$ approach as described previously (294). GABA_AR $\beta 3$ subunit primers: CATGTCCTTTGTGAAGGAGACG, GTCAAGCGTGAGGTTGAGAGG, product length 229 base pairs (BP); GABA_AR $\gamma 2$ subunit primers GCGCAGTTCTGTTGAAGTGG, CCATTGCTGTGACATAGGAGAC, product length 338 BP; Gephyrin primers: GCAGGGTATCTTGGATCCTCG, GCTCTGTCTTTGGAGGTAGC, product length 215 BP; 4) β -actin primers: AGCCATGTACGTAGCCATCC, ACCCTCATAGATGGGCACAG, product length 115 BP.

3.2.9 Western Blot and Immunoprecipitation

Protein concentration was determined by BCA protein assay for all biochemistry. Neurons were lysed in denaturing buffer for immunoprecipitation: 50mM Tris HCl, 1mM EDTA, 1% SDS, 2mM Na₃VO₄, 10mM NaF, 50mM N-ethylmaleimide, protease inhibitor cocktail (Sigma). Lysates were sonicated and heated at 50°C for 20 min, then diluted 1:5 in RIPA buffer (50mM Tris HCl pH 7.6, 150mM NaCl, 1% Igepal, 0.5 % Sodium deoxycholate, 1mM EDTA, 2mM Na₃VO₄, 10mM NaF, 50mM N-ethylmaleimide, protease inhibitor cocktail). Standard immunoprecipitation procedures were performed using overnight incubation with $\gamma 2$ subunit antibody or rabbit IgG (sci2027; Sigma), 1 h incubation with Protein A Sepharose 4B beads (Invitrogen), three RIPA buffer washes, and loading for SDS-PAGE. After electrophoresis and transfer to nitrocellulose membrane, samples were probed with primary antibody overnight followed by the appropriate horseradish peroxidase (HRP)-coupled secondary antibody.

3.2.10 Membrane and Subcellular Fractionation

Cultured neurons were lysed using fractionation buffer: 50mM Tris-HCl, 50mM NaCl, 1mM EDTA, 2mM Na₃VO₄, 10mM NaF, 320mM sucrose, 0.25% igepal, and protease inhibitor cocktail. Lysates were spun at 88,881g for 30 min at 4°C to separate pellet (membrane) from supernatant (cytosol). Fraction integrity was tested by localization specific markers in all experiments (270).

3.2.11 Co-immunoprecipitation

Mice were intraperitoneally (I.P.) injected with vehicle control or 10mg/kg DZP and sacrificed 12 h post-injection (n = 4 mice per treatment). Mouse cortical tissue was homogenized in co-IP buffer (50mM Tris HCl pH 7.6, 50mM NaCl, 0.25% Igepal, 1mM EDTA, 2mM Na₃VO₄, 10mM NaF, 50mM N-ethylmaleimide, and Sigma protease inhibitor cocktail) using a Dounce homogenizer. Tissue was solubilized with end-over-end mixing at 4°C for 15 min, and then spun at 1,000g to remove non-solubilized fractions. Each immunoprecipitation tube contained 375µg of tissue lysate brought up to 1ml volume using co-IP buffer. Lysates were precleared using Protein A Sepharose 4B beads (Invitrogen) for 1 h at 4°C. Lysate was then immunoprecipitated overnight with 2.5µg rabbit γ2 subunit antibody (224003, Synaptic Systems) or 2.5µg rabbit IgG (2027, Santa Cruz). The next day, 40 µl Protein A Sepharose slurry was added and mixed for 2 h at 4°C on a nutator. Beads were then washed 3x at 4°C on a nutator in 1ml co-IP buffer. Beads were denatured with SDS-PAGE loading buffer [Laemmli Sample buffer (Biorad) + β-mercaptoethanol] with heat at 70°C for 10 min and intermittent vortexing. Two immunoprecipitation reactions were

performed per animal and were pooled into a single tube without beads to be used for downstream in-gel digestion.

3.2.12 Mass Spectrometry and Data Processing

Immunoprecipitated proteins were separated by electrophoresis in Criterion XT MOPS 12% SDS-PAGE reducing gels (Bio-Rad), with subsequent protein visualization by staining with Coomassie blue. Each gel lane was divided into six slices. After de-staining, proteins in the gel slices were reduced with TCEP [tris(2-carboxyethyl)phosphine hydrochloride] and then alkylated with iodoacetamide before digestion with trypsin (Promega). HPLC-electrospray ionization-tandem mass spectrometry (HPLC-ESI-MS/MS) was accomplished by data-dependent acquisition on a Thermo Fisher Orbitrap Fusion Lumos Tribrid mass spectrometer. Mascot (Matrix Science; London, UK) was used to search the MS files against the mouse subset of the UniProt database combined with a database of common contaminants. Subset searching of the Mascot data, determination of probabilities of peptide assignments and protein identifications, were accomplished by Scaffold (v 4.8.4, Proteome Software). MS data files for each entire gel lane were combined via the “MudPIT” option. Identification criteria were: minimum of two peptides; 96% peptide threshold; 1% FDR; 99% protein threshold. One vehicle- and one DZP-treated animal were removed from analysis due to insufficient $\gamma 2$ subunit pulldown relative to all other groups. N = 3 animals per condition were used for downstream analysis. Protein clustering was applied in Scaffold and weighted spectrum values and exclusive unique peptides were exported for manual excel analysis. Student’s t-test analysis was performed using relative fold change (ratio) of DZP compared to vehicle group. In some cases peptides were only detected in vehicle or DZP treated groups, resulting in DZP/V ratio values of zero or undefined error (cannot divide by zero). These

were annotated as NF-DZP (not found in DZP samples) or NF-V (not found in vehicle samples) in the tables.

3.2.13 Bioinformatics Analysis

Ingenuity Pathways Analysis (IPA) (Ingenuity Systems) was used for cellular pathway analysis. Relative fold levels of DZP proteins compared to vehicle were used for analysis. To be suitable for IPA analysis, proteins NF-DZP were assigned a value of $-1E+99$, while proteins NF-V were assigned a value of $1E+99$. Significant enrichment in protein networks were calculated by right tailed Fisher's exact test. Z-score analysis is a statistical measure of an expected relationship direction and observed protein/gene expression to predict pathway activation or inhibition. IPA core analysis was searched to determine direct and indirect relationships within 35 molecules per network and 25 networks per analysis. All data repositories available through IPA were used to determine experimentally observed and highly predicted interactions occurring in mammalian tissue and cell lines. Ratio data were converted to fold change values in IPA, where the negative inverse ($-1/x$) was taken for values between 0 and 1, while ratio values greater than 1 were not affected. Proteins found to be enhanced in their association with $\gamma 2$ (Table 1) were searched in the *Mus musculus* GO Ontology database (released 2018-10-08) for GO biological process and GO molecular function and analyzed by the PANTHER overrepresentation test; significance was determined using Fisher's Exact with Bonferroni correction for multiple testing.

3.2.14 Statistics

Relevant statistical test information is described in the figure legends or within the individual methods sections. *p* values are reported in the results section if significance is between 0.01 and < 0.05 or if the data is approaching significance.

3.3 Results

3.3.1 12-24h Diazepam Decreases the GABA_A γ 2 Subunit and Gephyrin through Post-Translational Mechanisms

We first examined if DZP exposure reduced surface levels of γ 2-GABA_ARs and altered gephyrin Ser270 phosphorylation in cortical neurons by immunofluorescence (**Fig. 11A**). Cortical neurons were treated for 24 h with vehicle or 1 μ M DZP, then immunostained for surface γ 2, followed by permeabilization and immunostaining with GAD65 (glutamic acid decarboxylase 65, a marker for presynaptic GABAergic terminals) and the phospho-Ser270 specific gephyrin mAb7a antibody (72, 75). Image analysis identified no sizable change in surface synaptic ($91.6 \pm 5.3\%$) or extrasynaptic ($93.3 \pm 3.8\%$) γ 2 intensity in DZP treated neurons relative to control, but DZP induced a significant $18.9 \pm 7.4\%$ ($p = 0.033$) increase in synaptic phospho-gephyrin (**Fig. 11B**). No change in extrasynaptic phosphorylated Ser270 gephyrin was measured. We repeated this DZP treatment and examined total and phospho-gephyrin levels in dendrites (**Fig. 11C**). Again DZP significantly enhanced phospho-Ser270 gephyrin compared to vehicle ($132 \pm 12\%$; $p = 0.013$), while a decrease in overall gephyrin levels was found ($69.7 \pm 5.4\%$) (**Fig. 11D**).

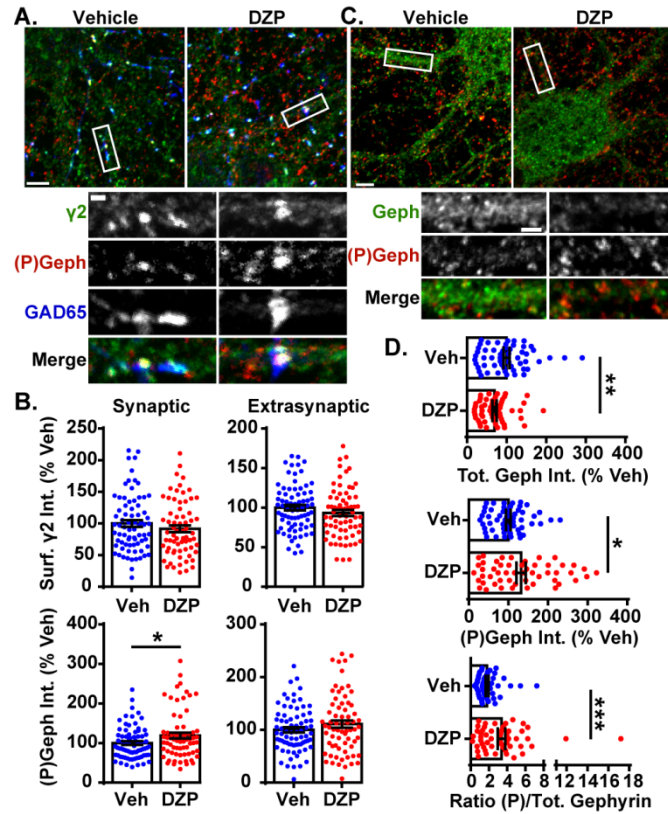


Figure 11. DZP Downregulates Gephyrin Independent of $\gamma 2$ Surface Levels.

(A) Cortical neurons were treated for 24 h with vehicle or 1 μ M DZP, then immunostained for surface $\gamma 2$ GABA_AR (green), followed by permeabilization and immunostaining for (P)Ser270 gephyrin (red), and GAD65 (blue). Panels below show enlargements of GABA_AR synapses on dendrites. (B) Dendrite surface synaptic and extrasynaptic $\gamma 2$ levels are not significantly altered by DZP. Synaptic phospho-gephyrin was enhanced in response to DZP (n = 69-74 neurons; 4 independent cultures). (C) Neurons were treated as in A followed by antibody staining for total gephyrin (green) and (P)Ser270 gephyrin (red). Panels below show enlargements of dendrite region. (D) The dendritic pool of gephyrin was decreased, while (P)Ser270 gephyrin levels were augmented, resulting in a dramatic increase in the ratio of phosphorylated gephyrin to total gephyrin (n = 52-59 neurons; 3 independent cultures). Int. = fluorescence intensity. Image scale bars: main panels = 5 μ m, enlargements = 1 μ m. *p \leq 0.05, **p < 0.01, ***p < 0.001, Student's t-test; error bars \pm S.E.M.

Accordingly, the mean ratio of phospho/total gephyrin was $78.1 \pm 21\%$ higher following DZP (**Fig. 11D**). Complimentary biochemical studies using membrane fractionation were used to compare cytosolic, membrane, and total protein pools in cortical neurons. In agreement with immunofluorescence data, membrane levels of $\gamma 2$ (0.929 ± 0.06) were not reduced after 1 μM DZP, although the total pool of $\gamma 2$ was diminished (0.793 ± 0.07) (**Fig. 12A,B**) compared to vehicle. Cytosolic levels of $\gamma 2$ (1.03 ± 0.06) were also unchanged. Comparatively, DZP reduced full-length gephyrin in every compartment measured relative to control (cytosol: 0.871 ± 0.03 ; membrane: 0.722 ± 0.06 , total: 0.695 ± 0.05). We confirmed the integrity of our fractions using cytosolic and membrane specific markers (Supplemental Figure 2; (270)).

Next we assessed if the decrease in gephyrin and $\gamma 2$ total levels at 24 hours was a result of altered gene expression. qRT-PCR experiments revealed no difference in gephyrin ($p = 0.206$), $\gamma 2$, or control GABA_AR $\beta 3$ subunit mRNA levels between vehicle and DZP treated neurons (**Fig. 12C**). To determine if post-translational modification of $\gamma 2$ also occurs coincident with decreased $\gamma 2$ protein levels, we examined ubiquitination of $\gamma 2$ in response to DZP exposure. We reasoned that changes in ubiquitination of $\gamma 2$ would likely precede the loss of total $\gamma 2$ seen at 24 h (**Fig. 12A,B**). GFP-ubiquitin transfected cortical neurons were treated with vehicle or 1 μM DZP for 12 h. Neurons were lysed under denaturing conditions to isolate the $\gamma 2$ subunit from the receptor complex. Immunoprecipitation of the $\gamma 2$ subunit revealed a 2.13 fold increase ($p = 0.015$) in ubiquitination in DZP treated neurons relative to vehicle (**Fig. 12D,E**). Furthermore, just as observed with 24 h DZP treatment, a reduced total pool of $\gamma 2$ was also found at 12 h ($p = 0.020$) (**Fig. 12D,E**). Notably, this is the first demonstration of endogenous $\gamma 2$ ubiquitination occurring in neurons (previous findings were of recombinant receptors in HEK cells) (159, 170). To investigate mechanisms underlying reduced full-length gephyrin levels, we examined gephyrin cleavage.

Gephyrin is degraded post-translationally by the protease calpain-1 (73, 295, 296), and gephyrin Ser270 phosphorylation promotes cleavage by calpain-1 (73). Consistent with the enhanced gephyrin Ser270 phosphorylation (**Fig. 11**) and reduced full-length levels (**Fig. 11,12**) we found a significant increase in the ratio of cleaved/full length gephyrin after 24 h DZP *in vitro* (**Fig. 12F,G**). We confirmed the identity of the gephyrin cleavage product using a well-characterized glutamate stimulation protocol that induces gephyrin cleavage in cultured neurons (295, 296), a process blocked by calpain-1 inhibition (**Fig. 13**).

Finally, we wanted to determine if similar mechanisms occur *in vivo* following DZP treatment. Prior publications show BZDs and metabolites are not present 24 h post-injection due to rapid drug metabolism in rodents (297-300). Furthermore, BZD uncoupling does not persist 24 h after a single dose (15 mg/kg) or 2 week daily DZP treatment, whereas uncoupling can be seen 12 h after a single injection, indicating this is the appropriate time point for measuring *in vivo* loss of $\gamma 2$ -GABA_AR function (271). Accordingly, mice were given a single intraperitoneal (IP) injection of 10 mg/kg DZP or vehicle control, and cortex tissues were harvested 12 h later. We found DZP significantly reduced the total pool of $\gamma 2$ ($87.3 \pm 3.0\%$) and full-length gephyrin ($73.9 \pm 9.1\%$; $p=0.046$) relative to vehicle treated mice at 12 h post injection (**Fig. 12H,I**). Plasma membrane compartment specific loss of these proteins was further assessed using subcellular fractionation of mouse cortical tissue. Synaptic (**Fig. 14A**) and extrasynaptic (**Fig. 14B**) membrane fractions were unable to detect a robust loss of $\gamma 2$ subunit or gephyrin at either localization after DZP treatment although a near significant decrease in extrasynaptic $\gamma 2$ levels was found ($-12.8\% \pm 4.0$; $p=0.053$) (**Fig. 14C**). These findings indicate both BZD-sensitive GABA_ARs and full-length gephyrin are downregulated by post-translational mechanisms after initial DZP treatment *in vitro* and *in vivo* to temper potentiation of GABA_AR function.

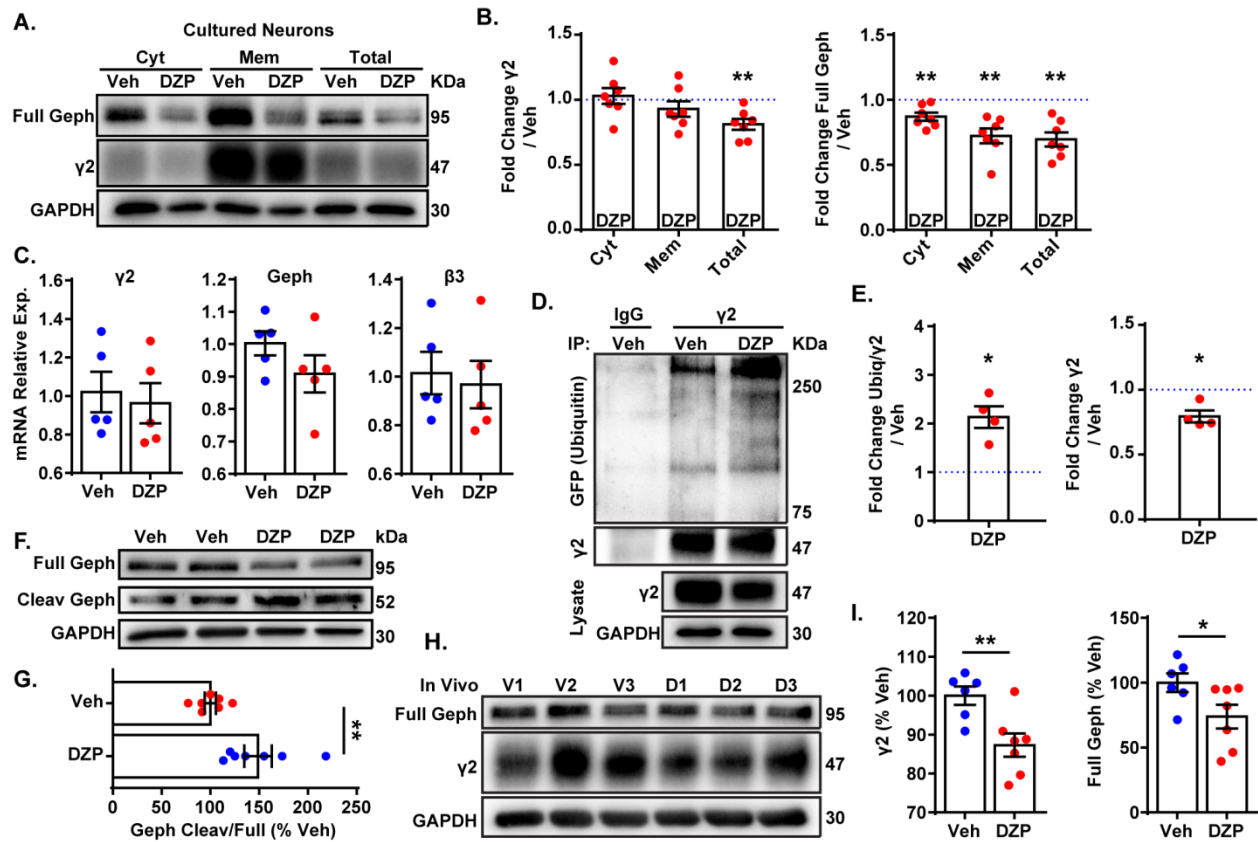


Figure 12. DZP Induces Degradation of $\gamma 2$ and Gephyrin *In Vitro* and *In Vivo*.

(A) Cortical neurons exposed to 1 μ M DZP or vehicle for 24 h were subjected to membrane fraction and western blot analysis. (B) Total $\gamma 2$ subunit and cytosolic, membrane, and total gephyrin were significantly reduced after DZP (n=4 independent cultures). (C) Quantitative RT-PCR revealed no change in $\gamma 2$ subunit, $\beta 3$ subunit or gephyrin mRNA expression following 24 h DZP *in vitro* (n=5 independent cultures). (D) GFP-ubiquitin transfected neurons were treated with vehicle or DZP for 12 h. Lysates were immunoprecipitated with control IgG or $\gamma 2$ antibody, followed by blotting with anti-GFP, $\gamma 2$ and GAPDH. (E) DZP treatment increased the levels of $\gamma 2$ ubiquitin conjugates and decreased $\gamma 2$ total levels. (F,G) DZP treatment enhanced the ratio of cleaved gephyrin fragments/full length gephyrin (n=4 independent cultures). (H) Representative western blots of cortical tissue collected from mice 12 h after a single IP injection of 10 mg/kg DZP or vehicle. Three mice shown from each treatment. (I) $\gamma 2$ subunit and gephyrin totals are significantly reduced in DZP-treated animals (6-7 mice per condition). (* $p \leq 0.05$, ** $p < 0.01$, **** $p < 0.0001$, Student's t-test; error bars \pm S.E.M.)

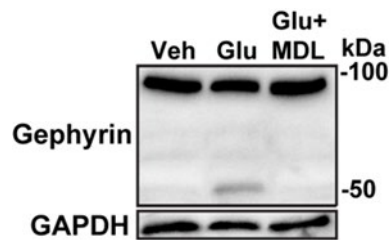


Figure 13. Calpain-1 Dependent Gephyrin Cleavage upon Glutamate Stimulation.

DIV 16 neurons were treated with vehicle or 100 μ M glutamate for 30min in HBS +/- 10 μ M calpain-1 inhibitor MDL-28170 (MDL). Neurons were then returned to conditioned media for 1.5 h prior to lysis. MDL-28170 treated neurons were in presence of inhibitor throughout experiment. Calpain-1 inhibition mitigates glutamate induced cleavage of gephyrin. Top band indicates full length gephyrin (95 kDa), bottom band indicates cleaved gephyrin (~50 kDa).

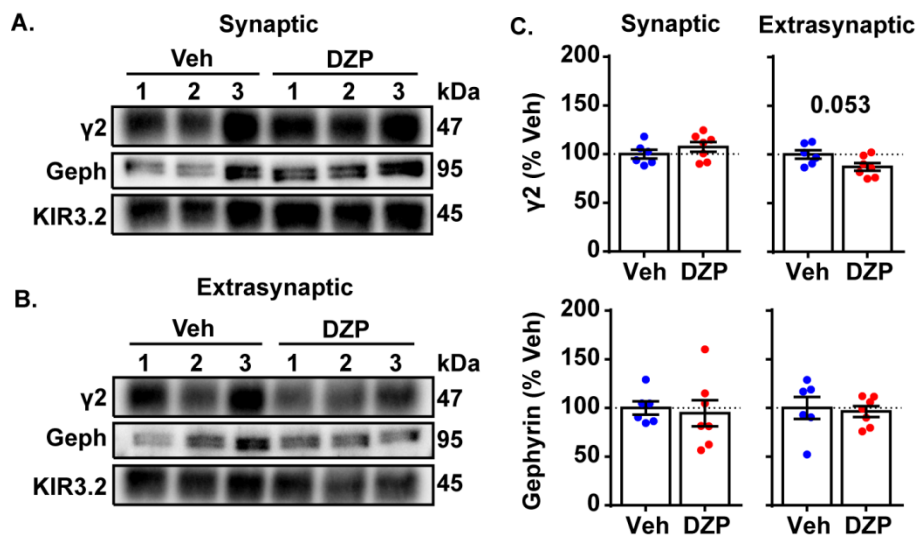


Figure 14. Subcellular Fractionation of DZP Treated Mice.

Cortical tissue collected from mice 12 h after a single IP injection of 10 mg/kg DZP or vehicle were subjected to subcellular fractionation to separate synaptic (A) and extrasynaptic fractions (B). Representative blots shown from animals 1-3 for each treatment. Western blot analysis was used to examine γ 2 subunit and gephyrin levels. KIR 3.2, an inward-rectifier potassium channel present at equal distribution in the plasma membrane (at both synaptic and extrasynaptic regions) was used as loading control. (C) Quantification of synaptic and extrasynaptic γ 2 subunit and gephyrin (6-7 mice per condition). (* $p \leq 0.05$, Student's t-test; error bars \pm S.E.M.).

3.3.2 GABA_AR Composition and Intracellular and Surface Trafficking are Changed by DZP *In Vitro*

We then investigated if surface $\gamma 2$ -containing GABA_ARs are more frequently targeted to lysosomes after DZP exposure by live-imaging. For these experiments we used our recently characterized optical sensor for synaptic GABA_AR ($\gamma 2^{\text{pH}}$ FAP). This dual reporter is composed of a $\gamma 2$ subunit tagged with an N-terminal pH-sensitive GFP, myc, and the fluorogen-activating peptide DL5 (212). The pH-sensitive GFP tag selectively identifies cell surface GABA_ARs and the DL5 FAP binds malachite green (MG) dye derivatives including MG-BTau (233, 240, 301). MG-BTau is cell impermeable and non-fluorescent until bound by DL5. Upon binding, MG-BTau fluoresces in the far red spectral region (~ 670 nm). This FAP-dye system allows for selective labeling of surface $\gamma 2$ -containing GABA_ARs which can then be tracked through various phases of trafficking (212). As previously shown, $\gamma 2^{\text{pH}}$ FAP GABA_ARs are expressed on the neuronal surface, form synaptic clusters, do not perturb neuronal development and show equivalent functional responsiveness to GABA and DZP both in the absence and presence of MG dyes (212). We transfected neurons with $\gamma 2^{\text{pH}}$ FAP and treated them with DZP for 8-16 h. Neurons were then pulse-labeled with 100 nM MG-BTau dye and returned to conditioned media at 37°C +/- DZP for 1 h. The lysosomal inhibitor leupeptin (200 μ M) and the lysosomal specific dye, LysoTracker (50 nM), were added after 30 min. At the end of the incubation, neurons were washed in 4°C saline to inhibit trafficking and immediately used for live-imaging experiments. Representative images demonstrate MG-BTau labeled $\gamma 2^{\text{pH}}$ FAP-GABA_ARs localized on the cell surface (**Fig. 15A**) and at synaptic clusters on dendrites (**Fig. 15B**) based on colocalization with surface specific pHGFP signal. MG-BTau further reveals internalized receptors at lysosomes (**Fig. 15C**). Image quantification showed synaptic $\gamma 2$ -GABA_AR intensity remained largely unchanged (**Fig. 15D**).

Importantly, we found a significant $8.0 \pm 2.5\%$ ($p = 0.015$) enhancement in the mean intensity of GABA_ARs labeled with MG-BTau at lysosomes following DZP (**Fig. 15E**). The area of GABA_ARs colocalized at lysosomes trended towards an increase in DZP treated cells ($140.2 \pm 23.6\%$; $p = 0.144$) but did not reach significance.

We complemented these lysosomal targeting studies with an NH₄Cl live-imaging approach that allows us to compare the ratio of cell surface vs. intracellular GABA_ARs in living neurons. $\gamma 2^{\text{pH}}$ FAP expressing neurons were treated with vehicle or DZP for 24 h. Additional control groups included the BZD antagonist Ro 15-1788 (1-2 h) to reverse the effects of DZP. Neurons were actively perfused with HEPES buffered saline (HBS) treatment and an initial image was taken of surface pHGFP receptor signal (**Fig. 15F**). Neurons were then exposed to pH 7.4 NH₄Cl solution to neutralize the pH gradient of all intracellular membrane compartments, revealing internal pools of $\gamma 2$ containing GABA_ARs. Analysis revealed no change in surface $\gamma 2$ levels between treatments (**Fig. 15G**) consistent with Fig. 11 and 12. However, the number of large intracellular vesicles (circular area $\sim 0.75 \mu\text{m}$) containing receptors was significantly enhanced ($p = 0.047$) (**Fig. 15H**), consistent with increased localization in intracellular vesicles. Ro 15-1788 and DZP + Ro 15-1788 treated neurons were not significantly different from vehicle. Overall, these findings suggest $\gamma 2$ -GABA_AR ubiquitination, intracellular accumulation, lysosomal targeting and degradation are part of the adaptive response to DZP.

To determine if $\gamma 2$ subunit ubiquitination is key for lysosomal targeting of GABA_ARs following DZP exposure, we created lysine to arginine mutated $\gamma 2$ subunits to block ubiquitination. Importantly, the lysine residues in the large intracellular domain have been implicated in $\gamma 2$ subunit degradation (159, 170). We created a construct of the $\gamma 2$ long isoform where eight closely compacted lysine residues previously found to be important for ubiquitination were mutated

($\gamma^{2^{pH}}FAPK8R$). Two additional lysine residues in the ICD at more distant locations may also be subject to ubiquitination; therefore an additional $\gamma^{2^{pH}}FAPK10R$ construct with these residues mutated was generated. First we examined if the $\gamma^{2^{pH}}FAPK8R$ and $\gamma^{2^{pH}}FAPK10R$ constructs could be expressed in primary cultured neurons (**Fig. 16 A,B**) and HEK293 cells (**Fig. 16 C,D**). We found that full length $\gamma^{2^{pH}}FAPK8R$ and $\gamma^{2^{pH}}FAPK10R$ are expressed in both cell types but at significantly lower levels in neurons (K8R: -65.0%; K10R: -70.8%) and in HEK293 cells (K8R: -22.3%; K10R: -35.1%) relative to wild type. This suggests that the eight closely encoded lysine residues in the $\gamma 2$ subunit may have a role in subunit stability during biosynthesis.

Given the similar expression levels of $\gamma^{2^{pH}}FAPK8R$ and $\gamma^{2^{pH}}FAPK10R$ in our biochemical data, we proceeded with the $\gamma^{2^{pH}}FAPK10R$ construct with two additional lysine residues mutated as it should conceivably be more resistant to ubiquitination. Cultured neurons expressing wild-type $\gamma^{2^{pH}}FAP$ and $\gamma^{2^{pH}}FAPK10R$ were exposed to DZP for 20-28 h and then pulse-labeled with MG-BTau dye and returned to conditioned media at 37°C +/- DZP for 1.5 h. At the end of the incubation, neurons were washed in 4°C saline to inhibit trafficking and immediately used for live-imaging experiments. LysoTracker (50 nM), was added 10 min prior to imaging. Representative images demonstrate MG-BTau labeled $\gamma^{2^{pH}}FAP$ and $\gamma^{2^{pH}}FAPK10R$ GABA_ARs localized on the cell surface (**Fig. 16E**) and at synaptic clusters on dendrites (**Fig. 16F**) indicating the $\gamma^{2^{pH}}FAPK10R$ traffics to the plasma membrane. As seen previously in **Fig. 15**, DZP increases MG-BTau labeled $\gamma^{2^{pH}}FAP$ GABA_AR colocalization at lysosomes (**Fig. 16G**). Enhanced association of $\gamma^{2^{pH}}FAPK10R$ with lysosomes was also observed after DZP. Image quantification (**Fig. 16H,I**) confirmed that DZP caused a significant increase in the intensity (+174.0% ± 72.5) and near significant increase in the area of (+153.1% ± 65.5) of MG-

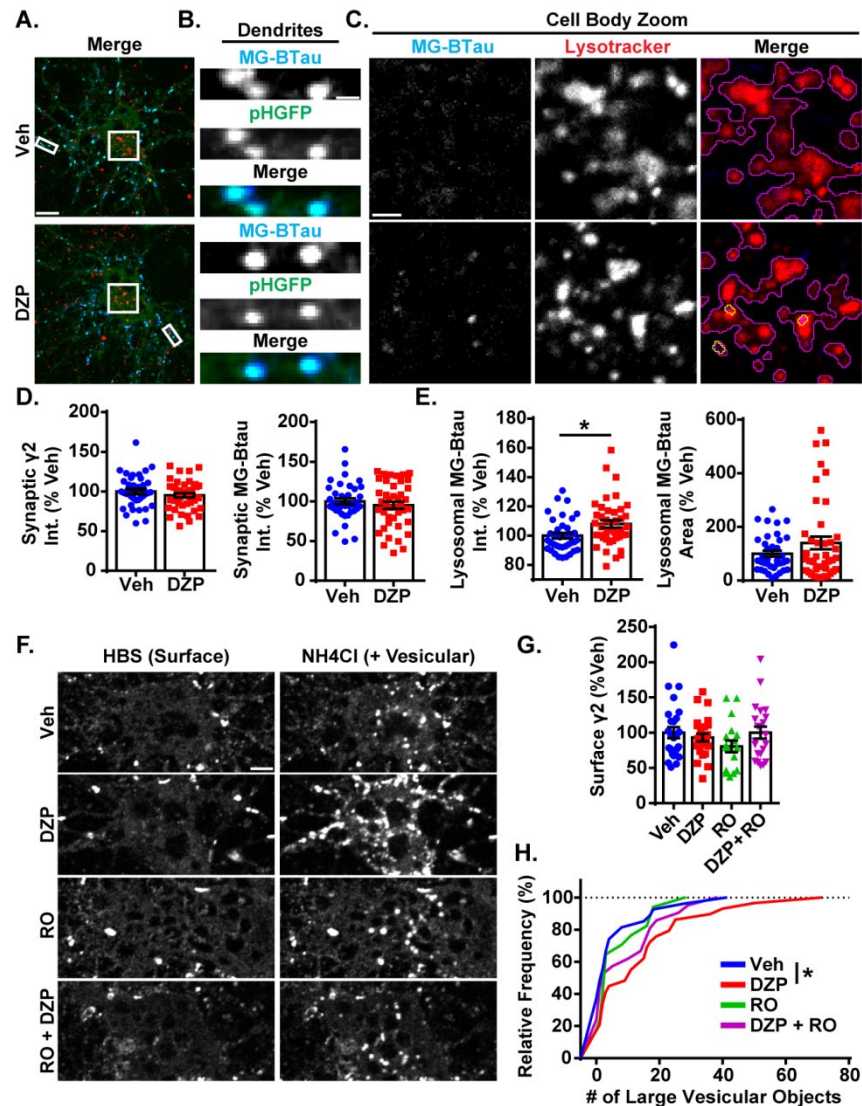


Figure 15. Lysosomal Targeting and Vesicular Accumulation of $\gamma 2$ -GABA_ARs in Response to DZP.

(A) $\gamma 2^{\text{ph}}$ FAP neurons were pretreated for 12-18 h with 1 μM DZP, then pulse-labeled with 100 nM MG-BTau dye for 2 min, and returned to conditioned media at 37°C +/- DZP for 1 h. 50 nM Lysotracker dye was added at the 30 min mark to identify lysosomes. MG-BTau = blue; pHGFP = green; Lysotracker = red. (n=37-42 neurons; 5 independent cultures). (B) Dendrite zoom images show MG-BTau labeling at $\gamma 2^{\text{ph}}$ FAP synapses. (C) Cell body zoom images highlighting colocalization of MG-BTau labeled GABA_ARs (yellow trace) at lysosomes (purple trace). (D) pHGFP and MG-BTau measurements reveal surface synaptic $\gamma 2$ -GABA_AR levels are not altered by DZP. (E) The pool of internalized MG-BTau GABA_ARs colocalized at lysosomes was enhanced in DZP treated neurons as measured by intensity (* $p \leq 0.05$, Student's t-test; error bars \pm S.E.M.). (F) Neurons treated 20-28 h with vehicle or DZP. The DZP

site antagonist Ro 15-1788 (5 μ M) was added 1-2 h prior to imaging to inhibit DZP binding at GABA_ARs. Neurons were first imaged in HBS, and then perfused with NH₄Cl (pH 7.4) to reveal intracellular γ 2^{pH}FAP receptors. DZP treated neurons accumulated more γ 2-GABA_ARs in large vesicular structures compared to vehicle. (n=20-27 neurons; 3-4 independent cultures). (G) Surface intensity of γ 2^{pH}FAP was not different between treatments (one-way ANOVA; error bars \pm S.E.M.). (H) DZP-treated neurons more frequently demonstrated accumulation of γ 2^{pH}FAP in large vesicles (* $p \leq 0.05$ Kolmogorov-Smirnov statistical test). Scale bars in μ m: A=10; B=1; C=2, F=5.

BTau labeled γ 2^{pH}FAP GABA_ARs at lysosomes compared to vehicle wild type. Dye-labeled γ 2^{pH}FAPK10R receptors also demonstrated an increase in intensity (+128.2% \pm 63.8) and area (+81.1% \pm 35.4) of colocalization with lysosomes relative to vehicle control. No significant difference in synaptic cluster measurements were found for either group. This data suggests that redundant ubiquitination of other GABA_AR subunits in complex with γ 2 likely mediates DZP-induced lysosomal targeting and that γ 2 ubiquitination alone is not a key step in this process.

Despite the increase in ubiquitination and lysosomal targeting of γ 2-GABA_ARs after DZP, we did not detect decreased overall surface or synaptically localized surface γ 2 levels. This suggested two possibilities, one being that DZP treatment only reduced total γ 2 levels to 80% of control in cultured cortical neurons and 85% *in vivo*, making a slight decrease in surface γ 2-GABA_ARs challenging to detect with current methods. Alternatively, there could be an increase in γ 2 subunit assembly with BZD-insensitive α subunits (γ 2 α 4 β) (302) with a concomitant reduction in surface levels of BZD-sensitive receptors (γ 2 α 1/2/3/5 β). Our previous work showed 24 h BZD exposure in hippocampal neurons causes decreased total and surface levels of the α 2 GABA_AR subunit via lysosomal mediated degradation, without any changes in receptor insertion or removal rate (169). To determine if α 2/ γ 2 GABA_ARs are specifically decreased by DZP treatment, we developed and employed an intermolecular FRET assay, using pH-sensitive GFP

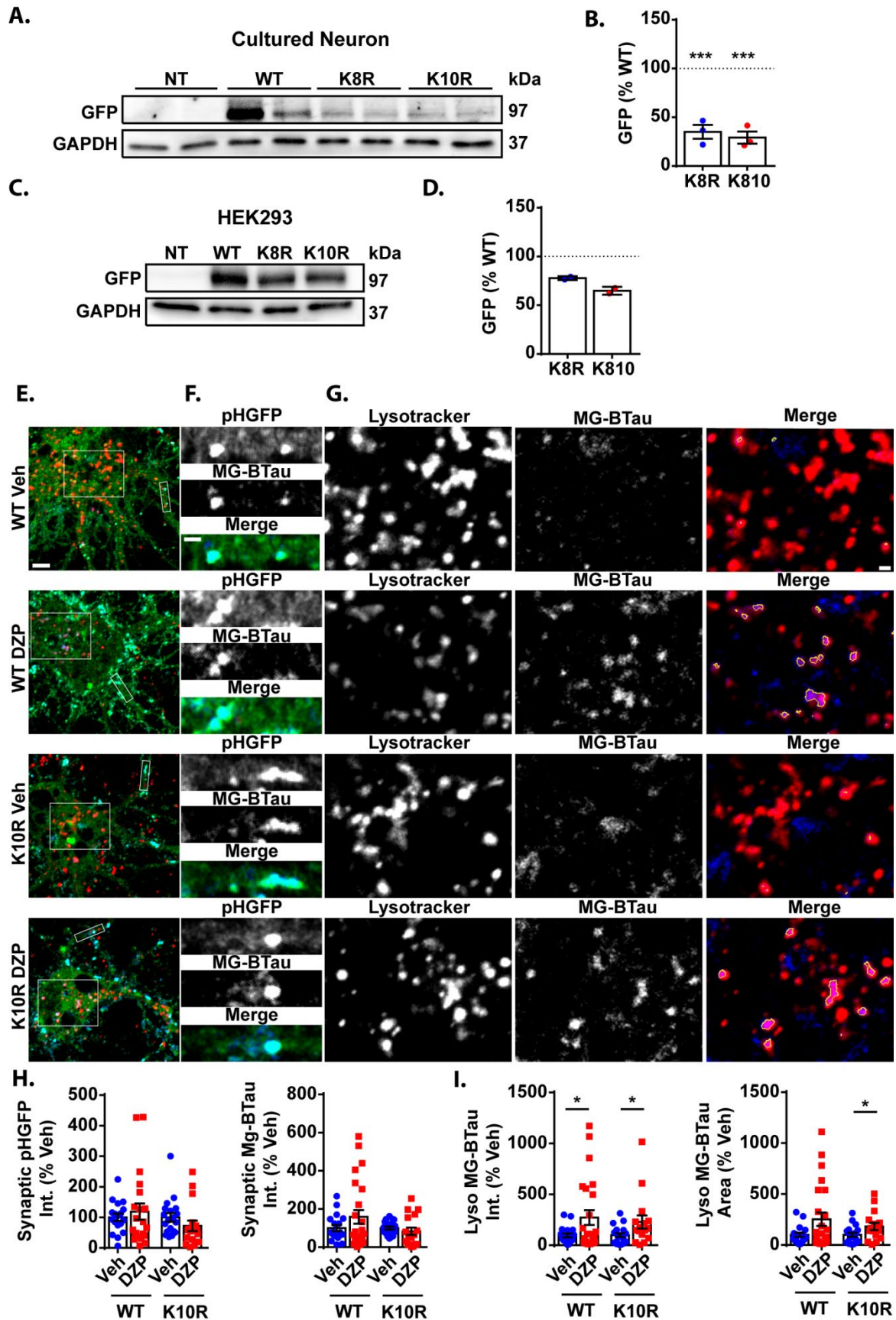


Figure 16. Characterization and Lysosomal Targeting of Lysine Mutant $\gamma 2$ in Response to DZP.

(A) Cortical neurons transfected with wild type (*WT*), *K8R* or *K10R* $\gamma 2^{pH}$ FAP constructs were assessed for full-length protein expression. NT = non-transfected. (B) Quantification revealed the *K8R* and *K10R* $\gamma 2^{pH}$ FAP were expressed at a significantly lower level than wild-type ($n = 3$ independent cultures; one-way ANOVA with post-hoc Tukey's Test; error bars \pm S.E.M.; *** $p \leq 0.001$). (C) Western blot analysis of HEK293 cells transfected with GABA_AR $\beta 3$ subunit along with *WT*, *K8R* or *K10R* $\gamma 2^{pH}$ FAP subunits or NT negative control. (D) Quantification determined full-length *K8R* and *K10R* $\gamma 2^{pH}$ FAP subunits are also expressed at lower levels in HEK293 cells relative to *WT* $\gamma 2^{pH}$ FAP ($n = 2$ independent cultures). (E) *WT* $\gamma 2^{pH}$ FAP and *K10R* $\gamma 2^{pH}$ FAP transfected neurons were pretreated for 12-18 h with 1 μ M DZP, then pulse-labeled with 100 nM MG-BTau dye for 2 min, and returned to conditioned media at 37°C +/- DZP for 1.5 h. 50 nM LysoTracker dye was added 10 min prior to live-imaging to identify lysosomes. MG-BTau = blue; pHGFP = green; LysoTracker = red. ($n = 16$ -24 neurons; 4 independent cultures). (F) Dendrite zoom images show MG-BTau labeling at $\gamma 2^{pH}$ FAP synapses. (G) Cell body zoom images highlighting colocalization of MG-BTau labeled *WT* and *K10R* $\gamma 2^{pH}$ FAP GABA_ARs (yellow trace) at lysosomes. (H) pHGFP and MG-BTau measurements reveal surface synaptic $\gamma 2$ -GABA_AR levels are not altered by DZP when compared against matching vehicle control in either *WT* or *K10R* $\gamma 2^{pH}$ FAP cells. (I) The intensity of internalized MG-BTau labeled GABA_ARs colocalized at lysosomes was enhanced in both $\gamma 2^{pH}$ FAP *WT* and *K10R* cells after DZP treatment relative to their respective vehicle controls (* $p \leq 0.05$, Student's t-test; error bars \pm S.E.M.). A significant increase in the area of MG-BTau lysosomal colocalization was also detected for $\gamma 2^{pH}$ FAP *K10R* neurons. Scale bars in μ m: E=5; F=1; G=1.

tagged $\alpha 2^{pH}$ (65) as a donor fluorophore and a red fluorescent protein (RFP) tagged $\gamma 2$ subunit ($\gamma 2^{RFP}$) as an acceptor. FRET is an accurate measurement of molecular proximity at distances of 10-100 Å and is highly efficient if donor and acceptor are within the Förster radius, typically 30-60 Å (3-6 nM), with the efficiency of FRET being dependent on the inverse sixth power of intermolecular separation (303). Synaptic GABA_ARs exist as five subunits assembled in $\gamma 2$ - α - β - α - β order forming a heteropentameric ion channel (**Fig. 17A**). We first expressed $\alpha 2^{pH}$ and $\gamma 2^{RFP}$ in neurons and examined their ability to participate in intermolecular FRET. Photobleaching of the

acceptor $\gamma 2^{\text{RFP}}$ channel enhanced donor $\alpha 2^{\text{pH}}$ signal (Supplementary Figure 4; (270)), confirming energy transfer from $\alpha 2^{\text{pH}}$ to $\gamma 2^{\text{RFP}}$. Next, we confirmed measurable FRET only occurs between $\alpha 2^{\text{pH}}/\gamma 2^{\text{RFP}}$ in surface GABA_AR at synaptic sites; FRET was blocked with quenching of donor $\alpha 2^{\text{pH}}$ when the extracellular pH was reduced from 7.4 to 6.0 (**Fig.17A,B**). Following FRET assay validation, $\alpha 2^{\text{pH}}/\gamma 2^{\text{RFP}}$ GABA_AR neurons were treated for 24 h with vehicle or DZP and examined for total synaptic $\alpha 2^{\text{pH}}$ and $\gamma 2^{\text{RFP}}$ fluorescence as well as the $\gamma 2$ FRET signal (**Fig. 17C**). These studies identified a DZP-induced reduction in synaptic $\alpha 2$ (-12.6%), synaptic $\gamma 2$ (-14.3%) and diminished association of $\alpha 2$ with $\gamma 2$ in synaptic GABA_ARs as measured by decreased FRET $\gamma 2$ signal (-10.6%) (**Fig. 17D**). In summary, this sensitive FRET method indicates that cortical neurons show a similar susceptibility for $\alpha 2$ subunit downregulation by BZD treatment as seen in hippocampal neurons (169). Furthermore it identifies a DZP-induced decrease in a specific pool of surface synaptic BZD-sensitive $\gamma 2$ -GABA_AR.

To gain additional mechanistic insight into the molecular mechanisms controlling phosphorylation and degradation of gephyrin observed in Fig. 11 and 12, we performed a DZP time series experiment to measure changes in expression or activation of the gephyrin regulating kinases ERK, GSK3 β , and CDK5. CDK5 and GSK3 β phosphorylate gephyrin at the Ser270 site (74, 75), while ERK phosphorylates a neighboring Ser268 residue (73). We first measured ERK activation by examining ERK phosphorylation across time points. DZP treatment caused a significant decrease in ERK phosphorylation at 45 min (-50.2%), 3 h (-44.5%) and 6 h (-51.2%), with a recovery in phosphorylation to vehicle levels occurring around 12 h and 24 h (Figure 5A,B). Total ERK levels were unchanged after DZP, except for a significant enhancement in expression at the 12 h time point, coinciding with recovery of ERK phosphorylation. We did not detect a change in the phosphorylation or total levels of GSK3 β (**Fig.18C,D**) or expression of CDK5

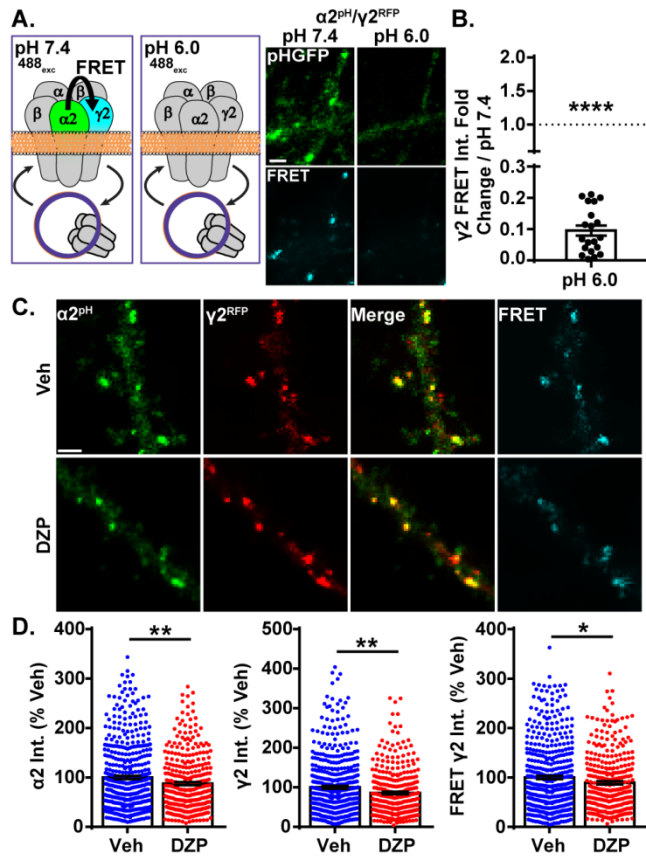


Figure 17. Intermolecular FRET Reveals Decreased Synaptic $\alpha 2/\gamma 2$ Surface GABA_ARs after DZP.

(A) Diagram and time-series images of cortical neurons expressing donor $\alpha 2^{pH}$ (green) and acceptor $\gamma 2^{RFP}$ during imaging and with imaging saline at pH 7.4 and pH 6.0. Surface $\alpha 2^{pH}$ (green) signal and intermolecular FRET (teal) between $\alpha 2/\gamma 2$ subunits occurs at pH 7.4, but is eliminated by brief wash with pH 6.0 extracellular saline and quenching of the $\alpha 2^{pH}$ donor pHGFP fluorescence. (B) Quantification of relative FRET at pH 7.4 and pH 6.0 ($n = 20$ synapses). (C) Neurons $\alpha 2^{pH}$ (green) and $\gamma 2^{RFP}$ (red) were treated with vehicle or DZP for 20-28 h +/- and then subjected to live-imaging. For each cell, an initial image used 488 nm laser excitation to identify surface $\alpha 2^{pH}$ and FRET $\gamma 2^{RFP}$. A second image was taken immediately afterwards to acquire $\gamma 2^{RFP}$ total levels (561 nm laser excitation). Dendritic lengths show multiple synaptic clusters with $\alpha 2/\gamma 2$ surface GABA_ARs. (D) Synaptic cluster intensity quantification of $\alpha 2^{pH}$, $\gamma 2^{RFP}$ and FRET $\gamma 2^{RFP}$ (at least 15 synapses per cell; $n = 335-483$ synapses; 6 independent cultures). Image scale bars = 2 μm (* $p \leq 0.05$, ** $p < 0.01$, **** $p < 0.0001$, paired t-test (B), Student's t-test (D); error bars \pm S.E.M.).

(**Fig. 18E,F**). This data suggests that kinases involved in gephyrin phosphorylation at Ser270 do not demonstrate global changes after DZP, suggesting that the kinases may be recruited to gephyrin, or that an unknown phosphatase responsible for dephosphorylating Ser270 is inhibited after DZP exposure. Conversely, ERK inactivation by DZP is predicted to decrease phosphorylation of the functionally relevant Ser268 site of gephyrin, which has also been implicated in gephyrin synaptic remodeling (73). Gephyrin point mutant studies suggest reduced phosphorylation at Ser268 coupled with enhanced Ser270 phosphorylation, or the inverse, promotes calpain-1 degradation and scaffold remodeling (73). This data provides evidence that a known kinase pathway responsible for fine-tuning GABA_AR synapse dynamics (304) and scaffold (73) is robustly inactivated by DZP.

We previously found 24 h BZD exposure reduces the amplitude of miniature inhibitory postsynaptic currents (mIPSCs) (169), suggesting changes in synaptic GABA_AR function. Having identified both reductions in full-length gephyrin (**Fig. 11,12**) and BZD sensitive GABA_ARs (**Fig. 12, 15**), we next tested if DZP treatment altered the synaptic retention properties of gephyrin and/or GABA_ARs. Neurons expressing $\gamma 2^{\text{pH}}$ FAP and RFP-gephyrin were used for live-imaging fluorescence recovery after photobleaching experiments (FRAP) to measure synaptic and extrasynaptic exchange following exposure to vehicle, 1 μM DZP, 5 μM Ro 15-1788, or DZP + Ro 15-1788. After an initial image was taken, dendrites were photobleached, and signal recovery was measured every 2 min over 30 min at synaptic sites and extrasynaptic regions (**Fig. 19A** synapses panel; **Fig.19B** larger dendritic region with white arrows denoting extrasynaptic region). MG-BTau dye was added directly after the photobleaching step to immediately re-identify the photobleached surface synaptic GABA_ARs, and improve spatial measurements (**Fig. 19B**). These experiments revealed synaptic $\gamma 2$ turnover rates were nearly doubled in DZP treated neurons, a

process reversed by Ro 15-1788 co-treatment (**Fig. 19C**). DZP also accelerated gephyrin synaptic exchange rates compared to vehicle, with Ro 15-1788 co-treatment restoring exchange to control levels. No significant correlation was found between cluster area measured and fluorescence recovery rates of $\gamma 2$ and gephyrin across all conditions, suggesting synaptic exchange rate is independent of cluster size (data not shown). Moreover, no statistical difference was found in $\gamma 2$ or gephyrin extrasynaptic exchange rates (**Fig.19D**). These findings suggest concurrent reduction of gephyrin and GABA_AR synaptic confinement is a compensatory response to mitigate prolonged DZP potentiation of GABA_ARs.

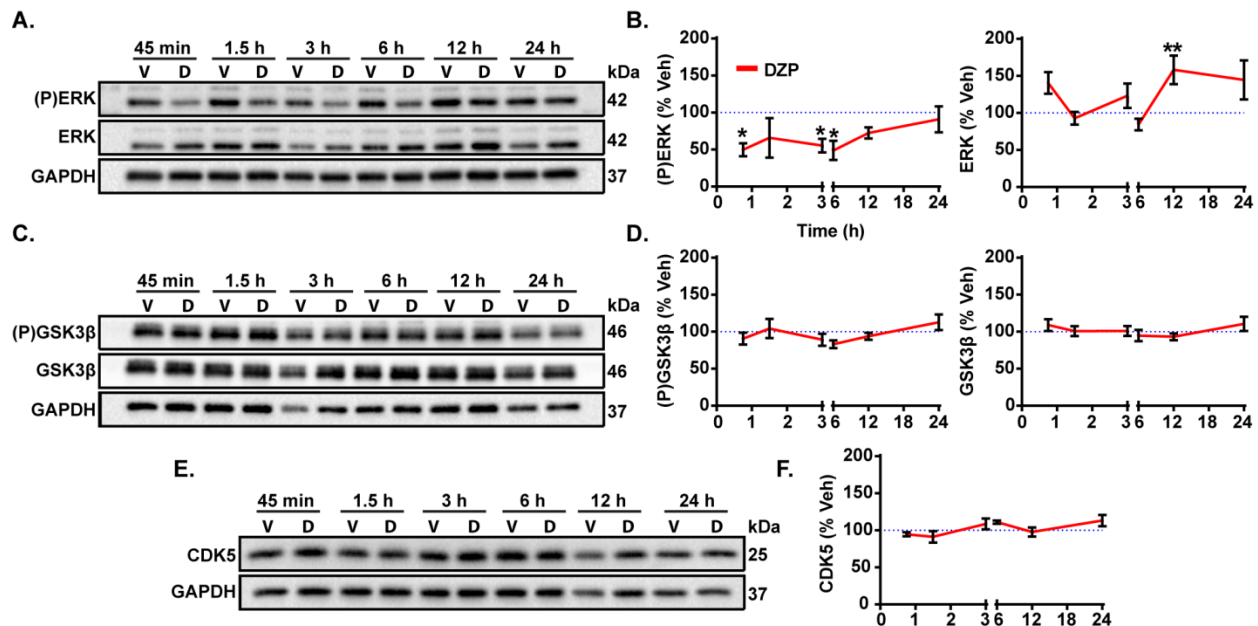


Figure 18. Gephyrin Regulating Kinases Following DZP Treatment.

DIV 16 cortical neurons were treated with vehicle (V) or DZP (D) at multiple time points. Known kinase regulators of gephyrin synaptic clustering were tested for total protein levels and activation status with phospho-specific antibodies as indicated. (P)ERK and total ERK (A,B), (P)GSK3β and total GSK3β (C,D) and CDK5 (E,F) western blot and quantification (n = 4 independent cultures). DZP inhibited ERK phosphorylation across multiple time points while GSK3β activation and total levels did not change. CDK5 total levels were also unchanged by DZP treatment. (*p ≤ 0.05, **p < 0.01, Two-way ANOVA followed by Sidak's multiple comparisons test; error bars ± S.E.M.).

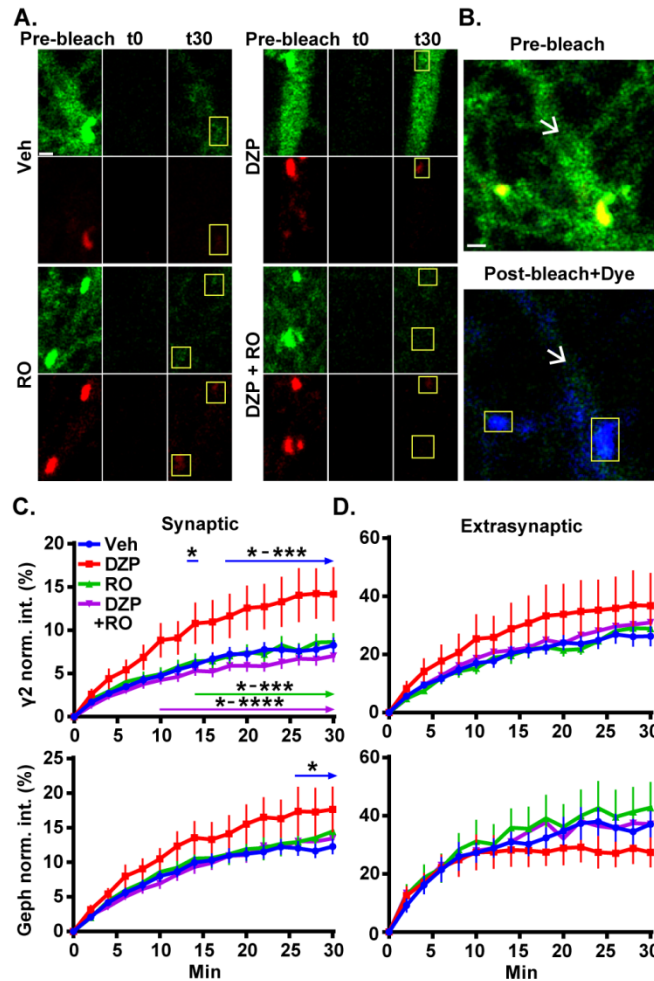


Figure 19. Prolonged DZP Exposure Accelerates $\gamma 2$ GABA_AR and Gephyrin Synaptic Exchange.

(A) Neurons expressing $\gamma 2^{\text{pH}}$ FAP (green) and RFP-gephyrin (red) were treated with vehicle or DZP for 20-28 h +/- Ro 15-1788 for the last 1-2 h. Neurons were imaged at 37°C in constant presence of treatment. Initial image of dendrites taken prior to photobleaching (Pre-bleach), then imaged post-bleach (t0) every 2 min for 30 min. Images of dendritic regions show synaptic cluster sites (yellow boxes) and extrasynaptic regions. (B) 10 nM MG-Btau dye (blue) was added immediately after bleaching events in A to resolve bleached $\gamma 2^{\text{pH}}$ FAP GABA_ARs and provide spatial accuracy for time series measurements. Panels show enlargement of vehicle dendritic regions identified in A. Yellow boxes indicate synaptic clusters and arrows indicate extrasynaptic region seen by pHGFP fluorescence in pre-bleach (green) followed by post-bleach labeling with MG-Btau (blue). (C, D) Fluorescence recovery of $\gamma 2$ GABA_AR and gephyrin measured at synaptic sites and extrasynaptic sites from A. Synapse = $\gamma 2^{\text{pH}}$ FAP cluster colocalized with

gephyrin cluster. Int. = fluorescence intensity. Image scale bars = 1 μm (* $p \leq 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$, two-way ANOVA; Tukey's multiple comparisons test; 4-8 synapses and one 10 μm extrasynaptic region per cell; n = 51-56 synapses from 16 neurons per treatment; 4 independent cultures; error bars \pm S.E.M.).

3.3.3 Label-Free Quantitative Proteomics of $\gamma 2$ GABA_AR Following DZP Injection *In*

Vivo

We next sought to observe DZP-induced changes in receptor trafficking *in vivo*. As an orthogonal approach, we utilized label-free quantitative proteomics to measure changes in the quantities of proteins associated with $\gamma 2$ -GABA_ARs in the cortex of mice after DZP. Cortical tissue was collected from DZP- or vehicle-treated mice 12 h post injection, lysed, and immunoprecipitated with anti- $\gamma 2$ subunit antibody or IgG control. Following label-free mass spectrometry analysis, spectrum counts were used to assess relative abundance of $\gamma 2$ -associated proteins. A total of 395 proteins were identified using our inclusion criteria: minimum of two peptides; identified in at least three samples overall or in two of three samples in a specific treatment group; demonstrated at least 3:1 enrichment over IgG control across at least three samples overall (Dataset 1; not included). The relative abundance of $\gamma 2$ -GABA_AR associated proteins in the DZP group compared to vehicle was used to determine which proteins were increased (**Table 1**) or decreased (**Table 2**). As a result we identified 46 proteins with elevated levels of interaction with $\gamma 2$ -GABA_ARs, including 10 proteins that were only found in the DZP treated group (Table 1, not found in vehicle samples, NF-V). Notably, we found a significant ($p < 0.05$) increase in $\gamma 2$ association with 14-3-3 protein family members tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein gamma (also known as 14-3-3 γ) and tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon (also

known as 14-3-3 ϵ), the phosphatase protein phosphatase 3 catalytic subunit alpha (also known as calcineurin/PPP3CA) and a near significant increase in the GABA_AR $\alpha 5$ subunit ($p = 0.057$), suggesting DZP induced changes in GABA_AR surface trafficking (305, 306), synaptic retention (162, 180, 182, 183, 307), and receptor composition (308). In contrast, 23 proteins were found to co-immunoprecipitate with $\gamma 2$ less in DZP animals relative to control, seven of which were only present in the vehicle treatment group (**Table 2**, not found in DZP, NF-DZP). Interestingly, the calcium-sensitive kinase CaMKII α , which can regulate GABA_AR membrane insertion, synaptic retention and drug binding properties (26, 70-72), was found to be significantly decreased in interaction with $\gamma 2$ -GABA_AR following DZP injection *in vivo*.

To better understand the consequences of the DZP-induced shift in the $\gamma 2$ -GABA_AR protein interaction network, protein fold change data was subjected to core Ingenuity Pathway Analysis (IPA). Top enriched canonical pathways with $-\log(p\text{-value}) > 6.2$ are shown in Figure 20. Notably, GABA receptor signaling pathways were highly enriched, as expected, although IPA was unable to determine pathway activation status by z-score analysis. $\gamma 2$ -GABA_AR association with proteins involved in 14-3-3 mediated signaling and Ras homolog gene family, member A (RhoA) signaling pathways were greatly increased after DZP (**Fig. 20A**, orange), while interaction with proteins involved in eukaryotic initiation factor 2 (EIF2) signaling and sirtuin signaling pathways were reduced (**Fig. 20A**, blue) relative to vehicle. We further examined alterations in functional network association relevant to receptor trafficking by checking the predicted activation status of select pathways when only using proteins which were found to be increased or decreased (**Table 1, 2**). **Fig. 20B** lists $\gamma 2$ -GABA_AR major functional pathways found to be altered by DZP, contributing to processes such as endocytosis (z-score = 2.626), organization of cytoskeleton (z-score = 0.672), and development of neurons (z-score = -0.293). Significant protein changes ($p <$

0.05) conserved between two or more pathways include decreased γ 2-GABA_AR association with CAMKII α and CDK5 and enhanced association with calcineurin/PPP3CA, the intracellular trafficking protein RAB35 and the cytoskeletal protein NEFH (also known as heavy neurofilament protein). As an additional measurement, we performed gene ontology (GO) database analysis of proteins which were found to be increased in DZP treated mice relative to vehicle control (**Table 3**). GO analysis identified enrichment in γ 2 association with proteins involved in intracellular trafficking and cellular localization biological pathways after DZP, consistent with IPA analysis findings. Taken together, these results suggest DZP modifies intracellular and surface trafficking of γ 2-GABA_ARs both *in vitro* and *in vivo*.

Table 1. Proteins Demonstrating Increased Association with γ 2-GABA_ARs after DZP *In Vivo* by Mass Spectrometry.

Ratio DZP/V is fold change in DZP animals' peptide spectral counts (SC) relative to control vehicle treated animals.

NF-V = not found in vehicle samples. N = 3 animals per treatment condition, $p < 0.1$, t-test.

| Ratio DZP/V | P-Value | UniProtKB | Gene ID | Entrez Gene Name | Location | Type(s) |
|-------------|---------|------------|---------|--|---------------------|----------------------------|
| 9.6 | 8.9E-02 | Q14BI2 | GRM2 | glutamate metabotropic receptor 2 | Plasma Membrane | G-protein coupled receptor |
| 9.5 | 4.3E-02 | P12960 | CNTN1 | contactin 1 | Plasma Membrane | enzyme |
| 7.0 | 5.9E-02 | P11276 | FN1 | fibronectin 1 | Extracellular Space | enzyme |
| 5.4 | 2.7E-02 | E9Q4P0 | KXD1 | KxDL motif containing 1 | Cytoplasm | other |
| 5.4 | 3.1E-02 | Q62277 | SYN | synaptophysin | Cytoplasm | transporter |
| 5.0 | 5.0E-03 | Q9QXY6 | EHD3 | EH domain containing 3 | Cytoplasm | other |
| 5.0 | 7.8E-02 | P48774 | GSTM3 | glutathione S-transferase mu 3 | Cytoplasm | enzyme |
| 4.9 | 1.9E-05 | P38647 | HSPA9 | heat shock protein family A (Hsp70) member 9 | Cytoplasm | other |
| 4.7 | 6.4E-02 | Q91V41 | RAB14 | RAB14, member RAS oncogene family | Cytoplasm | enzyme |
| 4.2 | 6.4E-02 | P48758 | CBR1 | carbonyl reductase 1 | Cytoplasm | enzyme |
| 4.2 | 7.2E-02 | Q8K3F6 | KCNQ3 | potassium voltage-gated channel subfamily Q member 3 | Plasma Membrane | ion channel |
| 4.2 | 3.3E-02 | A0A0R4J036 | Nefm | neurofilament, medium polypeptide | Plasma Membrane | other |
| 4.0 | 7.9E-02 | Q921I1 | TF | transferrin | Extracellular Space | transporter |
| 3.8 | 8.6E-02 | Q9CYZ2 | TPD52L2 | tumor protein D52 like 2 | Cytoplasm | other |
| 3.3 | 4.2E-02 | Q99KI0 | ACO2 | aconitase 2 | Cytoplasm | enzyme |
| 2.6 | 8.0E-02 | Q9EQF6 | DPYSL5 | dihydropyrimidinase like 5 | Cytoplasm | enzyme |
| 2.4 | 2.2E-02 | P56480 | ATP5F1B | ATP synthase F1 subunit beta | Cytoplasm | transporter |
| 2.4 | 9.2E-02 | P46096 | SYT1 | synaptotagmin 1 | Cytoplasm | transporter |
| 2.4 | 3.7E-02 | Q6P1J1 | CRMP1 | collapsin response mediator protein 1 | Cytoplasm | enzyme |
| 2.2 | 3.8E-02 | Q9DB20 | ATP5PO | ATP synthase peripheral stalk subunit OSCP | Cytoplasm | transporter |
| 1.9 | N.A. | P61027 | RAB10 | RAB10, member RAS oncogene family | Cytoplasm | enzyme |
| 1.8 | 9.6E-02 | P63017 | HSPA8 | heat shock protein family A (Hsp70) member 8 | Cytoplasm | enzyme |
| 1.8 | 1.8E-02 | P63011 | RAB3A | RAB3A, member RAS oncogene family | Cytoplasm | enzyme |
| 1.8 | 1.3E-02 | P17426-2 | AP2A1 | adaptor related protein complex 2 subunit alpha 1 | Cytoplasm | transporter |
| 1.7 | 9.1E-02 | P18760 | CFL1 | cofilin 1 | Nucleus | other |
| | | | | | | |

Table 1. Continued

| | | | | | | |
|------|---------|--------|-----------|---|-----------------|-------------------------|
| 1.7 | 8.2E-02 | Q9Z2I9 | SUCLA2 | succinate-CoA ligase ADP-forming beta subunit | Cytoplasm | enzyme |
| 1.7 | 4.0E-02 | P63328 | PPP3CA | protein phosphatase 3 catalytic subunit alpha | Cytoplasm | phosphatase |
| 1.7 | 7.1E-02 | Q8R191 | SYNGR3 | synaptogyrin 3 | Plasma Membrane | other |
| 1.6 | 5.7E-02 | Q8BHJ7 | GABRA5 | gamma-aminobutyric acid type A receptor alpha5 subunit | Plasma Membrane | ion channel |
| 1.6 | 1.8E-02 | O35129 | PHB2 | prohibitin 2 | Cytoplasm | transcription regulator |
| 1.6 | 1.6E-02 | P61982 | YWHAG | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein gamma (14-3-3 gamma) | Cytoplasm | other |
| 1.5 | 5.3E-02 | P07901 | HSP90A A1 | heat shock protein 90 alpha family class A member 1 | Cytoplasm | enzyme |
| 1.5 | 7.8E-03 | P67778 | PHB | prohibitin | Nucleus | transcription regulator |
| 1.5 | 8.1E-02 | Q3UGC7 | EIF3J | eukaryotic translation initiation factor 3 subunit J | Cytoplasm | translation regulator |
| 1.5 | 7.5E-02 | Q8VEM8 | SLC25A3 | solute carrier family 25 member 3 | Cytoplasm | transporter |
| 1.3 | 3.3E-02 | P60710 | ACTB | actin beta | Cytoplasm | other |
| NF-V | 7.9E-04 | P62259 | YWHAE | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon (14-3-3 epsilon) | Cytoplasm | other |
| NF-V | 1.0E-02 | P63044 | VAMP2 | vesicle associated membrane protein 2 | Plasma Membrane | other |
| NF-V | 1.6E-02 | P46660 | INA | internexin neuronal intermediate filament protein alpha | Cytoplasm | other |
| NF-V | 3.7E-02 | Q9QYM9 | TMEFF2 | transmembrane protein with EGF like and two follistatin like domains 2 | Cytoplasm | other |
| NF-V | 4.1E-02 | Q6PHN9 | RAB35 | RAB35, member RAS oncogene family | Cytoplasm | enzyme |
| NF-V | 6.0E-02 | P19246 | NEFH | neurofilament heavy | Cytoplasm | other |
| NF-V | 6.3E-02 | Q9CZ13 | UQCRC1 | ubiquinol-cytochrome c reductase core protein 1 | Cytoplasm | enzyme |
| NF-V | 1.2E-06 | Q9CQQ7 | ATP5PB | ATP synthase peripheral stalk-membrane subunit b | Cytoplasm | transporter |
| NF-V | 2.8E-06 | P80317 | CCT6A | chaperonin containing TCP1 subunit 6A | Cytoplasm | other |
| NF-V | 2.8E-06 | Q9CWS0 | DDAH1 | dimethylarginine dimethylaminohydrolase 1 | Cytoplasm | enzyme |

Table 2. Proteins Demonstrating Decreased Association with γ 2-GABA_ARs after DZP *In Vivo* by Mass Spectrometry.

Ratio DZP/V is fold change in DZP animals' peptide SC relative to control vehicle treated animals. NF-DZP = not found in DZP samples. N = 3 animals per treatment condition, $p < 0.1$, t-test.

| <i>Ratio DZP/V</i> | <i>P-Value</i> | <i>UniProtKB</i> | <i>Gene ID</i> | <i>Entrez Gene Name</i> | <i>Location</i> | <i>Type(s)</i> |
|--------------------|----------------|------------------|----------------|--|-----------------|-------------------------|
| 0.2 | 3.4E-02 | P62717 | RPL18A | ribosomal protein L18a | Cytoplasm | other |
| 0.2 | 3.9E-02 | P62874 | GNB1 | G protein subunit beta 1 | Plasma Membrane | enzyme |
| 0.2 | 4.2E-02 | Q60900-2 | ELAVL3 | ELAV like RNA binding protein 3 | Nucleus | other |
| 0.2 | 5.8E-02 | Q920I9 | WDR7 | WD repeat domain 7 | Cytoplasm | other |
| 0.3 | 2.0E-02 | P53026 | RPL10A | ribosomal protein L10a | Nucleus | other |
| 0.3 | 3.4E-02 | Q91VM5 | Rbmxl1 | RNA binding motif protein, X-linked like-1 | Nucleus | other |
| 0.4 | 6.9E-02 | P49312 | Hnrnpa1 | heterogeneous nuclear ribonucleoprotein A1 | Nucleus | other |
| 0.4 | 8.5E-02 | Q8BG05 | Hnrnpa3 | heterogeneous nuclear ribonucleoprotein A3 | Nucleus | transporter |
| 0.4 | 7.9E-02 | Q922F4 | TUBB6 | tubulin beta 6 class V | Cytoplasm | other |
| 0.5 | 5.2E-02 | P62334 | PSMC6 | proteasome 26S subunit, ATPase 6 | Nucleus | peptidase |
| 0.5 | 2.9E-04 | P11798 | CAMK2A | calcium/calmodulin dependent protein kinase II alpha | Cytoplasm | kinase |
| 0.5 | 3.6E-02 | E9PV14 | EPB41L1 | erythrocyte membrane protein band 4.1 like 1 | Plasma Membrane | other |
| 0.7 | 6.8E-02 | P16330 | CNP | 2',3'-cyclic nucleotide 3' phosphodiesterase | Cytoplasm | enzyme |
| 0.7 | 7.6E-02 | O35643 | AP1B1 | adaptor related protein complex 1 subunit beta 1 | Cytoplasm | transporter |
| 0.8 | 1.4E-02 | P68369 | TUBA1A | tubulin alpha 1a | Cytoplasm | other |
| 0.8 | 8.0E-02 | P52480 | PKM | pyruvate kinase M1/2 | Cytoplasm | kinase |
| NF-DZP | 1.5E-02 | P61358 | RPL27 | ribosomal protein L27 | Cytoplasm | other |
| NF-DZP | 3.5E-02 | Q9Z1X4-3 | ILF3 | interleukin enhancer binding factor 3 | Nucleus | transcription regulator |
| NF-DZP | 5.5E-02 | Q80UJ0 | ELAVL2 | ELAV like RNA binding protein 2 | Cytoplasm | other |
| NF-DZP | 2.8E-06 | Q3UHB8 | CCDC177 | coiled-coil domain containing 177 | Other | other |
| NF-DZP | 2.8E-06 | P49615 | CDK5 | cyclin dependent kinase 5 | Nucleus | kinase |
| NF-DZP | 2.8E-06 | Q6ZWV3 | RPL10 | ribosomal protein L10 | Cytoplasm | translation regulator |
| NF-DZP | 2.8E-06 | Q9CQ69 | UQCRCQ | ubiquinol-cytochrome c reductase complex III subunit VII | Cytoplasm | enzyme |

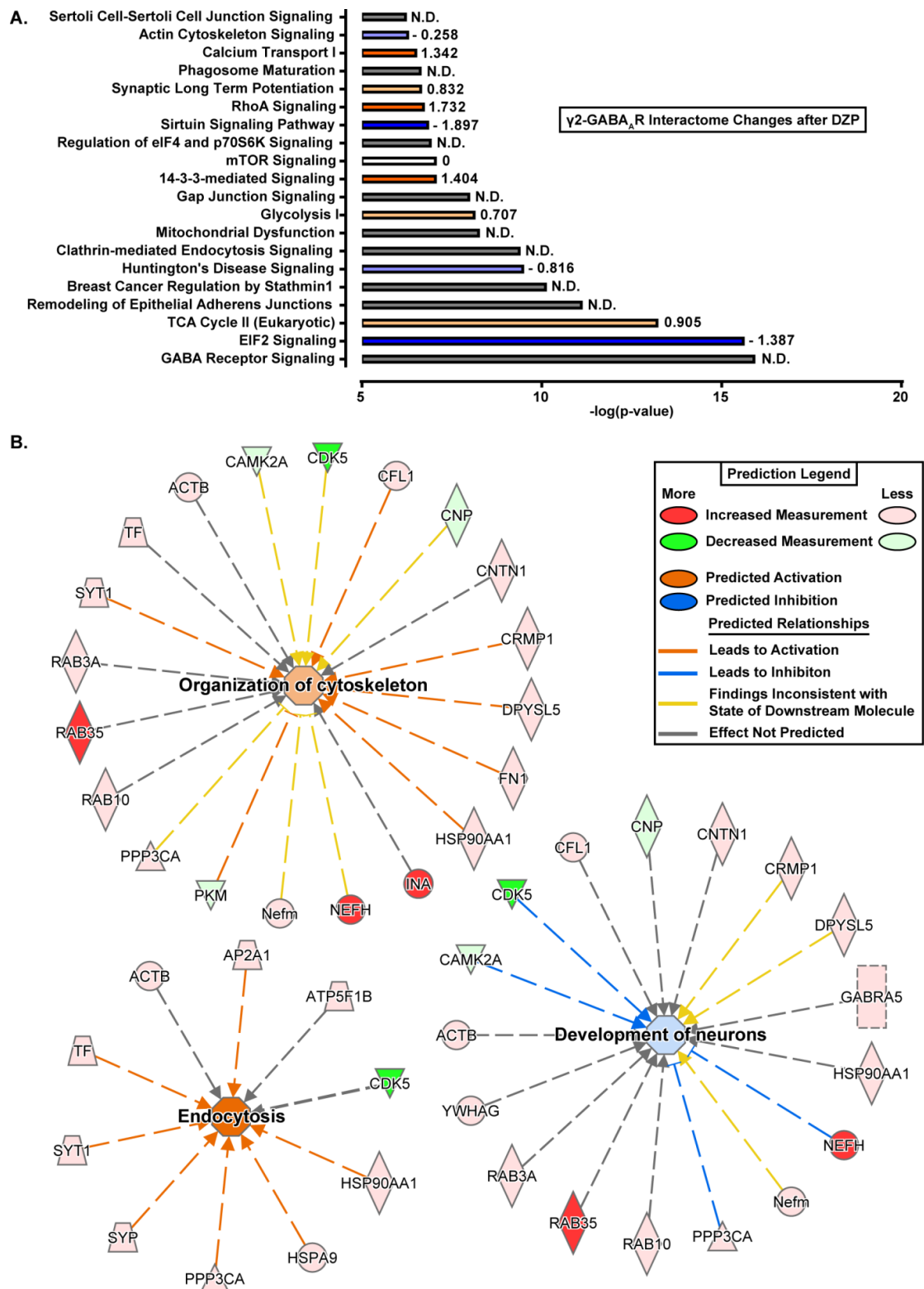


Figure 20. Ingenuity Pathway Analysis Reveals Shifts in Protein Interaction Networks After DZP Exposure.

(A) Canonical pathways found to be enriched with $\gamma 2$ -GABA_ARs and differentially expressed following DZP administration *in vivo*. Enriched pathways with $-\log(p\text{-value})$ greater than 6.2 were considered as calculated by Fisher's exact test right-tailed. Values to right of bars represent pathway activation z-score. Positive z-score represents predicted upregulation of a pathway (orange), negative z-score predicts inhibition (blue), z-score = 0 represents no change in pathway (white), while not determined (N.D.) conveys the analysis program was unable to determine a significant change (grey). Intensity of color represents size of z-score value. (B) Functional network association of select pathways when using proteins which were found to be increased or decreased with a $p < 0.1$. Major functional pathways altered by DZP include endocytosis (z-score = 2.626), organization of cytoskeleton (z-score = 0.672), and development of neurons (z-score = -0.293). Significant protein changes ($p < 0.05$) conserved between two or more pathways include decreased $\gamma 2$ -GABA_AR association with CAMKII α and CDK5 and enhanced association with calcineurin/PPP3CA, the intracellular trafficking protein RAB35 and the cytoskeletal protein NEFH (also known as heavy neurofilament protein). Red = increased measurement, green = decreased measurement, orange = activation of pathway, blue = inhibition of pathway, yellow = findings inconsistent with state of downstream molecule, grey = effect not predicted.

Table 3. GO Analysis Reveals Enrichment of Intracellular Trafficking, Transport, and Protein Localization Pathways after DZP.

Proteins found to have enhanced association ($p < 0.1$) with $\gamma 2$ -GABA_ARs during Scaffold analysis were searched in the GO Ontology database for biological process pathway enrichments. PANTHER Overrepresentation test and Fisher's Exact test with Bonferroni correction for multiple testing for significance.

| <i>GO Biological Process</i> | <i>GO Term ID</i> | <i>Fold Enrichment</i> | <i>P-Value</i> |
|---------------------------------------|-------------------|------------------------|----------------|
| transport | GO:0006810 | 4.2 | 9.8E-09 |
| establishment of localization | GO:0051234 | 4.0 | 2.5E-08 |
| establishment of localization in cell | GO:0051649 | 6.8 | 2.0E-07 |
| localization | GO:0051179 | 3.3 | 2.5E-07 |
| intracellular transport | GO:0046907 | 7.2 | 1.6E-06 |
| regulation of localization | GO:0032879 | 4.3 | 3.7E-06 |
| intracellular protein transport | GO:0006886 | 9.1 | 7.8E-06 |
| regulation of transport | GO:0051049 | 5.1 | 2.2E-05 |
| cellular localization | GO:0051641 | 4.8 | 4.8E-05 |
| protein transport | GO:0015031 | 6.1 | 2.2E-04 |

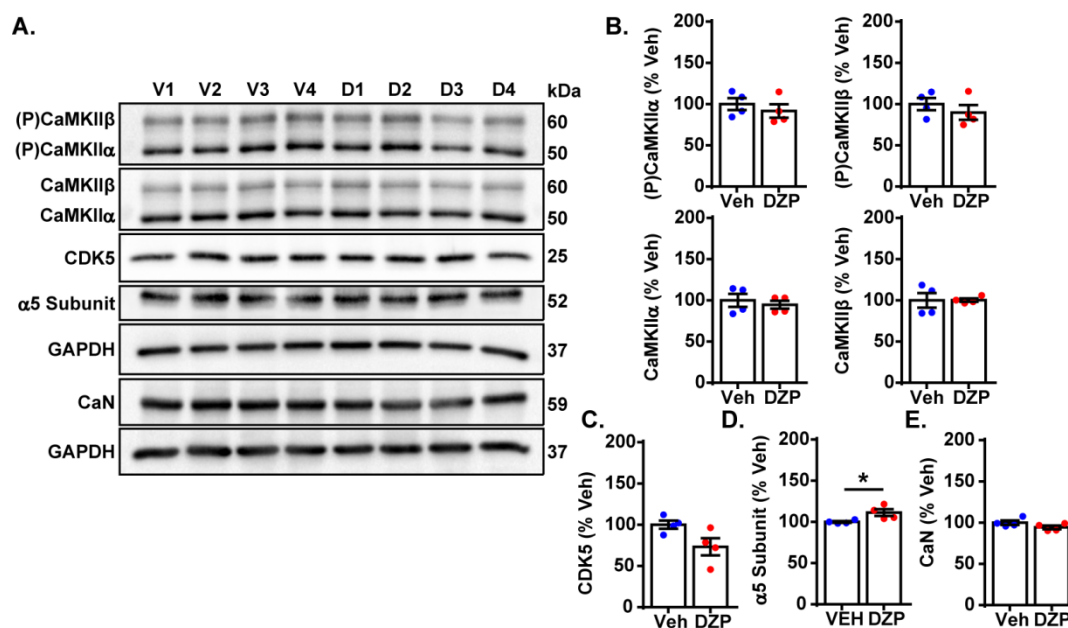


Figure 21. Biochemical Evaluation of Proteins Found to be Altered in their Association with γ 2-GABA_ARs after DZP by Proteomics.

Western blot analysis (A) of cortical tissue from mice treated with vehicle or DZP for 12 h. Quantification of T286/T287 (P)CaMKII and overall CaMKII α/β subunits (B), CDK5 (C), GABA_AR α 5 (D) subunit and calcineurin (CaN) (E). The α 5 subunit demonstrated a global increase in protein levels after DZP, while no other proteins were significantly altered (* $p \leq 0.05$, Student's t-test; $n = 4$ mice per treatment; error bars \pm S.E.M.).

To determine if the changes in association with key proteins identified to be altered in their association with γ 2 after DZP was a result of changes in total overall protein levels, we performed western blot analysis of cortical tissue from mice treated with vehicle or DZP for 12 h (**Fig. 21**). Quantification revealed that phosphorylated T286/T287 ((P)CaMKII) and overall CaMKII α/β subunits, CDK5 and CaN were not significantly altered by DZP. In contrast, the α 5 subunit exhibited a statistically significant increase in response to DZP relative to vehicle. These findings suggest that higher levels of expression of the α 5 subunit leads to increased α 5/ γ 2 containing

GABA_ARs, while a change in localization or interaction of CaMKII α/β , CDK5 and CaN underlie the diminished association with γ 2 after DZP exposure seen by proteomics.

3.4 Discussion

This work identifies key trafficking pathways involved in GABA_AR neuroplasticity in response to initial DZP exposure. Using a combination of biochemical and imaging techniques, we identified total γ 2 subunit levels are diminished in response to 12-24 h of DZP exposure *in vitro* and *in vivo*. Concurrent with the decrease in the overall γ 2 pool, we found DZP treatment enhanced ubiquitination of this subunit. Use of an innovative optical sensor for BZD sensitive GABA_AR (γ 2^{pH}FAP) in combination with MG dye pulse-labeling approaches revealed DZP exposure moderately enhanced targeting of surface γ 2-GABA_ARs to lysosomes. Live-imaging experiments with pH 7.4 NH₄Cl revealed increased intracellular receptor pools, providing further evidence that DZP enhances γ 2-GABA_AR lysosomal accumulation, a response reversed by BZD antagonist Ro 15-1788 treatment. We used novel intersubunit FRET based live-imaging to identify that surface synaptic α 2/ γ 2 GABA_ARs were specifically decreased after DZP, suggesting these receptor complexes were subjected to ubiquitination, lysosomal targeting, and degradation. In addition to DZP modulation of receptor trafficking, the postsynaptic scaffolding protein gephyrin demonstrated significant plasticity including increased Ser270 phosphorylation and production of gephyrin proteolytic fragments, concurrent with a decrease in total and membrane full-length gephyrin levels and ERK inactivation. Given the fundamental role of gephyrin in scaffolding GABA_ARs and regulating synaptic confinement, we used simultaneous FRAP live-imaging of receptors and scaffold in neurons to monitor inhibitory synaptic dynamics. We found ~24 h DZP

exposure accelerates both the rate of gephyrin and GABA_AR exchange at synapses as shown by enhanced fluorescence recovery rates. Control experiments using the BZD antagonist Ro 15-1788 were able to reverse the DZP induced loss of synaptic confinement, reducing gephyrin and GABA_AR mobility back to vehicle levels. Finally, we used label-free quantitative mass spectrometry and bioinformatics to identify key changes in $\gamma 2$ -GABA_AR protein association *in vivo* suggesting alterations in trafficking at the cell surface and intracellularly. Collectively, this work defines a DZP-induced reduction of gephyrin scaffolding coupled with increased synaptic exchange of gephyrin and GABA_ARs. This dynamic flux of GABA_ARs between synapses and the extrasynaptic space was associated with enhanced $\gamma 2$ -GABA_AR accumulation in intracellular vesicles and $\gamma 2$ -GABA_AR subtype specific lysosomal degradation. We propose DZP treatment alters these key intracellular and surface trafficking pathways ultimately diminishing responsiveness to DZP.

Numerous classical studies have examined gene and protein expression adaptations in GABA_AR subunits after BZD exposure with minimal agreement that a specific change occurs (32, 33, 46). Here molecular mechanistic insight is provided, through direct measurements of enhanced ubiquitination of the $\gamma 2$ subunit (**Fig. 12**), lysosomal targeting (**Fig. 14,15**), reduced surface synaptic $\alpha 2/\gamma 2$ GABA_AR levels (**Fig. 17**), and reduced synaptic confinement (**Fig. 19**) of DZP-sensitive GABA_ARs. Together this suggests BZD exposure primarily decreases synaptic retention of $\gamma 2$ containing GABA_AR while downregulating surface levels of the $\alpha 2$ subunit. Ubiquitination of the $\gamma 2$ subunit by the E3 ligase Ring Finger Protein 34 (RNF 34) (170) is the only currently known mechanism targeting internalized synaptic GABA_ARs to lysosomes (159). Due to the requirement of the $\gamma 2$ subunit in all BZD-sensitive GABA_ARs, it is likely that ubiquitination of the $\gamma 2$ subunit is a contributing factor for increased lysosomal-mediated degradation in response to

DZP, although not required (**Fig. 16**). Despite a small decrease in the $\gamma 2$ total protein, changes in surface levels were not significant by biochemical approaches, consistent with evidence that $\gamma 2$ -GABA_AR surface levels are tightly regulated to maintain baseline inhibition and prevent excitotoxicity. For example, in heterozygous $\gamma 2$ knockout mice a 50% reduction in $\gamma 2$ levels appears to be compensated by increased cell surface trafficking, resulting in only an approximately 25% reduction in BZD binding sites in the cortex and a limited reduction in synaptic GABA_AR clusters (309, 310). In contrast, homozygous $\gamma 2$ knockout mice show a complete loss of behavioral drug response to BZD and over 94% of the BZD sites in the brain (GABA binding sites unchanged) and early lethality (311). Similarly, studies have shown that prolonged GABA_AR agonist or BZD application increases $\gamma 2$ GABA_AR internalization in cultured neurons, with inconsistent changes in surface GABA_AR levels detected (160, 312). Importantly, by using high sensitivity surface GABA_AR intersubunit FRET measurements we were able to detect a decrease in BZD sensitive $\alpha 2/\gamma 2$ GABA_ARs (**Fig. 17**).

The role of inhibitory scaffolding changes in responsiveness to BZD has been largely under investigated. Phosphorylation of gephyrin at Ser270 is mediated by CDK5 and GSK3 β , while a partnering and functionally relevant Ser268 site is regulated by ERK (73). DZP time series experiments revealed a global decrease in ERK phosphorylation but not GSK3 β , without a change in total kinase levels of ERK, GSK3 β or CDK5 over the course of the assay (except 12 h ERK) (**Fig. 18**). A previous model by Tyagarajan SK, et al. (2013) using gephyrin point mutants at Ser268 and Ser270 suggested that enhanced Ser270 phosphorylation coupled with decreased Ser268 phosphorylation by ERK promotes gephyrin remodeling and calpain-1 degradation. This is consistent with the ERK inactivation measured in our data and the increase in gephyrin Ser270 phosphorylation demonstrated by immunofluorescence after DZP (**Fig. 11**), enhanced gephyrin

degradation and decreased full-length gephyrin levels (**Fig. 11,12**). Calpain-1 mediated gephyrin cleavage can occur within 1 minute in hippocampal membranes (313), and cleavage products are increased following *in vitro* ischemia at 30 min and up to 48 hours following ischemic events *in vivo* (295). Gephyrin cleavage may be occurring at earlier time points than the DZP 24 h mark measured here (**Fig. 12 F,G**), coinciding with ERK dephosphorylation as early as 45 min (Figure 5A,B). One limitation of our results is that measuring total and phospho levels of these kinases does not directly address changes in association or regulation of gephyrin, although it does provide an additional piece of evidence supporting gephyrin cleavage by calpain-1 and scaffold remodeling. Accordingly, our previous work found 30 min treatment with the GABA_AR agonist muscimol in immature neurons (depolarizing) leads to ERK/BDNF signaling and decreased Ser270 phosphorylated gephyrin levels at synapses and overall (304). Thus, ERK activation status negatively correlates with the level of phosphorylation at gephyrin Ser270.

Recent work has demonstrated 12 h DZP treatment of organotypic hippocampal slices expressing eGFP-gephyrin causes enhanced gephyrin mobility at synapses and reduced gephyrin cluster size (314). Here we found the synaptic exchange rate of $\gamma 2$ GABA_ARs and gephyrin to be nearly doubled at synapses in cortical neurons after ~24 h DZP exposure (**Fig. 19**). $\gamma 2$ extrasynaptic fluorescence recovery in DZP treated neurons was variable but also trended towards an increase relative to controls (**Fig. 19**), which could be a result of increased diffusion of receptors out of the synaptic space. This effect occurred coincident with the formation of truncated gephyrin cleavage products (**Fig. 12**), which has previously been shown to decrease $\gamma 2$ synaptic levels (295). These findings are also consistent with our previous work showing RNAi gephyrin knockdown doubles the rate of $\gamma 2$ -GABA_AR turnover at synaptic sites (54). Later quantum dot single particle tracking studies confirmed $\gamma 2$ synaptic residency time is linked to gephyrin scaffolding levels (252).

Importantly, GABA_AR diffusion dynamics also reciprocally regulate gephyrin scaffolding levels (307), suggesting gephyrin and GABA_ARs synaptic residency are often functionally coupled. Accordingly, γ 2 subunit and gephyrin levels both decrease in responses to other stimuli including status epilepticus (315) or prolonged inhibition of IP₃ receptor-dependent signaling (180). Additionally, chemically-induced inhibitory long-term potentiation (iLTP) protocols demonstrate gephyrin accumulation occurs concurrent with the synaptic recruitment of GABA_ARs within 20 min (287). Collectively, these proteins display a high degree of interdependence across different experimental paradigms of inhibitory synapse plasticity occurring over minutes to days.

Increasing receptor synaptic retention enhances synaptic currents, while enhanced receptor diffusion via decreased scaffold interactions reduces synaptic currents. For example, reduction of gephyrin binding by replacement of the α 1 GABA_AR subunit gephyrin binding domain with non gephyrin binding homologous region of the α 6 subunit results in faster receptor diffusion rates and a direct reduction in mIPSC amplitude (285). Similarly, enhanced diffusion of GABA_ARs following estradiol treatment also reduces mIPSCs in cultured neurons and in hippocampal slices (316). In contrast, brief DZP exposure (< 1h) reduces GABA_AR synaptic mobility (69) without a change in surface levels (70), consistent with initial synaptic potentiation of GABA_AR neurotransmission by DZP. Together with our current findings, this suggests post-translational modifications on GABA_AR subunits or gephyrin that enhance receptor diffusion are a likely key step leading to functional tolerance to BZD drugs.

It is a significant technical challenge to examine dynamic alterations in receptor trafficking occurring *in vivo*. To overcome this we examined changes in γ 2-GABA_AR protein association following DZP injection in mice using quantitative proteomics and bioinformatics analysis. This work revealed shifts toward γ 2-GABA_AR association with protein pathway networks associated

with endocytosis and organization of cytoskeleton (**Fig. 20B, Table 3**), confirming similar fluctuations in membrane and intracellular trafficking occur *in vivo* and *in vitro* after DZP. We also found that shifts in association of proteins involved in the development of neurons (CaMKII α , CDK5, NEFH, calcineurin/PPP3CA) suggested an inhibition in this pathway after DZP (**Fig. 20B**). When considering all protein hits between vehicle and DZP, γ 2-GABA_AR association with proteins involved in 14-3-3 mediated signaling and RhoA signaling pathways were greatly increased after DZP (**Fig. 20A**, orange), while interaction with proteins involved in EIF2 signaling and sirtuin signaling pathways were reduced (**Fig. 20A**, blue). 14-3-3 proteins are heavily linked in GABA_AR intracellular to surface trafficking (305, 306), and the RhoA signaling pathway is directly involved in actin cytoskeleton organization (317) and α 5-GABA_AR anchoring (106), providing further evidence of GABA_AR shifts in membrane and cytosolic trafficking after DZP exposure.

Recent inhibitory synapse proteomics studies have identified a number of new protein synaptic constituents or modulators of GABA_AR function (87, 318-321). We show here that proteins known to have roles in synaptic function and trafficking of membrane receptors show changes in their association with γ 2-receptors. For example, the calcium-sensitive kinase CaMKII α was found to be significantly decreased in interaction with γ 2-GABA_AR following DZP, which can regulate GABA_AR membrane insertion, synaptic retention and drug binding properties (119, 178, 287, 322) (Table 2). Calcineurin/PPP3CA has been recognized as a key regulator of GABA_AR synaptic retention and plasticity (162, 180, 182, 183, 307) and has been linked to the response to DZP *in vitro* (312). Here we provide the first evidence that DZP exposure enhances the association of calcineurin with γ 2-GABA_ARs *in vivo*. Furthermore, DZP was found to enhance γ 2 association with 14-3-3 protein family members (**Table 1**), which are known mediators of

GABA_AR surface and intracellular trafficking (305, 306). $\alpha 5$ subunit coassembly with $\gamma 2$ (**Table 1**) and overall levels (**Fig. 21**) were elevated after DZP. Interestingly, the $\alpha 5$ subunit is required for the development of BZD sedative tolerance in mice (308). It is notable that our proteomic studies are in part limited by the specificity of our antibody used and general downstream effects of reduced neuronal activity. Future follow up studies using the DZP site antagonist R015-1788 will be needed to dissect the individual roles of proteins found to be significantly altered in their association with GABA_AR, and their physiological and pharmacological importance to BZD tolerance and inhibitory neurotransmission.

Through application of novel and highly sensitive fluorescence imaging approaches combined with *in vivo* proteomics, we provide unprecedented resolution of GABA_AR synapse plasticity induced by BZDs at both the level of the single neuron and cortex. Our study reveals that sustained initial DZP treatment diminishes synaptic BZD sensitive GABA_AR availability through multiple fundamental cellular mechanisms: through reduction of the post-synaptic scaffolding protein gephyrin; shifts toward intracellular trafficking pathways and targeting of receptors for lysosomal degradation; and enhanced synaptic exchange of both gephyrin and GABA_ARs. Proteomic and bioinformatics studies using DZP-treated mouse brain tissue provide further evidence that altered $\gamma 2$ -GABA_AR surface and intracellular trafficking mechanisms play a critical role to the response to DZP *in vivo*. These results define key events leading to BZD irresponsiveness in initial sustained drug exposure. Future studies utilizing this dual approach will address the neuroadaptations produced by long term BZD use to systematically identify the effects of a critical drug class that has seen a tripling in prescription numbers over the last two decades (323).

4.0 Inhibitory and Excitatory Synaptic Neuroadaptations in the Diazepam Tolerant Brain

Joshua Lorenz-Guertin performed animal injections, sample collection, biochemistry data collection and analysis, behavior, mass spectrometry data analysis. Megan L. Brady performed an open-field behavioral assay. Sabya Das performed biochemistry experiments on tissue from seven day treated animals and assisted with behavioral experiments. Tija C. Jacob, Matthew J. Bambino, Katarina Vajn and Matthew L. MacDonald assisted with mass spectrometry data analysis. Tija C. Jacob and Matthew L. MacDonald built and curated SRM libraries. The Macdonald laboratory performed mass spectrometry experiments. Nadezda Povysheva performed electrophysiology experiments and analysis.

4.1 Introduction

BZDs are positive allosteric modulators that potentiate GABA_AR inhibition by increasing the binding affinity of GABA and increasing channel opening frequency (32). Sustained treatment with BZD drugs is intimately associated with the development of tolerance, dependence, withdrawal and addiction (33). BZD efficacy diminishes after prolonged or high dose acute exposure (271, 272), with tolerance to the sedative/hypnotic effects and anti-convulsant properties forming most quickly (46, 273-275). Since the development of BZDs in the early 1960s, intense research efforts have attempted to understand the adaptive response to BZDs. Direct comparison of these studies has proved challenging due to inconsistent findings likely as a result of methodological differences (33). Regardless, three important key characteristics were identified: BZD drugs demonstrate reduced affinity for the GABA_AR after prolonged exposure (allosteric uncoupling; described in section 3.1), the effects of BZD could be reversed by concurrent treatment with the BZD site antagonist flumazenil (including behavioral dependence, withdrawal and tolerance (324-326)), and DNA/RNA level changes of GABA_AR subunit expression are

inconsistent across experimental models (32). Considering these findings en masse, it is likely that rapidly tunable post-translational modifications, protein levels of GABA_AR subunits, or other non-GABA_AR inhibitory synapse components, may provide important mechanistic information underlying BZD irresponsiveness. For instance, BZD potentiation of recombinant GABA_ARs in HEK293 cells is reduced when $\gamma 2$ subunit Ser327 residue is phosphorylated (150) and 7-14 days of DZP treatment in rats causes increased phosphorylation at this site (327). Moreover, protein level changes in GABA_AR subunit composition dictates the ability to bind BZD drugs (2), impacts localization at synapses and interacting proteins (328) and determines general channel properties (329). GABA_ARs exist primarily in heteropentamers composed of two α , two β and a $\gamma 2$ subunit, possibly containing two different α subunits, which impacts receptor pharmacology (330-332). As stated in previous sections, $\alpha 1/2/3/5$ subunits directly adjacent to $\gamma 2$ form the BZD binding pocket, while $\alpha 4$ and $\alpha 6$ are BZD insensitive. Notably, $\alpha 4/\beta/\gamma 2$ GABA_ARs exist in small α subunit heterogeneous populations (333, 334), and increased expression of these BZD-insensitive GABA_ARs could shift receptor pharmacology and contribute to tolerance by reducing BZD binding.

Neurotransmission relies on a delicate balance of both inhibitory and excitatory input, and thus synaptic neuronal proteins involved in both of these processes are likely involved in the response to BZDs. Excitatory glutamatergic receptors consist of ionotropic and metabotropic subtypes. Ionotropic glutamate receptors are heteromeric ligand-gated cation channels inwardly permeable to K⁺, Na⁺, or Ca²⁺ ions following glutamate binding. The NMDA (N-methyl-D-aspartate) receptor class is crucial for synaptic plasticity and is comprised of two obligatory GluN1 subunits and two GluN2/3 subunits with differing regulatory characteristics. The predominant GluN2 isoforms are GluN2A and GluN2B. GluN2B is predominantly expressed in

the early postnatal brain and remains open longer after activation compared to GluN2A, which is expressed at higher levels later in over development (335). As a result, NMDA receptor function and role in synaptic plasticity is closely correlated with dynamic changes in the composition of GluN2 subunit isoforms. AMPA (alpha-amino-3-hydroxy-5-methyl-4-isoxazole-4-propionic acid) receptors are heterotetrameric ligand-gated ion channels composed of multiple subunits (GluR1-4). AMPA receptors are also important for the establishment of long-term excitatory potentiation and synaptic plasticity. AMPA receptors exhibit faster kinetics and lower glutamate affinity than NMDA receptors, thus the balance of AMPA/NMDA receptors is key to neuronal excitatory neurotransmission for short-term integration of synaptic inputs and long-term transformation of circuits (336-338).

Glutamatergic sensitization or upregulation has been postulated to be important in the development of BZD tolerance and addiction/withdrawal (339), as excessive excitation could require BZDs to be administered persistently or at higher doses to achieve the intended therapeutic effect. Early mouse studies using the AMPA antagonist GYKI 52466 and the NMDA receptor antagonist CPP revealed BZD withdrawal syndromes occur in separate AMPA and NMDA dependent phases (340). NMDAR current has also been shown to be decreased two days post cessation of one week treatment with the BZD flurazepam in CA1 hippocampal neurons, although this effect could be reversed by treatment with the non-competitive NMDAR antagonist MK-801 one day after BZD cessation (299). Multiple studies support the role of enhanced NMDA receptor function in withdrawal behaviors (341-343) and upregulation of GluN1 and GluN2B NMDAR subunits after DZP by [3H]MK801 binding and biochemistry (344, 345). Moreover, MK801 and ifenprodil (GluN2B subtype NMDAR antagonist) suppressed withdrawal-induced

pentylentetrazole (PTZ) seizure susceptibility in DZP treated mice (342), cumulatively supporting the idea of NMDAR upregulation in response to DZP withdrawal.

Fewer studies have focused on the role of NMDAR contribution to the formation BZD tolerance. Importantly, NMDARs are implicated in tolerance to a number of other pharmacological drug classes including opioids (346), ethanol (347) and barbiturates (348). Some behavioral data suggests co-administration of the highly potent NMDAR competitive antagonist CPP, but not the AMPAR antagonist GYKI 52466, prevents development of DZP sedative behavioral tolerance in mice (349). MK801 also prevented the development of tolerance to locomotor effects (350) of DZP in rats, while tolerance to the anticonvulsant response of the BZD lorazepam was moderately prevented by CPP in mice (341). Interestingly, lorazepam reduced binding of the BZD binding site agent [3H]flumazenil in multiple brain regions, an effect that was not reversed by CPP co-treatment, suggesting downregulation of GABA_ARs was not reversible by NMDAR inhibition. This finding could imply distinct contributions of GABA_ARs and NMDARs to neuroadaptations in BZD tolerance.

Understanding the role of both GABAergic and glutamatergic contributions in BZD withdrawal and tolerance studies has been limited by using non-comprehensive experimental approaches. Moreover, these studies lack insight about the key molecular signaling networks undermining functional changes in synaptic function. To gain a more holistic perspective of the neuroadaptive changes occurring during BZD tolerance, we analyzed inhibitory and excitatory synaptic protein levels and function by biochemical and electrophysiology approaches in mice who demonstrate DZP sedative tolerance behaviorally. To generate a more complete understanding of DZP-induced neuroplasticity, we used state of the art selected reaction monitoring (SRM) mass spectrometry to quantify over 500 proteins, interrogating glutamatergic,

GABAergic and other signaling pathways. No existing studies have used a high-throughput quantitative and targeted proteomics based method to reveal the complex neuroadaptations of the BZD tolerant rodent brain. We assessed our proteomic findings using bioinformatics analysis to determine changes in activation states of key biological pathways to predict changes in cellular activity and function. Collectively our findings reveal complex alterations in both synaptic inhibitory and excitatory neurotransmission that share overlapping mechanisms with ethanol and opiate tolerance.

4.2 Methods and Materials

4.2.1 Mice

All experiments were approved by the Institutional Animal Care and Use Committee of the University of Pittsburgh and conducted in accordance with the National Institutes of Health Guidelines for the Care and Use of Laboratory Animals. C57BL/6J 8-10 week old male mice (Jackson Laboratory) were maintained on a reverse 12 h dark/light schedule. Mice were habituated to the University of Pittsburgh animal facility for at least three days prior to initiation of experiments. Mice were housed under 12 h light/dark cycles and had ad libitum access to food.

4.2.2 Diazepam Treatment and Open-Field Behavior Assay

Mice were randomly assigned to vehicle (40% PEG, 10% EtOH, 5% Na Benzoate, 1.5 % Benzyl alcohol) or DZP (Hospira) treatments. All animals received a saline injection at day -1 and

vehicle injection at day 0. On day 1, mice received either a DZP (10mg/kg) or vehicle injection and this treatment continued once daily for seven days in the morning. Mice were injected with vehicle or DZP approximately 45 min prior to testing for locomotor activity in an open field using automated activity monitors (Med Associates, St Albans, VT). Mice were allowed to freely explore the chamber for 20 min during which time ambulatory distance traveled was recorded. Brain tissue was immediately collected and flash frozen following day 7 behavior studies where applicable. Mice that were only used for biochemistry experiments were given the same dosing regimen, including a dose approximately 45 min prior to sacrifice (two treatments total for 24 h timepoint mice and four treatments total for 72 h timepoint mice).

4.2.3 Antibodies

Primary antibodies: rabbit GAPDH (WB) (14C10, Cell Signaling); rabbit CaMKII α/β Phospho Thr286 (WB) (p1005-286, Phosphosolutions); rabbit CaMKII pan (WB) (4436, Cell Signaling); rabbit GluN1 (WB) (5704, Cell Signaling); mouse GluN2B (WB) (610417, BD Biosciences); rabbit GluN2A (WB) (1500, Phosphosolutions), rabbit GABA_AR α 1 subunit (WB) (06-868, Millipore); rabbit GABA_AR α 4 subunit (WB) (845-GA4C, Phosphosolutions); rabbit GABA_AR α 5 subunit (WB) (2224503, Synaptic Systems); rabbit GABA_AR β 3 subunit (WB) (863-GB3C, Phosphosolutions); rabbit γ 2 GABA_AR subunit (WB) (224003, Synaptic Systems); rabbit gephyrin (WB) (sc-14003, Santa Cruz); rabbit KIR3.2 (WB) (APC-006, Alomone Labs).

4.2.4 Subcellular Fractionation

Subcellular fractionation was performed as previously described (351). Mouse cortical tissue was homogenized using a dounce homogenizer in homogenization buffer (HB) (in mM): 20 Tris-HCl, 2 EDTA, 640 Sucrose, 40 Na pyrophosphate, 20 NaF, 40 β -glycerophosphate, 4 Na_3VO_4 , Sigma protease inhibitor cocktail (adjusted to pH 7.4 with NaOH at 4°C). After homogenization, samples were spun 1000rcf for 10mins at 4°C. The supernatant was removed and was either stored (Total) or used for subcellular fractionation. Samples were spun at 15,000 rcf for 30 min at 4°C. The supernatant was removed and the pellet was resuspended in 496 μL H_2O with protease inhibitor and sat on ice for 15 min. 3.75 μL 1M HEPES NaOH was then added and lysis continued on ice for 15 min. Samples were then spun for 20 min at 25,000 rpm at 4°C. Supernatant was discarded and 75 μL HB was added followed by addition of 75 μL 2x Triton buffer (final concentration in mM): 20 Tris-HCl, 2 EDTA, 2 EGTA, 20 NaF, 4 Na_3VO_4 , Sigma protease inhibitor cocktail). Samples were sonicated at 25%, 3 pulses, 5s each under ice to dissolve the pellet. 150 μL 1x Triton buffer (with 1% Triton X-100) was then added and incubated for 30 min on ice. Next, samples were spun 100,000 rcf for 60 min at 4°C; the supernatant (extrasynaptic fraction) was removed and stored on ice. The pellet was homogenized in HB and sonicated, followed by the addition of 1% SDS prior to storage at -80°C (Synaptic). The extrasynaptic fraction was concentrated using acetone precipitation overnight, followed by homogenization in HB, sonication, and addition of 1% SDS. Samples were run using SDS-PAGE and transferred to nitrocellulose membrane. Samples were probed with primary antibody overnight followed by the appropriate horseradish peroxidase (HRP)-coupled secondary antibody.

4.2.5 Electrophysiological Recordings

Experiments were performed on prefrontal cortex (PFC) slices from 3-7 month old C57BL/6J male mice. Mice were deeply anesthetized with chloral hydrate and decapitated. The brain was quickly removed and immersed in ice-cold pre-oxygenated artificial cerebrospinal fluid (ACSF). Coronal slices containing PFC were made as previously described (352). Throughout experiments, ACSF (31-32°C, perfused with a 95% O₂/5% CO₂) of the following composition was used (in mM): 126 NaCl, 2.5 or 10 KCl, 1.25 NaH₂PO₄, 1 MgSO₄, 2 CaCl₂, 24 NaHCO₃, 10-20 glucose; pH~7.3.

Whole-cell recordings were performed from layer 2-3 neurons visualized by IR-DIC video microscopy as previously described (353). Pyramidal neurons were identified by their apical dendrites and triangular somata. Patch electrodes (5-10 MΩ open-tip resistance) were filled with a solution containing (in mM): 140 CsCl, 0.1 CaCl₂, 2 MgCl₂, 2.5 Phosphocreatine, 1.1 EGTA, 2 ATP-Mg, 1 GTP-Na and 10 HEPES, adjusted to 7.2 with 1 M CsOH. Voltage and current recordings were performed with a Multi-Clamp 700A amplifier (Axon Instruments, Union City, CA). Signals were filtered at 2 kHz and acquired at a sampling rate of 10 kHz using Clampex 10.2 software (Molecular Devices Corporation, Sunnyvale, CA). Access resistance typically was 10-20 MΩ and remained relatively stable during experiments (≤30% increase). Corrections were made for liquid junction potential (-13 mV). We used: gabazine (10 μM) and picrotoxin (100 μM) to inhibit GABA_AR; 2,3-dihydroxy-6-nitro-7-sulfamoylbenzo(F)quinoxaline (NBQX; 20 μM) to inhibit kainate and α-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid receptors (AMPA_Rs); D-2-amino-5-phospho-pentanoic acid (AP-5; 50 μM) to inhibit NMDA_Rs; tetrodotoxin (TTX; 1 μM) to inhibit voltage-gated Na⁺ channels; diazepam (3 μM) and GABA (20 μM) as an GABA_AR

agonist. Gabazine, picrotoxin, GABA, diazepam, NBQX, and AP-5 were purchased from Abcam (Cambridge, MA); TTX from Sigma (St. Louis, MO).

Miniature inhibitory postsynaptic currents (mIPSCs) were recorded at -70 mV in NBQX, AP-5, TTX. Miniature excitatory post-synaptic currents (mEPSCs) were recorded at -70 mV in Gabazine and TTX. Spontaneous and miniature events were analyzed using the MiniAnalysis Program (Synaptosoft, Decatur, GA) as previously described (353).

To record evoked AMPA/NMDA receptor EPSC (eEPSC), a bipolar stimulating electrode was placed on the border of white matter and layer 6 (352) with pulses delivered at 0.1 Hz frequency. eEPSCs were recorded at +40 mV in the presence of gabazine to block GABA_AR mediated currents. After eEPSCs were recorded for ~5 min, AP-5 was added to isolate AMPAR mediated responses. The AMPA/NMDA ratio was calculated as previously described (354). First, the average NMDAR current was calculated by subtracting the average isolated AMPAR current from the initial average eEPSC prior to AP-5 application. Second, the AMPA/NMDA ratio was calculated as a ratio of the peak amplitude of the currents. Amplitude of evoked synaptic responses was measured on averaged traces as the most positive current value compared to baseline current using Clampfit.

Tonic GABA_AR current was measured as the shift in baseline produced by the application of GABA_AR blocker picrotoxin in the presence of NBQX, AP-5, TTX and GABA. The baseline current was measured in the Clampfit during three consecutive 0.2-min intervals before the application of picrotoxin and 3 min after its application when baselines reach plateau.

Two-tailed paired t-test was used for group comparisons using Excel (Microsoft Corp., Redmond, WA). Values are presented as mean \pm SEM.

4.2.6 Mass Spectrometry

Mouse cortical tissue from 10 vehicle and 10 DZP treated mice was homogenized individually using a dounce homogenizer in HB (in mM): 20 Tris-HCl, 2 EDTA, 640 Sucrose, 40 Na pyrophosphate, 20 NaF, 40 β -glycerophosphate, 4 Na_3VO_4 , Sigma protease inhibitor cocktail (adjusted to pH 7.4 with NaOH at 4°C). After homogenization, samples were spun 1000 rcf for 10 min at 4°C. The supernatant (total) was used for downstream mass spectrometry. Total protein concentration in the homogenate preparations were assessed by micro BCA (Pierce). Targeted MS was performed in a similar fashion as described previously (355): 10 μg homogenate or pooled controls were mixed with 10 μg of [$^{13}\text{C}_6$]brain ISTD (355) prepared from stable isotope labeling in mammals (SILAM) mouse cortex tissue (Cambridge Isotopes). The [$^{13}\text{C}_6$]lysine-labeled brain proteome internal standard ([$^{13}\text{C}_6$]brain ISTD) was prepared by homogenizing cerebral cortex tissue from a Stable Isotope Labeling in Mammals (SILAM) mouse (Cambridge Isotopes). These animals were raised on a diet in which the only source of Lysine was $^{13}\text{C}_6$ labeled, resulting in near complete (99%) labeling of the animal proteome in three generations. Labeling efficiency of each [$^{13}\text{C}_6$]brain ISTD preparation was confirmed prior to use.

Mass spectrometry analyses were conducted on a TSQ Quantiva triple stage quadrupole mass spectrometer (ThermoFisher Scientific, Location) with an Ultimate 3000 HPLC (Dionex). Two μl (~ 1 μg protein) was loaded on to a 3 μm 120A; 105mm REPROSIL-Pur C18 Picochip (New Objective) at 1 $\mu\text{l}/\text{min}$ for 12 min and eluted at 400nl/min over a 25 min gradient from 3-35% mobile phase B (Acetonitrile, 0.1% formic acid). Selected reaction monitoring (SRM) transitions were scheduled with 60 second windows. Transitions were monitored, allowing for a cycle time of 1 sec, resulting in a dynamic dwell time never falling below 10 msec. The MS instrument parameters were as follows: capillary temperature 275°C, spray voltage 1350 V, and a

collision gas of 1.4 mTorr (argon). The resolving power of the instrument was set to 0.7 Da (Full Width Half Maximum) for the first and third quadrupole. Data were acquired using a Chrom Filter peak width of 4.0 sec.

Method development began by building upon our previously described SRM libraries (355-358) with the selection of additional proteins of interest included in published multidimensional MS/MS analyses of synaptic enrichments from mouse and human brain tissue (355, 359, 360) as well as the NIST Tandem Mass Spectral Library and the library generated by pilot immunoprecipitation-proteomic studies of γ 2-GABA_ARs. Targets for inclusion in the LC-SRM/MS assay were selected with a bias toward well annotated synaptic proteins, such as glutamate receptors, kinases, phosphatases, vesicular fusion, amino acid metabolism, protein trafficking and scaffolding as well as proteins found to interact with the GABA_AR. Peptides for proteins of interest were then filtered based on the following criteria: 1) presence of lysine and 2) non-redundant to a selected protein or protein group (determined by BLAST search). Acceptable peptide sequences, along with MS2 spectra, were imported into Skyline (361). Initially, five mass transitions were selected for each target peptide and its “heavy” counter-part. To ensure that the desired peptide was assayed, rigorous selection criteria were employed for the inclusion of peptide SRM transitions. Candidate “light”/“heavy” peptide SRMs were evaluated manually in Skyline for A) retention time, B) similar y-ion ratios (within 25%) to each other and database MS2 spectra, and D) a signal-to-noise ratio greater than 3. Peptide SRM pairs for which more than one identical peak was observed was omitted. Ultimately, 961 peptides unique to 571 proteins (or protein groups) were quantified in mouse samples. Statistics were performed by Student’s t-test analysis in Excel.

4.2.7 Bioinformatics Analysis

Ingenuity Pathways Analysis (IPA) (Ingenuity Systems) was used for cellular pathway analysis. Proteins with peptides which were found to have increased or decreased DZP/Veh ratios with a $p < 0.1$ were used for analysis. This statistical cutoff was used to achieve adequate numbers of proteins to be used for comparison and prediction based analysis. Duplicate proteins were averaged within IPA to determine relative ratio changes. Significant enrichment in protein networks were calculated by right tailed Fisher's exact test. Z-score analysis is a statistical measure of an expected relationship direction and observed protein/gene expression to predict pathway activation or inhibition. IPA core analysis was searched to determine direct and indirect relationships within 35 molecules per network and 25 networks per analysis. All data repositories available through IPA were used to determine experimentally observed and highly predicted interactions occurring in mammalian tissue and cell lines. Ratio data were converted to fold change values in IPA, where the negative inverse ($-1/x$) was taken for values between 0 and 1, while ratio values greater than 1 were not affected.

4.2.8 Statistics

Relevant statistical test information is described in the figure legends or within the individual methods sections.

4.3 Results

4.3.1 Mice Rapidly Form Tolerance to the Sedation Actions of DZP

We first sought to establish a model of DZP sedative tolerance in mice. All animals received a saline injection at day -1 and vehicle injection at day 0. On day 1, mice received either a DZP (10mg/kg) or vehicle injection. DZP-treated mice demonstrated sedation and a significant decrease in distance traveled compared to vehicle treated animals (**Fig. 22**). By day 3, the distance traveled was not significantly different between groups, indicating DZP-treated mice had become tolerant to the sedative effects of DZP. Similar rapidly forming behavioral tolerance to the sedative actions of DZP has been reported by multiple groups (47, 297, 349, 362). To confirm functional loss of DZP sensitivity in the cortex, we measured miniature inhibitory postsynaptic currents (mIPSCs) and potentiation by DZP using slice electrophysiology at the end of the seven day protocol (**Fig. 23A**). There was no significant difference between vehicle (Veh) and DZP treated animals mIPSC amplitude (**Fig. 23B**), frequency (**Fig. 23C**) or tau (decay) (**Fig. 23D**), suggesting no major change in pre- or post-synaptic GABAergic neurotransmission. In contrast, DZP potentiation (**Fig. 23E**) of current amplitude (**Fig. 23F**) and tau decay (**Fig. 22G**) in vehicle animals was significantly higher than animals treated for seven days with DZP, suggesting functional tolerance to the positive allosteric effects of the drug. These results are consistent with previous publications suggesting loss of DZP sensitivity occurs independent of changes in basal GABAergic neurotransmission (363-365).

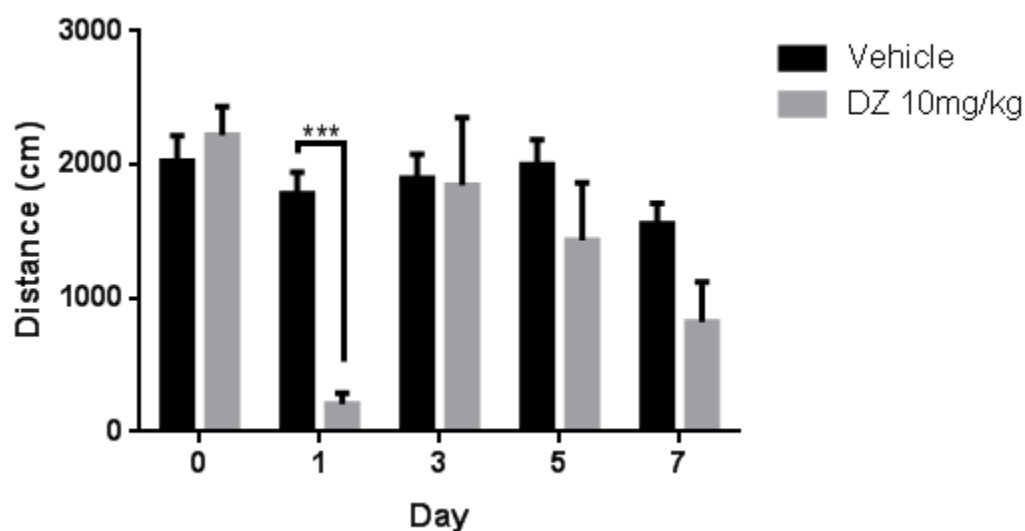


Figure 22. Repeated DZP Treatment Rapidly Leads to Sedative Tolerance in Mice.

Animals were administered treatment by IP injection once daily and then tested for sedative tolerance 45min later in the open field behavioral test on the days indicated. All animals received a saline injection at day -1 and vehicle injection at day 0. Mice received either a DZP (10mg/kg) or vehicle injection on days 1-7. DZP-treated mice demonstrated sedation and a significant decrease in distance traveled compared to vehicle treated animals. By day 3, the distance traveled was not significantly different between groups, indicating DZP-treated mice had become tolerant to the sedative effects of DZP. Two-way ANOVA found a significant effect of time ($p < 0.0001$), treatment ($p = 0.0261$), and a significant interaction ($p = 0.0020$), with a post-hoc Sidak test indicating a significant difference between vehicle and DZP treated animals at day 1 ($p < 0.001$), $n=16$ vehicle treated mice, $n=14$ DZP-treated mice.

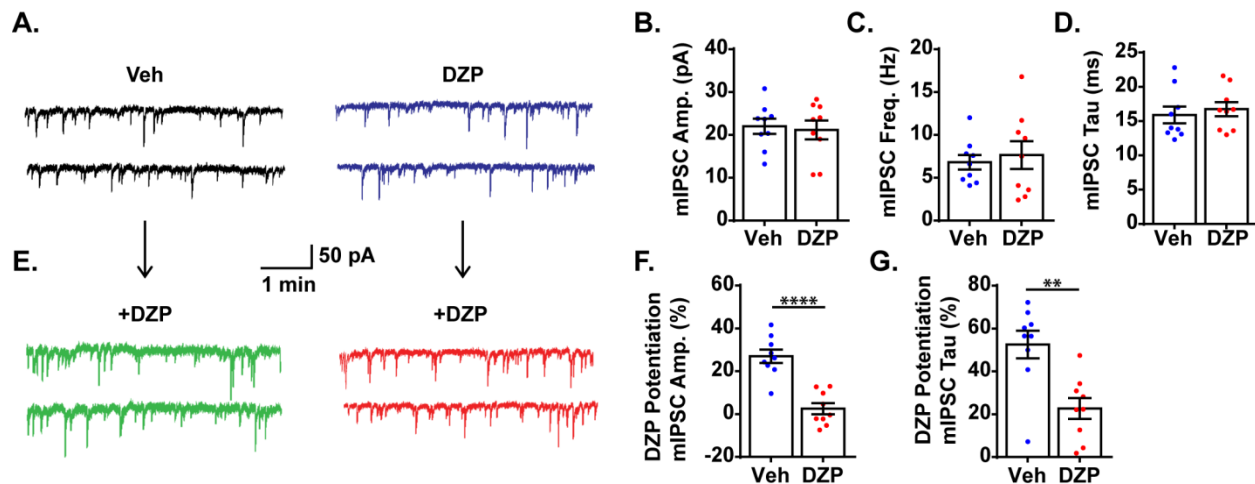


Figure 23. Repeated DZP Exposure Leads to Loss of DZP Potentiation of GABA_A Synaptic Currents.

(A) mIPSCs in vehicle (Veh) (black and green) and DZP (blue and red) treated mice ($V_{\text{hold}} = -70$ mV). (B) mIPSC amplitude, (C) frequency and (D) tau were not different in DZP treated mice compared to Veh. (E,F,G) DZP potentiation of current amplitude and tau is significantly larger in Veh animals relative to DZP (** $p \leq 0.01$, **** $p \leq 0.0001$ Student's t-test; $n=9$ per treatment group ; error bars \pm S.E.M.).

4.3.2 Inhibitory Synapse Protein Levels and Localization after DZP

We next sought to determine if GABA_AR subunits involved in the sedation response to DZP (308, 366, 367) were altered by seven day drug treatment. Levels of gephyrin, the key synaptic scaffolding protein for GABAergic synapses, the DZP-insensitive GABA_AR $\alpha 4$ subunit, and the highly expressed GABA_AR $\beta 3$ subunit were also measured. Subcellular fractionation (351) was used to measure the total, synaptic and extrasynaptic cortical levels of these proteins to determine membrane localization and overall changes (**Fig. 24A,B,C**). Unexpectedly, this analysis revealed a significant increase in the overall pool of GABA_AR $\alpha 1$ ($+71.4\% \pm 11.6$), $\beta 3$ ($+48.8\% \pm 7.2$) and $\gamma 2$ ($+32.9\% \pm 5.7$) subunits in the DZP group relative to the vehicle animals

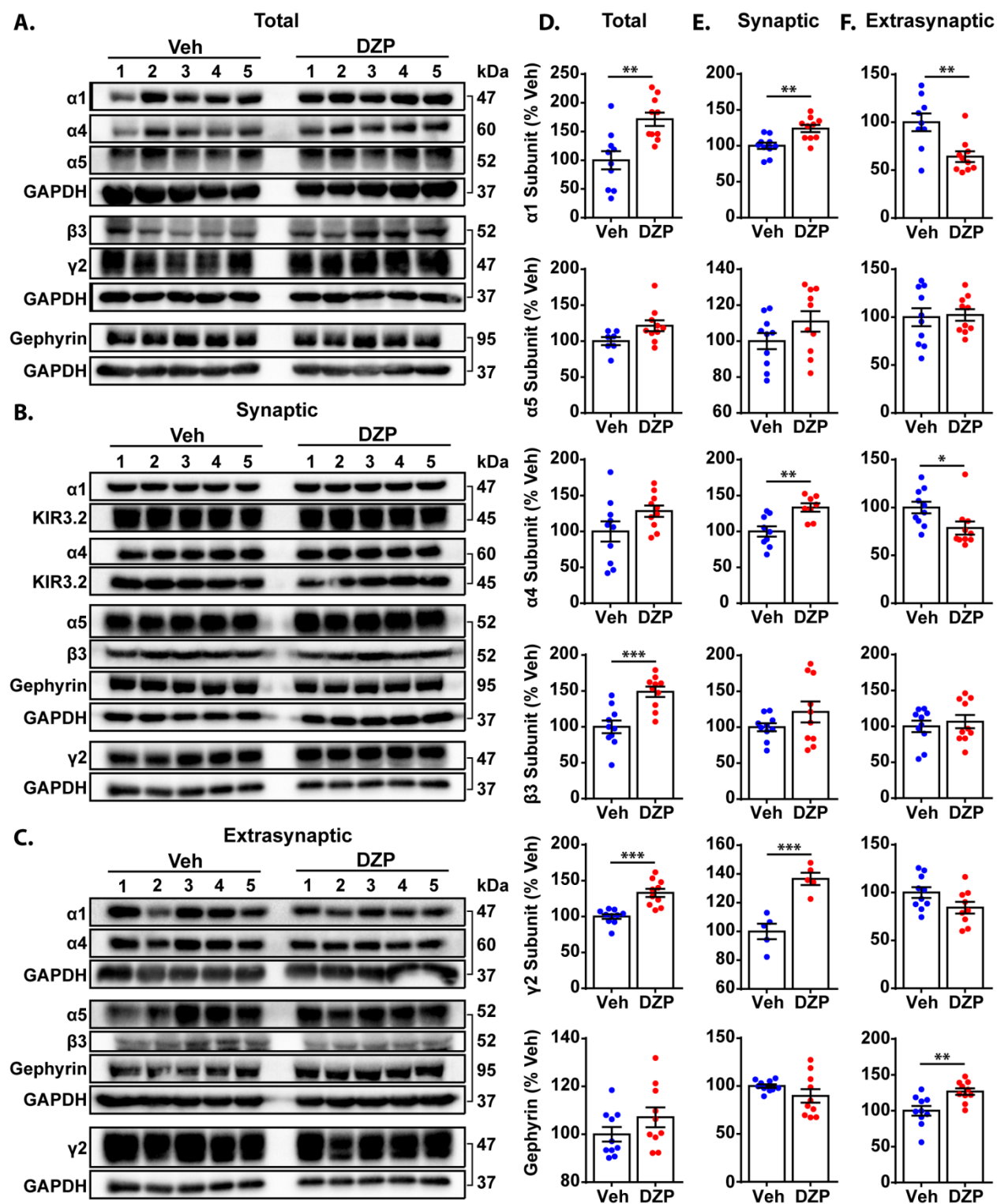


Figure 24. GABA_AR Subunits and Gephyrin are Altered by Seven Day DZP Treatment *In Vivo*.

Mice treated IP once daily for seven days with vehicle or DZP were assessed for GABA_AR subunit and gephyrin cortical tissue total (A), synaptic (B), and extrasynaptic levels (C) by western blot analysis. Representative blots show

mice 1-5 from each treatment. Quantification revealed a significant increase in the overall levels of $\alpha 1$, $\beta 3$, $\gamma 2$ subunits (D). Synaptic levels of (E) $\alpha 1$, $\alpha 4$ and $\gamma 2$ subunits were also enhanced, while extrasynaptically $\alpha 1$ and $\alpha 4$ were decreased (F). DZP also increased extrasynaptic gephyrin (* $p \leq 0.05$, ** $p < 0.01$, *** $p < 0.001$, Student's t-test; $n = 10$ mice per treatment (experimental error resulted in $n < 10$ for some measurements); error bars \pm S.E.M.).

(Fig. 24D). An increase in $\alpha 5$ subunit levels also approached statistical significance ($+21.4\% \pm 7.6$; $p = 0.054$). No change in $\alpha 4$ or gephyrin total levels was detected **(Fig. 24A,D)**. Synaptic fractions revealed an enrichment of $\alpha 1$ ($+24.1\% \pm 5.0$), the DZP-insensitive $\alpha 4$ subunit ($+33.4\% \pm 5.8$) and $\gamma 2$ ($+36.6\% \pm 4.3$) at synaptic sites **(Fig. 24B,E)**. The enhancement of $\alpha 1$ and $\alpha 4$ subunits in the synaptic fraction also occurred concomitantly with a significant reduction in the extrasynaptic pools of these subunits **(Fig. 23C,F)**, suggesting a recruitment of these subunits to synapses away from extrasynaptic sites during seven day DZP exposure. A significant increase in extrasynaptic gephyrin levels ($+26.7\% \pm 4.6$) was also detected, indicating inhibitory scaffold function or clustering may be altered as well.

Next we performed slice electrophysiology recordings to determine if the DZP-induced shift of $\alpha 1$ and $\alpha 4$ subunits away from the extrasynaptic space and into the synapse would alter tonic inhibition. Whole-cell patch clamp recordings in cortical slices were used to measure changes in the tonic current. Bath application of the GABA_AR pore blocker picrotoxin revealed a dramatic decrease in the tonic current of neurons from DZP treated mice compared to vehicle **(Fig. 25)**. Whole-cell current change, measured as a difference between baseline before and after picrotoxin application was used for control. These experiments revealed seven day DZP exposure produces a shift in synaptic GABA_AR composition where $\alpha 4$ and $\alpha 1$ subunits are

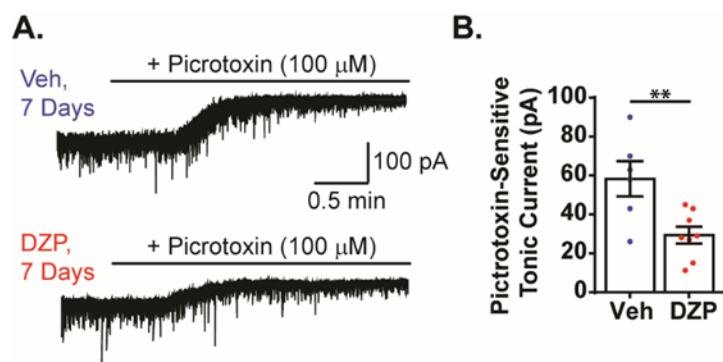


Figure 25. Tonic Inhibition is Reduced in DZP Treated Mice.

(A) Picrotoxin-sensitive changes in holding current were used to measure tonic inhibition in cortical slices from vehicle or DZP treated mice. (B) Quantification revealed a significant reduction in DZP (n = 8) treated animals tonic inhibition relative to vehicle (n = 6) injected mice (**p ≤ 0.01, Student's t-test; error bars ± S.E.M.).

elevated and a corresponding reductions of these subunits at extrasynaptic sites occurs concurrent with decreased baseline tonic inhibition.

4.3.3 DZP Treatment Increases NMDA Receptor Levels and Function

Given the neuroadaptations seen in inhibitory GABA_AR subunit synaptic proteins and prior evidence for glutamatergic system sensitization in the development of BZD tolerance, we hypothesized that an equivalent increase in excitation may also occur to achieve appropriate E/I balance in a homeostatic manner. Moreover, previous studies link enhanced NMDAR function to various types of drug tolerance (346-348), including evidence it has a role in DZP behavioral sedative tolerance (349, 350). We examined the subunit levels of this receptor after seven day DZP treatment. Analysis revealed increased total levels of GluN2A (+17.8% ± 4.7) and GluN2B (+53.7% ± 13.4) subunits in the cortex of DZP treated mice relative to vehicle (**Fig. 26A,C**) with an enrichment of GluN2A subunit (21.6 ± 4.1) at synapses (**Fig. 26B, D**). Collectively this data

suggests compensatory upregulation of excitatory receptors occurs after DZP exposure. Next we examined functional changes in excitatory neurotransmission by first measuring AMPA miniature excitatory postsynaptic currents (mEPSC) (**Fig. 27A**). We found no significant difference between treatment groups in AMPA mEPSC amplitude (**Fig. 27B**), frequency (**Fig. 27C**) and tau (**Fig. 27D**), suggesting pre- and post-synaptic mechanisms regulating AMPA receptor activation were not altered by seven day DZP exposure. In contrast, we found that the AMPA/NMDA ratio in DZP treated mice was nearly half that of vehicle in evoked excitatory postsynaptic current (eEPSC) measurements (**Fig. 27E,F**), consistent with upregulation of NMDAR functional activity. Together these functional results, combined with biochemical data indicate GluN2A and GluN2B NMDAR subunit upregulation, enhanced synaptic GluN2A levels and increased NMDAR activity following seven day DZP injections.

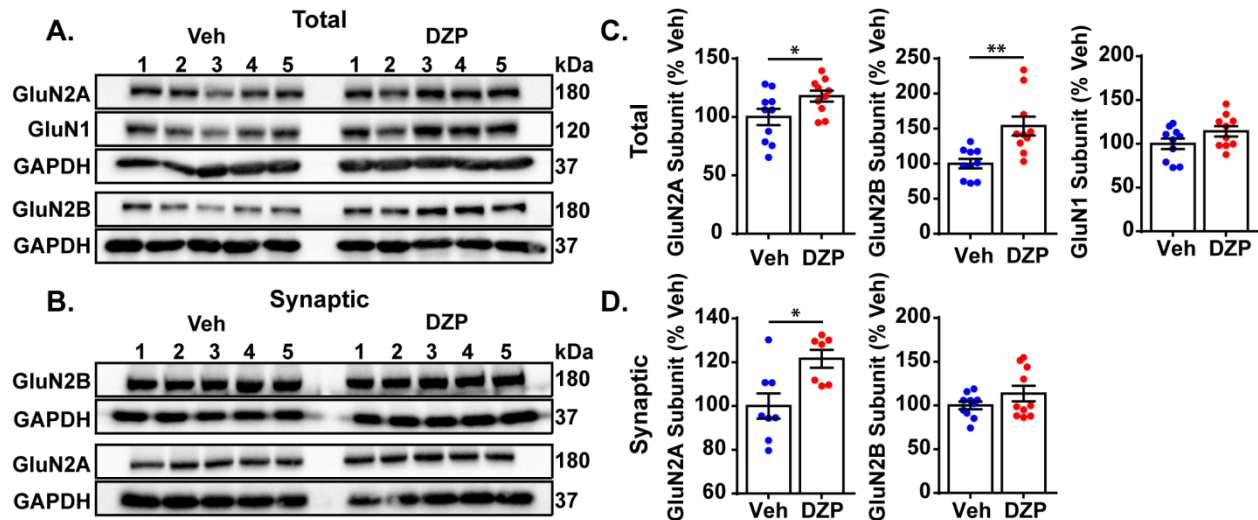


Figure 26. NMDA Receptor Subunit Levels are Increased by Seven Day DZP Treatment *In Vivo*.

Mice treated IP once daily for seven days with vehicle or DZP were assessed for NMDA receptor subunit cortical tissue total (A) and synaptic (B) levels by western blot analysis. Representative blots for mice 1-5. Quantification revealed a significant increase in the overall levels of the GluN2A and GluN2B subunits (C). GluN2A synaptic levels were also found to be significantly enhanced after DZP exposure (D) (* $p \leq 0.05$, ** $p < 0.01$, Student's t-test; $n = 10$ mice per treatment (experimental error resulted in $n < 10$ for some measurements); error bars \pm S.E.M.).

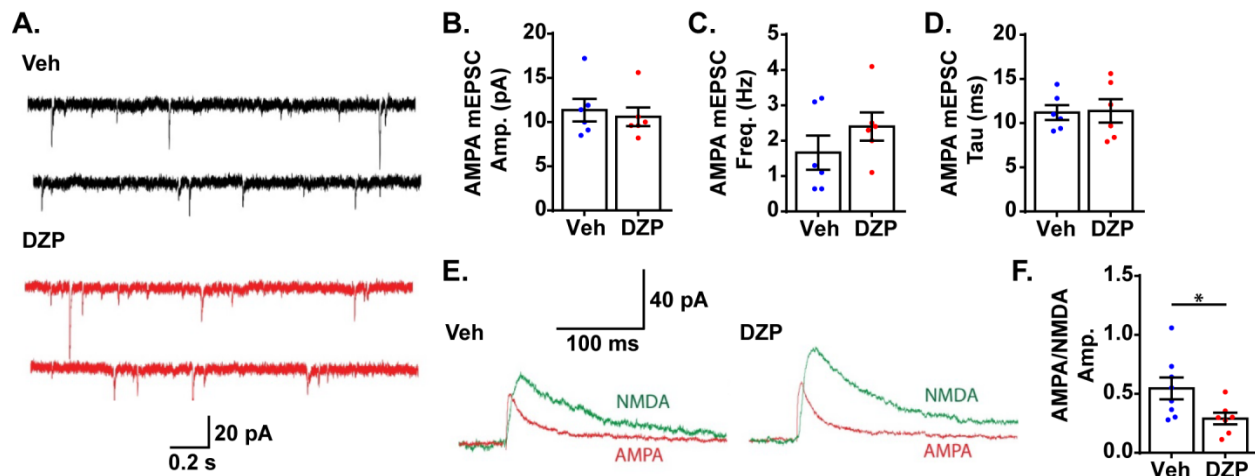


Figure 27. NMDAR Function is Increased in DZP Treated Mice.

(A) AMPAR EPSC traces in vehicle (black) and DZP (red) treated animals ($V_{\text{hold}} = -70$ mV). (B) AMPAR mEPSC (B) amplitude, (C) frequency and (D) decay were unchanged at day seven of DZP treatment ($n=6$). (* $p \leq 0.05$, Student's t-test; error bars \pm S.E.M.). (E,F) The AMPA/NMDA ratio ($V_{\text{hold}} = +40$ mV) was significantly lower ($p < 0.05$, Student's t test) in DZP treated ($n = 7$) compared to vehicle-treated mice ($n = 8$).

4.3.4 Inhibitory and Excitatory Proteins Adaptions Occur at Earlier DZP Timepoints

To determine if key inhibitory and excitatory proteins altered after seven day DZP treatment are also changed at earlier stages of drug exposure, we tested the cortical tissue of mice treated for a 24 h period (two treatments) or 72h period (four treatments) with vehicle or DZP. This experiment revealed a significant increase in total GABA_AR $\alpha 1$ ($+49.5\% \pm 16.0$), $\alpha 4$ ($+25.3\% \pm 5.5$) and $\alpha 5$ ($+32.0\% \pm 4.4$) subunits after 24 h DZP exposure relative to vehicle (**Fig. 28A,B**). GABA_AR $\beta 3$ subunit, $\gamma 2$ subunit, and gephyrin were not significantly altered. Increased $\alpha 1$ subunit levels persisted across 72 h of DZP treatment, while $\alpha 4$ and $\alpha 5$ subunits were not detectably different than vehicle. Notably, $\beta 3$ and $\gamma 2$ subunit overall levels were enhanced at 72 h in the DZP treated group, consistent with findings at day seven (**Fig. 24**).

The excitatory NMDA receptor subunit GluN2A was upregulated after 24 h of DZP treatment ($+21.1\% \pm 4.4$), without a detectable change in GluN1 or GluN2B subunits (**Fig. 28C,D**). In contrast, DZP elevated the GluN1 ($+30.3\% \pm 3.3$) and GluN2B ($+35.2\% \pm 11.8$) subunits after 72 h, but the GluN2A subunit returned to vehicle levels.

Collectively, these results suggest that GABA_AR subunits found to be elevated after seven day DZP treatment can be detected at higher levels earlier in the DZP treatment timeline axis. Notably the GABA_AR $\alpha 1$ subunit is elevated as early as the 24 h time point and persists through day seven. NMDA receptor subunits are also found to be differentially increased at earlier DZP treatment time points, suggesting NMDA receptor plasticity at multiple stages following drug exposure.

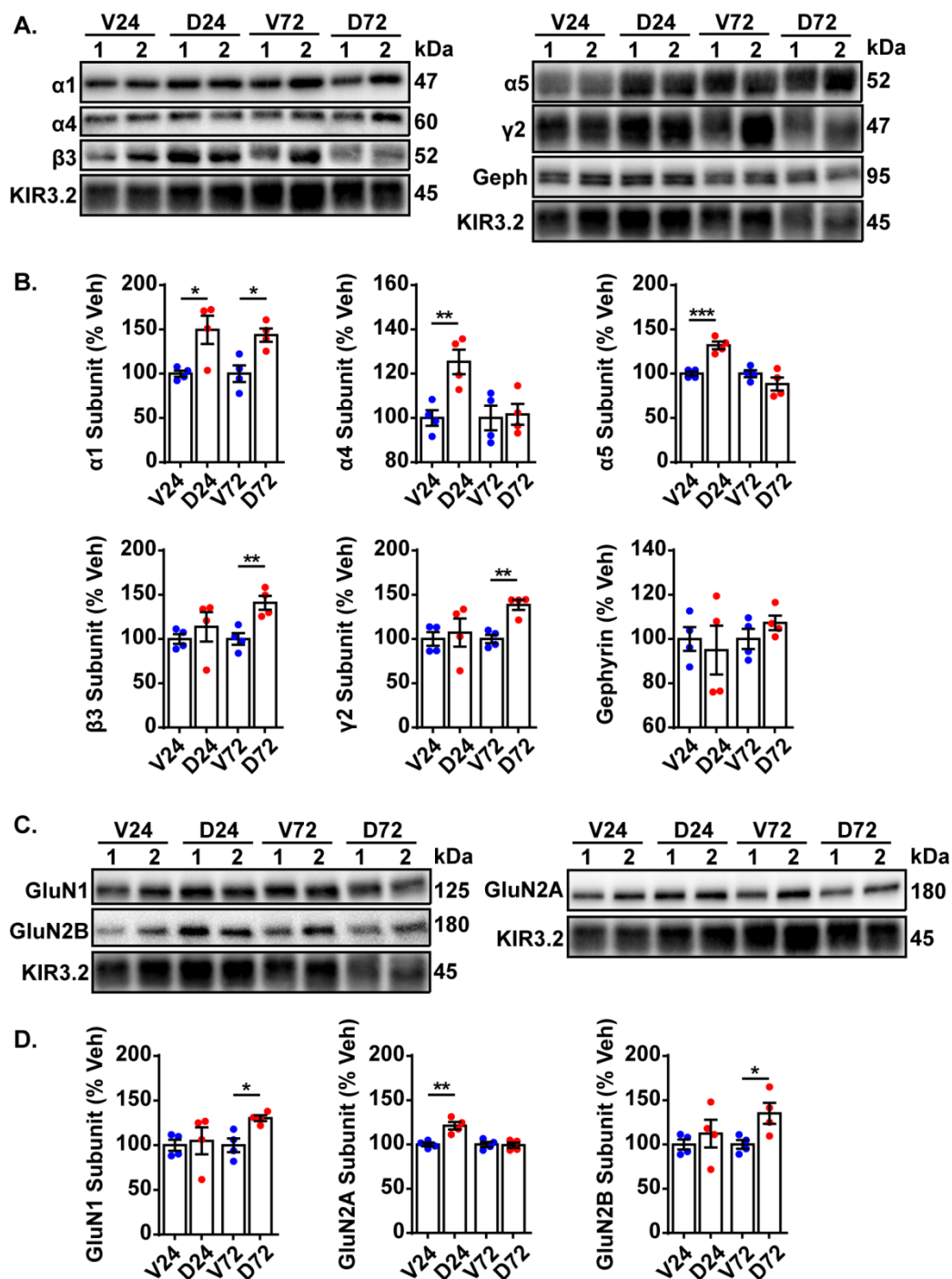


Figure 28. Key Inhibitory and Excitatory Proteins are Upregulated at Earlier DZP Treatment Timepoints.

Mice were treated with DZP or vehicle for 24 h (two doses) or 72 h (four doses). Total cortical lysates of GABA_AR subunits and gephyrin (A,B) and NMDAR subunits (C,D) were examined by western blot. Representative blots for mice 1-2 from each treatment. Quantification revealed significantly increased levels of $\alpha 1$, $\alpha 4$ and $\alpha 5$ GABA_AR subunits and NMDAR GluN2A subunit after 24 h DZP. The $\alpha 1$ subunit remained elevated after 72 h DZP treatment,

while $\alpha 4$, $\alpha 5$ and GluN2A subunits returned to vehicle levels. Conversely, the GABA_AR subunits $\beta 3$ and $\gamma 2$, and NMDAR subunits GluN2B and GluN1, were increased at the 72 h DZP treatment time point (* $p \leq 0.05$, ** $p < 0.01$, *** $p < 0.001$, Student's t-test; $n = 4$ mice per treatment; error bars \pm S.E.M.).

4.3.5 Quantitative Mass Spectrometry Identifies Changes in Neuronal Synaptic

Proteome with DZP Treatment

Changes in the major GABA_AR and NMDAR subunits contributing to inhibitory and excitatory neurotransmission are only a small fraction of the possible signaling network altered by DZP treatment. To gain a more comprehensive understanding of the protein profile of a DZP tolerant brain, we performed a quantitative proteomic screening against 500+ key synaptic proteins in vehicle versus DZP treated cortical tissue. This experiment identified a total of 962 unique peptides across 10 vehicle and 10 DZP samples. The peptide abundance of proteins in the DZP group compared to vehicle was used to determine which proteins were increased (**Table 4**) or decreased (**Table 5**). As a result we identified 108 protein peptides with elevated levels of interaction in seven day DZP treated animals, while 16 protein peptides were decreased. These experiments revealed robust changes in the Ca²⁺/calmodulin-dependent protein kinase II (CaMKII), a dodecameric holoenzyme that regulates key processes including synaptic plasticity. CaMKII is expressed in four isoforms $\alpha/\beta/\delta/\gamma$, with α and β being the most highly expressed in the forebrain at a ratio of about three α per β subunit (368). Individual CAMKII subunits can have distinct regulatory properties (369), localization (370), and developmental expression in neurons, for instance the δ and γ subunits are highly and selectively expressed early in development but strongly decrease in expression over time (371). Here we identified highly elevated peptide levels

of the α , β and δ subunits in cortical tissue of DZP treated mice, suggesting a global upregulation of CaMKII function or activity (**Table 4**).

Protein kinase C (PKC) is critical for NMDAR function and trafficking alongside CaMKII (372, 373), and PKC epsilon (1.20 fold increase, $p = 0.0060$) and gamma (1.30 fold increase, $p = 0.026$) isozymes were significantly enriched in DZP treated mice (**Table 4**). PKC ϵ reduces GABA $_A$ R sensitivity to ethanol and BZDs *in vitro* and *in vivo* by phosphorylating the $\gamma 2$ subunit S327 residue (150), while PKC γ is critical in tolerance mechanisms to other drugs like opioids (374, 375). DZP also significantly increased the levels of the growth associated protein 43 (GAP-43) (1.50 fold increase, $p = 0.019$) (**Table 4**) which is involved in excitatory neuron driven epileptogenesis (376), is integral for growth cone dynamics (377-379) and PKC phosphorylation of GAP-43 promotes excitatory long-term potentiation (380, 381). Increased levels of other pro-excitatory synapse proteins including discs large MAGUK scaffold protein 2 (DLGAP2) (382) (1.20 fold increase, $p = 0.027$) and the protein tyrosine kinase 2 beta (FAK2/CAK β /Pyk2) (1.30 fold increase, $p = 0.0036$) were also measured. FAK2 can be recruited to excitatory synapses to mediate PSD-95 scaffolding maintenance, promotes NMDA receptor levels, upregulate NMDAR function by activating Src and is involved in long term potentiation (LTP) (383-386).

Interestingly, DZP evoked presynaptic plasticity is also suggested by increases in piccolo peptides (1.60 fold increase, $p = 0.033$), which functions as a large scaffold protein that redundantly contributes to the synaptic vesicle readily releasable pool with bassoon (387). Importantly, combined knockdown of piccolo and bassoon does not affect basic synaptic vesicle release (387, 388). The synaptotagmin 7 (SYT7) and 1 (SYT1) proteins were also enriched in DZP treated animals. SYT7 is a major regulator of the readily releasable neurotransmitter pool and was recently identified to work postsynaptically with SYT1 in hippocampal neurons as

redundant Ca^{2+} -sensors for Ca^{2+} -dependent exocytosis of AMPA-receptors during LTP (389), although no change in mEPSCs was detected. Combined knockout of SYT1 and SYT7 is needed to block LTP, and SYT1/SYT7 double knockout does not alter mEPSCs, suggesting no change in baseline synaptic AMPAR activity, consistent with our electrophysiology data showing no changes in AMPAR mEPSC after DZP (**Fig. 27**). Elevated peptide levels of the membrane trafficking RAB3A protein (1.10 fold increase, $p = 0.0036$) were also measured, which regulates exocytosis of synaptic vesicles and is the most abundant RAB in the brain (390). Conversely, DZP animals exhibited decreased Dynamin 3 expression (**Table 5**), which is a large GTPase crucial for presynaptic endocytosis and neurotransmission (391), is a component of the metabotropic glutamate receptor excitatory postsynapse (392), and mediates developmental synaptogenesis (393).

Cyclic nucleotide (namely cAMP and cGMP) levels are tightly regulated by phosphodiesterases (PDEs) (394) and we identified a DZP-induced enrichment (1.40 fold increase, $p = 0.042$) of the PDE2 enzyme which is particularly key for the regulation of performance and cognitive functions (395, 396) and inhibition of this enzyme is a key target for ongoing cognitive therapies (397). Interestingly, a decrease in the GABA_AR subunit beta family (isoform 1/2/3) was determined by our analysis (**Table 5**). Our biochemical data predicts a significant increase in $\beta 3$ subunit levels, suggesting a decrease in either isoform $\beta 1$ and/or $\beta 2$, which is consistent with multiple studies showing decreased $\beta 2$ subunit mRNA after BZD exposure (32). We were unable to detect a statistically significant difference in other GABA_AR subunits or NMDAR subunits using our quantitative proteomics method in part due to variability and the limitations of our methodology in measuring hydrophobic membrane proteins (398).

Table 4. Protein Peptides Demonstrating Increased Levels after DZP Treatment by Mass Spectrometry.

Ratio D/V is fold change in DZP animals' relative peptide levels to control vehicle treated animals, t-test. Significant ($p < 0.05$) and near significant results ($p < 0.1$) shown.

| D/V | P-Value | Uniprot | Entrez Gene Name | Peptide Sequence | Location | Type(s) |
|-----|----------|---------|---|---------------------------|-----------------|-------------------------|
| 1.6 | 3.27E-02 | Q9QYX7 | piccolo presynaptic cytomatrix protein | ASPVPAPAEPPP QK | Cytoplasm | transporter |
| 1.6 | 6.57E-04 | P28652 | calcium/calmodulin dependent protein kinase II beta | FYFENLLAK | Cytoplasm | kinase |
| 1.6 | 4.01E-02 | Q9R0N7 | synaptotagmin 7 | VDLTQMQTFWK | Cytoplasm | transporter |
| 1.6 | 5.28E-02 | O35136 | neural cell adhesion molecule 2 | IIELSQTAK | Plasma Membrane | other |
| 1.5 | 5.61E-02 | P55095 | glucagon | AQDFVQWLMNT K | Cytoplasm | other |
| 1.5 | 1.63E-03 | Q6PHZ2 | calcium/calmodulin dependent protein kinase II delta | QETVDCLK | Cytoplasm | kinase |
| 1.5 | 3.69E-04 | P11798 | calcium/calmodulin dependent protein kinase II alpha | FTEEYQLFEELG K | Cytoplasm | kinase |
| 1.5 | 2.98E-04 | P11798 | calcium/calmodulin dependent protein kinase II alpha | AGAYDFPSPEW DTVTPEAK | Cytoplasm | kinase |
| 1.5 | 3.46E-04 | P11798 | calcium/calmodulin dependent protein kinase II alpha | VLAQGEYAAK | Cytoplasm | kinase |
| 1.5 | 1.88E-02 | P06837 | growth associated protein 43 | QADVPAAVTDA AATTAAEDAAT K | Plasma Membrane | other |
| 1.4 | 1.11E-03 | P28652 | calcium/calmodulin dependent protein kinase II beta | FTDEYQLYEDIG K | Cytoplasm | kinase |
| 1.4 | 3.70E-03 | Q6PHZ2 | calcium/calmodulin dependent protein kinase II delta | FTDEYQLFEELG K | Cytoplasm | kinase |
| 1.4 | 1.49E-03 | P11798 | calcium/calmodulin dependent protein kinase II alpha | ITAAEALK | Cytoplasm | kinase |
| 1.4 | 1.16E-03 | P11798 | calcium/calmodulin dependent protein kinase II alpha | VTEQLIEAISNGD FESYTK | Cytoplasm | kinase |
| 1.4 | 9.09E-02 | Q91XM9 | discs large MAGUK scaffold protein 2 | VNEVDVSEVSH SK | Plasma Membrane | kinase |
| 1.4 | 1.44E-02 | P46096 | synaptotagmin 1 | LTVVILEAK | Cytoplasm | transporter |
| 1.4 | 4.26E-02 | Q922S4 | phosphodiesterase 2A | EFFSQGDLEK | Cytoplasm | enzyme |
| 1.4 | 6.94E-02 | Q6P9K8 | CASK interacting protein 1 | VGYFPSSLGEAI VK | Nucleus | transcription regulator |
| 1.4 | 6.25E-02 | Q80Z24 | neuronal growth regulator 1 | CYLEDGASK | Plasma Membrane | other |
| 1.3 | 4.26E-02 | Q922D8 | methylenetetrahydrofolate dehydrogenase, cyclohydrolase and formyltetrahydrofolate synthetase 1 | GDLNDCFIPCTP K | Cytoplasm | enzyme |
| 1.3 | 6.86E-02 | Q9CS84 | neurexin 1 | SADYVNLALK | Plasma Membrane | transporter |
| 1.3 | 4.93E-02 | Q9Z140 | copine 6 | SDPFMEIYK | Plasma Membrane | transporter |
| 1.3 | 5.14E-02 | P60879 | synaptosome associated protein 25 | FCGLCVCPCK | Plasma Membrane | transporter |
| 1.3 | 3.60E-03 | Q9QVP9 | protein tyrosine kinase 2 beta/proline-rich tyrosine kinase 2 | DMPHNALDK | Cytoplasm | kinase |

Table 4. Continued

| | | | | | | |
|-----|----------|---------|---|-----------------------|---------------------|-----------------------|
| 1.3 | 8.31E-02 | P46660 | internexin neuronal intermediate filament protein alpha | NLQSAEEWYK | Cytoplasm | other |
| 1.3 | 1.61E-02 | P08551 | neurofilament light | NMQNAEEWFK | Cytoplasm | other |
| 1.3 | 7.76E-02 | P06837 | growth associated protein 43 | EGDGSATTDAA PATSPK | Plasma Membrane | other |
| 1.3 | 3.20E-02 | Q8CHH9 | septin 8 | SLSLGGHVGFD SLPDQLVSK | Extracellular Space | other |
| 1.3 | 4.17E-02 | Q8R3V5 | SH3 domain containing GRB2 like, endophilin B2 | VEEFLYEK | Cytoplasm | other |
| 1.3 | 3.92E-02 | P46096 | synaptotagmin 1 | VPYSELGGK | Cytoplasm | transporter |
| 1.3 | 9.14E-02 | O35526 | syntaxin 1A | HSAILASPNPDE K | Cytoplasm | transporter |
| 1.3 | 8.00E-03 | Q9Z1G4 | ATPase H ⁺ transporting V0 subunit a1 | QAEIENPLEDPV TGDYVHK | Cytoplasm | transporter |
| 1.3 | 2.63E-02 | P63318 | protein kinase C gamma | GSDELYAIK | Cytoplasm | kinase |
| 1.2 | 8.66E-02 | A2A9R6 | ELAV like RNA binding protein 4 | DANLYVSGLPK | Cytoplasm | translation regulator |
| 1.2 | 2.72E-02 | Q8BJ42 | DLG associated protein 2 | SSWSTLTVSQA K | Plasma Membrane | other |
| 1.2 | 7.60E-03 | Q9JME5 | adaptor related protein complex 3 subunit beta 2 | LLTQYVLSLAK | Cytoplasm | transporter |
| 1.2 | 1.22E-02 | Q8BUV3 | gephyrin | TLIINLPGSK | Plasma Membrane | enzyme |
| 1.2 | 8.44E-02 | Q922S4 | phosphodiesterase 2A | ATDQVVALACAF NK | Cytoplasm | enzyme |
| 1.2 | 9.81E-02 | P46097 | synaptotagmin 2 | VFLLPDK | Cytoplasm | transporter |
| 1.2 | 2.11E-02 | Q3TXX4 | solute carrier family 17 member 7 | YIEDAIGESAK | Plasma Membrane | transporter |
| 1.2 | 2.51E-02 | P25444 | ribosomal protein S2 | TYSYLTPDLWK | Cytoplasm | other |
| 1.2 | 9.67E-02 | P53994 | RAB2A, member RAS oncogene family | YIIIGDTGVGK | Cytoplasm | enzyme |
| 1.2 | 1.51E-02 | P46460 | N-ethylmaleimide sensitive factor, vesicle fusing ATPase | GILLYGPPGCGK | Cytoplasm | transporter |
| 1.2 | 6.90E-02 | Q9CQC9 | secretion associated Ras related GTPase 1B | LVFLGLDNAGK | Cytoplasm | enzyme |
| 1.2 | 1.14E-02 | P35276 | RAB3D, member RAS oncogene family | LVDIICDK | Cytoplasm | enzyme |
| 1.2 | 6.55E-02 | Q01097 | glutamate ionotropic receptor NMDA type subunit 2B | VFASTGYGIAIQ K | Plasma Membrane | ion channel |
| 1.2 | 5.96E-03 | P16054 | protein kinase C epsilon | DFIWGVIGK | Cytoplasm | kinase |
| 1.2 | 6.29E-02 | P58281 | OPA1 mitochondrial dynamin like GTPase | VVVVGDSAGK | Cytoplasm | enzyme |
| 1.2 | 8.40E-03 | Q91V41 | RAB14, member RAS oncogene family | TGENVEDAFLEA AK | Cytoplasm | enzyme |
| 1.2 | 7.25E-02 | Q9WUK 2 | eukaryotic translation initiation factor 4H | GFCYVEFDEVD SLK | Cytoplasm | translation regulator |
| 1.2 | 4.51E-02 | Q8BMS1 | hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit alpha | FVDLYGAQK | Cytoplasm | enzyme |
| 1.2 | 5.28E-02 | P63318 | protein kinase C gamma | ITDFGMCK | Cytoplasm | kinase |
| 1.2 | 6.06E-02 | Q925E7 | protein phosphatase 2 regulatory subunit Bdelta | FLESPDFQPNIA K | Nucleus | other |

Table 4. Continued

| | | | | | | |
|-----|----------|--------|--|-------------------|-----------------|-------------|
| 1.2 | 3.69E-02 | P46460 | N-ethylmaleimide sensitive factor, vesicle fusing ATPase | TTIAQQVK | Cytoplasm | transporter |
| 1.2 | 2.70E-02 | Q91V92 | ATP citrate lyase | FGGALDAAAK | Cytoplasm | enzyme |
| 1.2 | 6.57E-02 | P31324 | protein kinase cAMP-dependent type II regulatory subunit beta | VVDVIGTK | Cytoplasm | kinase |
| 1.2 | 1.59E-02 | Q80TJ1 | calcium dependent secretion activator | DIVTPVPQEEVK | Plasma Membrane | other |
| 1.2 | 7.03E-02 | P60766 | cell division cycle 42 | WVPEITHHCPK | Plasma Membrane | enzyme |
| 1.2 | 4.32E-02 | P47857 | phosphofructokinase, muscle | VLVVHDFEGLAK | Cytoplasm | kinase |
| 1.2 | 2.73E-02 | P28474 | alcohol dehydrogenase 5 (class III), chi polypeptide | GTAFGGWK | Cytoplasm | enzyme |
| 1.2 | 8.97E-02 | Q6PGN3 | doublecortin like kinase 2 | TAHSFEQVLTDITEAIK | Cytoplasm | kinase |
| 1.1 | 6.85E-03 | Q9CVB6 | actin related protein 2/3 complex subunit 2 | IIEETLALK | Cytoplasm | other |
| 1.1 | 7.61E-02 | O08539 | bridging integrator 1 | LNQNLNDVLVSL EK | Nucleus | other |
| 1.1 | 2.42E-02 | Q76MZ3 | protein phosphatase 2 scaffold subunit Aalpha | VLELDNVK | Cytoplasm | phosphatase |
| 1.1 | 7.81E-03 | P62761 | visinin like 1 | STEFNEHELK | Cytoplasm | other |
| 1.1 | 7.33E-02 | P17710 | hexokinase 1 | FLLSESGSGK | Cytoplasm | kinase |
| 1.1 | 4.10E-02 | P14869 | ribosomal protein lateral stalk subunit P0 | TSFFQALGITTK | Cytoplasm | other |
| 1.1 | 5.69E-02 | O88935 | synapsin I | IHGEIDIK | Plasma Membrane | transporter |
| 1.1 | 5.65E-02 | O88935 | synapsin I | TYATAEPFIDAK | Plasma Membrane | transporter |
| 1.1 | 2.83E-02 | P63011 | RAB3A, member RAS oncogene family | LVDVICEK | Cytoplasm | enzyme |
| 1.1 | 4.81E-02 | Q62351 | transferrin receptor | DAWGPGAAK | Plasma Membrane | transporter |
| 1.1 | 5.65E-02 | Q63844 | mitogen-activated protein kinase 3 | DVYIVQDLMETD LYK | Cytoplasm | kinase |
| 1.1 | 9.08E-02 | Q9CQE8 | RNA transcription, translation and transport factor | NFIVWLEDQK | Nucleus | other |
| 1.1 | 8.04E-02 | P11499 | heat shock protein 90 alpha family class B member 1 | YESLTDPSK | Cytoplasm | enzyme |
| 1.1 | 2.01E-02 | P17710 | hexokinase 1 | NILIDFTK | Cytoplasm | kinase |
| 1.1 | 2.48E-02 | Q63844 | mitogen-activated protein kinase 3 | APEIMLNSK | Cytoplasm | kinase |
| 1.1 | 9.53E-02 | Q8K0T0 | reticulon 1 | SVLQAVQK | Cytoplasm | other |
| 1.1 | 9.69E-02 | Q76MZ3 | protein phosphatase 2 scaffold subunit Aalpha | LTQDQDQDVVK | Cytoplasm | phosphatase |
| 1.1 | 9.26E-02 | P70168 | karyopherin subunit beta 1 | SSAYESLMEIVK | Nucleus | transporter |
| 1.1 | 5.94E-02 | P62827 | RAN, member RAS oncogene family | LVLVGDDGGTGK | Nucleus | enzyme |
| 1.1 | 5.75E-02 | P68254 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein theta | YDDMATCMK | Cytoplasm | other |
| 1.1 | 7.56E-02 | P39053 | dynammin 1 | LQSQLLSIEK | Cytoplasm | enzyme |

Table 4. Continued

| | | | | | | |
|-----|----------|--------------------|--|----------------------------------|-----------------|-----------------------|
| 1.1 | 7.43E-02 | P68368 | tubulin alpha 4a | TIGGGDDSF _{TT} FCETGAGK | Cytoplasm | other |
| 1.1 | 9.39E-02 | P40124 | cyclase associated actin cytoskeleton regulatory protein 1 | NSLDCEIVSAK | Plasma Membrane | other |
| 1.1 | 2.46E-02 | P62631 | eukaryotic translation elongation factor 1 alpha 2 | QLIVGVNK | Cytoplasm | translation regulator |
| 1.1 | 1.16E-02 | P49615 | cyclin dependent kinase 5 | DLLQNLLK | Nucleus | kinase |
| 1.1 | 4.38E-02 | Q7TMM ₉ | tubulin beta 2A class IIa | INVYYNEAAGNK | Cytoplasm | other |
| 1.1 | 9.45E-02 | P05213 | tubulin alpha 1b | SIQFVDWCPTGF _K | Cytoplasm | other |
| 1.1 | 6.81E-02 | Q8CHC4 | synaptojanin 1 | NQTLTDWLLDA _{PK} | Cytoplasm | phosphatase |
| 1.1 | 2.10E-02 | P68369 | tubulin alpha 1a | GHYTIGK | Cytoplasm | other |
| 1.1 | 9.94E-02 | P39054 | dynammin 2 | LQSQLLSLEK | Plasma Membrane | enzyme |
| 1.1 | 3.91E-02 | P84078 | ADP ribosylation factor 1 | DAVLLVFANK | Cytoplasm | enzyme |

Table 5. Protein Peptides Demonstrating Decreased Levels after DZP Treatment by Mass Spectrometry.

Ratio D/V is fold change in DZP animals' relative peptide levels to control vehicle treated animals, t-test. Significant ($p < 0.05$) and near significant results ($p < 0.1$) shown.

| D/V | P-Value | Uniprot | Entrez Gene Name | Peptide Sequence | Location | Type(s) |
|-----|----------|---------|---|----------------------|-----------------|-------------------------|
| 0.6 | 1.65E-02 | Q8BZ98 | dynamin 3 | RPLVLQLVTSK | Cytoplasm | enzyme |
| 0.7 | 4.19E-02 | P63080 | gamma-aminobutyric acid type A receptor beta1/2/3 subunit | VADQLWVPDT YFLNDK | Plasma Membrane | ion channel |
| 0.7 | 5.99E-02 | P61027 | RAB10, member RAS oncogene family | SFENISK | Cytoplasm | enzyme |
| 0.7 | 2.21E-02 | Q9D6M3 | solute carrier family 25 member 22 | GAAVNLTLPVTP EK | Cytoplasm | transporter |
| 0.7 | 8.23E-02 | P84096 | ras homolog family member G | YLECSALQQD GVK | Cytoplasm | enzyme |
| 0.7 | 7.25E-02 | Q60597 | oxoglutarate dehydrogenase | VIPENGPAAQD PHK | Cytoplasm | enzyme |
| 0.7 | 3.36E-02 | P63038 | heat shock protein family D (Hsp60) member 1/HSP60 | GIIDPTK | Cytoplasm | enzyme |
| 0.8 | 8.65E-02 | P35436 | glutamate ionotropic receptor NMDA type subunit 2A | FSYIPEAK | Plasma Membrane | ion channel |
| 0.8 | 2.99E-02 | O08915 | aryl hydrocarbon receptor interacting protein | EGEIAQFLCDI K | Nucleus | transcription regulator |
| 0.9 | 9.43E-02 | P15105 | glutamate-ammonia ligase | ACLYAGVK | Cytoplasm | enzyme |
| 0.9 | 6.64E-02 | Q02053 | ubiquitin like modifier activating enzyme 1 | QFLDYFK | Cytoplasm | enzyme |
| 0.9 | 7.17E-02 | P05063 | aldolase, fructose-bisphosphate C | DNAGAATEEFI K | Cytoplasm | enzyme |
| 0.9 | 9.88E-02 | Q9D051 | pyruvate dehydrogenase E1 beta subunit | VVSPWNSEDA K | Cytoplasm | enzyme |
| 0.9 | 9.71E-02 | Q8BG32 | proteasome 26S subunit, non-ATPase 11 | EQSILELGSL AK | Cytoplasm | other |
| 0.9 | 1.71E-02 | P35979 | ribosomal protein L12 | QAQIEVVPSAS ALIIK | Nucleus | other |
| 0.9 | 5.53E-02 | P19096 | fatty acid synthase | AGLYGLPK | Cytoplasm | enzyme |

To gain a more complete understanding of the functional outcome of DZP-induced changes in the synaptic proteome, we subjected our quantitative proteomics data to IPA bioinformatics analysis. Top enriched canonical pathways with $-\log(p\text{-value}) > 6.2$ are shown in **(Fig. 29A)**. Analysis determined the synaptogenesis signaling pathway to be the most abundantly enriched and was predicted to be robustly upregulated as determined by z-score analysis. Synaptic LTP and CREB signaling in neurons pathways were also found to be activated, suggesting increased synaptic remodeling and strengthening of excitatory synapses, consistent with increased peptide levels for actin related protein 2/3 complex subunit 2 (ARP 2/3) **(Table 4)**, an important driver of

dendritic spine maturation and synapse unsilencing (399). Predicted activation of other interesting pathways including 14-3-3 mediated signaling, melatonin signaling and Huntington's disease signaling was also observed.

We further examined alterations in functional network association by checking the predicted activation status of select pathways when only using proteins which were found to be increased or decreased with a $p < 0.1$ (**Table 4,5**). Functional network association of key biological pathways (**Fig. 29B**) predicted activation of the release of neurotransmitter (z-score = 3.112), development of neurons (z-score = 2.886), and long-term potentiation (z-score = 1.902) pathways in DZP mice relative to vehicle control. Significant protein changes ($p < 0.05$) conserved between two or more pathways include increased peptide levels of CaMKII subunits α/β , PRKCG (PKC γ) and RAB3A. Taken together, these results suggest seven day DZP treatment *in vivo* results in synaptic remodeling, pre- and post-synaptic plasticity and strengthening of excitatory synapses.

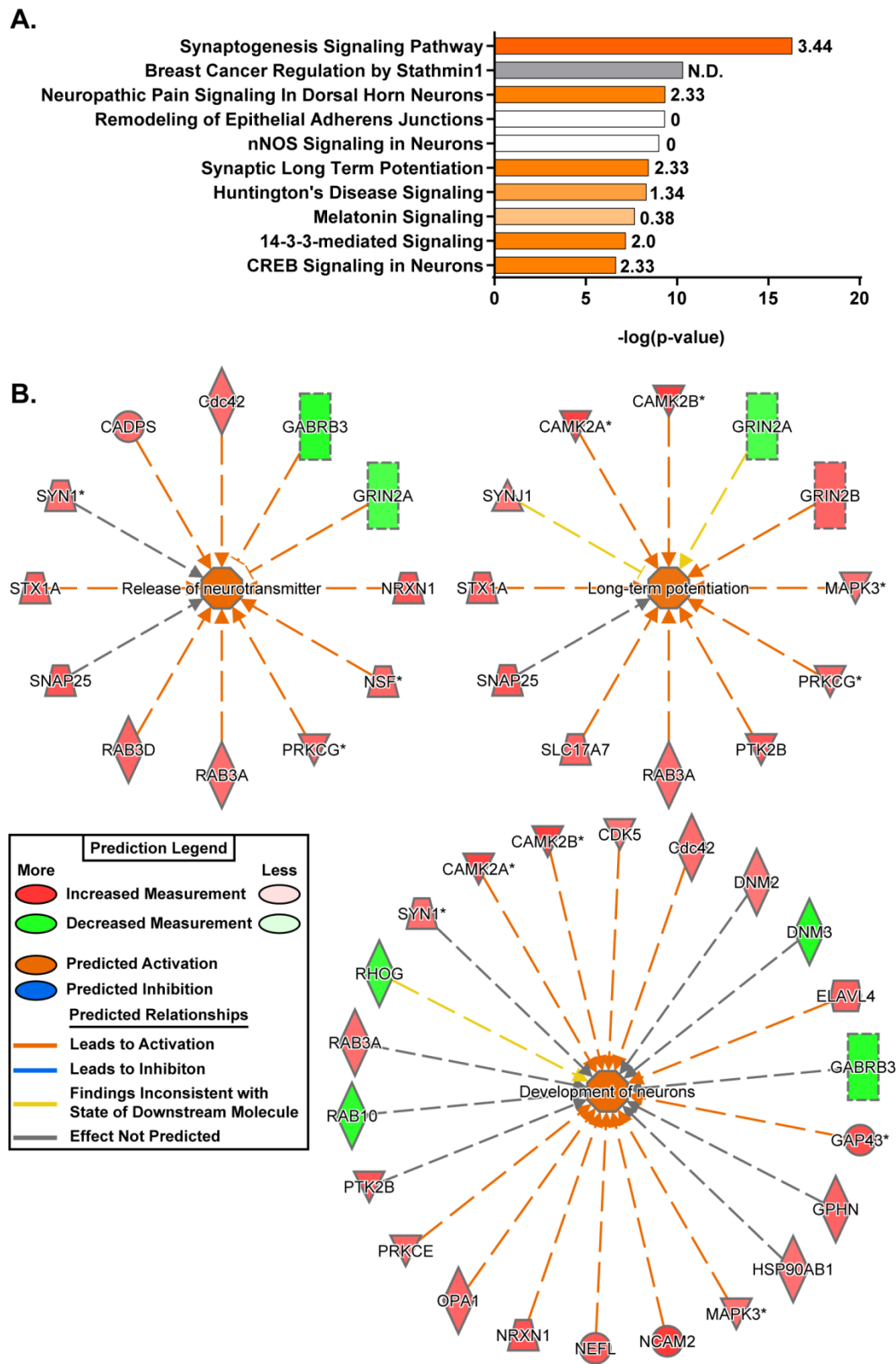


Figure 29. IPA Analysis Reveals Activation of Key Biological Networks Following DZP Treatment.

(A) Canonical pathways found to be differentially expressed following DZP administration *in vivo*. Enriched pathways with $-\log(p\text{-value})$ greater than 6.2 were considered as calculated by Fisher's exact test right-tailed. Values to right of bars represent pathway activation z-score. Positive z-score represents predicted upregulation of a pathway (orange), negative z-score predicts inhibition (blue), z-score = 0 represents no change in pathway (white), while not determined (N.D.) conveys the analysis program was unable to determine a significant change (grey). Intensity of color represents size of z-score value. (B) Functional network association of select pathways when using proteins which were found to be increased or decreased with a $p < 0.1$. Major functional pathways altered by DZP include release of neurotransmitter (z-score = 3.112), development of neurons (z-score = 2.886), and long-term potentiation (z-score = 1.902). Significant protein changes ($p < 0.05$) conserved between two or more pathways include increased peptide levels of CaMKII subunits α/β , PRKCG (PKC γ) and RAB3A. Red = increased measurement, green = decreased measurement, orange = activation of pathway, blue = inhibition of pathway, yellow = findings inconsistent with state of downstream molecule, grey = effect not predicted.

4.3.6 Western Blot Analysis of CaMKII Activation and Levels

To further validate the observed increase in CaMKII subunit peptide levels after DZP treatment in our proteomics data (**Table 4**), we performed western blot analysis on the cortical tissue of these mice. As an additional measure we also examined activation of CaMKII based on the phosphorylation state of the Thr286/287 residue, which is important for autonomous activation of the kinase (400), targeting to specific subcellular domains such as excitatory synapses (401) and regulation of LTP (402, 403). These experiments were unable to detect a statistical difference in the total $\alpha/\beta/\delta$ or Thr286/287 phosphorylation levels of α/β CaMKII (**Fig. 30A,B**). The inability to measure a change in CaMKII subunit levels equivalent to that seen in mass spectrometry experiments could be a result of the constraints of western blot analysis when considering antibody detection limitations and single molecular weight band measurements that may not comprehensively represent all forms of a protein including splice variants or various post-

translational modifications (368). Collectively, further tests will be needed to confirm that the alterations in CaMKII observed after DZP by proteomics are not false positive findings.

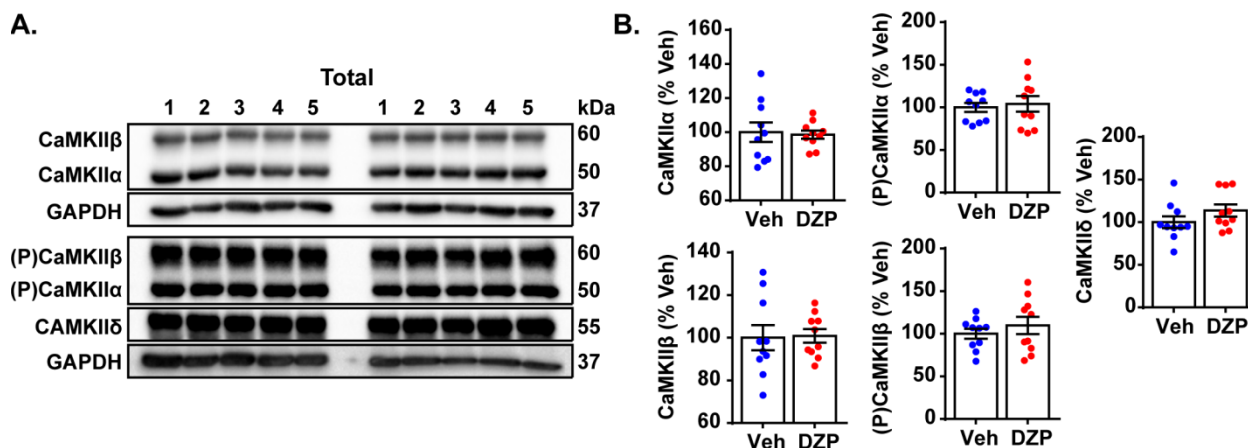


Figure 30. Western Blot Analysis was Unable to Detect a Change in CaMKII Subunit Expression after DZP.

Mice treated seven days with vehicle or DZP were assessed for phosphorylation status of CaMKII Thr286/287 residues and total CaMKII subunit cortical tissue levels (A). (B) Quantification revealed no change in phosphorylation or subunit levels of CaMKII (Student's t-test; $n = 10$ mice per treatment; error bars \pm S.E.M.).

4.4 Discussion

The neuroadaptive signature of a DZP tolerant brain has been elusive for researchers in part due to experimental limitations. Herein we find mice with tolerance to the sedative actions of DZP have modified GABA_AR subunit protein levels and localization in the cortex, highlighted by the DZP-insensitive $\alpha 4$ subunit and the highly abundant $\alpha 1$ subunit moving away from the extrasynaptic space into the synapse (**Fig. 24**). Slice electrophysiology experiments confirmed DZP insensitivity in animals treated for seven days with this drug, while no significant change in mIPSC amplitude was detected between treatments (**Fig. 23**). This suggests the total numbers of

GABA_ARs at synapses are not changed but a modification of the receptor pharmacological profile had occurred, consistent with increased incorporation of $\alpha 4$ into $\gamma 2$ GABA_ARs. Further supporting this proposed shift in GABA_AR subtypes away from the extrasynaptic space, DZP treated animals demonstrated a marked reduction in tonic inhibitory current (**Fig. 25**). Biochemical analysis of cortical tissue further revealed an enrichment of NMDAR subunits GluN2A and GluN2B (**Fig. 26**), culminating with an decrease in AMPA/NMDA ratio in slice electrophysiology studies without a change in AMPA mEPSCs (**Fig. 27**), suggesting overall increased NMDAR activity. Examining total levels of key inhibitory and excitatory proteins at earlier DZP treatment time points identified increases in GABA_AR $\beta 3$, $\gamma 2$ and NMDAR GluN2B subunit by day three of DZP exposure, concomitant with behavioral sedative tolerance (**Fig. 28**). Quantitative proteomic experiments screening hundreds of pivotal synaptic proteins in the cortex of vehicle versus DZP treated mice revealed upregulation of a number of proteins involved in synaptogenesis and remodeling, excitatory LTP and drug tolerance (**Table 4 and Fig. 29**). The most robust increase found by mass spectrometry was the pro-excitatory CaMKII kinase $\alpha/\beta/\delta$ subunit levels (**Table 4**), where all measured peptides were elevated by around 1.5 fold (number of peptides for CaMKII kinase $\alpha/\beta/\delta$ subunits were 4/2/2). Our inability to detect this by western blot analysis is likely due to methodological limitations including antibody specificity, limitations in sensitivity of measurements with highly abundant proteins, and single molecular weight band measurements (**Fig. 30**). In summary, our work demonstrates DZP sedative tolerance is associated with synaptic GABA_AR compositional changes, increased NMDAR levels and activity, enhanced expression of positive NMDAR modulators and synapse remodeling and excitatory synapse strengthening. These findings are clear factors that would contribute to a hyperexcitable and DZP-insensitive

brain state promoting symptoms observed during BZD withdrawal: heightened seizure susceptibility, anxiety, panic, and sleep disturbances.

One key finding in this study was the apparent shift in the $\alpha 4$ subunit to the synapse away from the extrasynaptic space. The $\alpha 4$ subunit does not bind classical BZD agonists like DZP, and receptor function is enhanced, rather than inhibited, by antagonists/inverse agonists at the BZD binding site and also is sensitive to modulation by neurosteroids, anesthetics, and ethanol (1, 219, 302, 404). Interestingly, the expression of the $\alpha 4$ subunit is highly malleable to a number of stimuli including alcohol exposure withdrawal (219, 405-407), progesterone-withdrawal (408, 409), social isolation in rats (410), electroshock seizures (411), absence seizures induced by gamma-hydroxybutyric acid (412) and pilocarpine-induced seizures (413). Chronic intermittent ethanol (CIE) treatments leads to a reduced behavioral hypnotic response to BZDs, associated with increased $\alpha 4$ and $\gamma 2$ total levels and decreased decay time of GABA_AR-mediated mIPSCs and potentiation by DZP (407). Similarly, we identified a DZP-induced increase in synaptic $\alpha 4$ and $\gamma 2$ subunit levels by western blot analysis (**Fig. 24**) coupled with minimal potentiation by DZP in electrophysiology studies (**Fig. 23**). Dorsal ganglion cells (DGCs) from temporal lobe epilepsy animal models also show diminished DZP responsiveness following accumulation of $\alpha 4$ at synaptic sites (414). Furthermore, electrophysiology recordings in hippocampal slices found an extrasynaptic to synaptic switch of $\alpha 4$ appears after CIE, demonstrating potentiation by RO 15-4513, which acts as a partial agonist at $\alpha 4/\gamma 2$ GABA_ARs, but functions as an inverse agonist at receptors with classical BZD pharmacology ($\alpha 1/\alpha 2/\alpha 5\beta 2$). This was further confirmed by electron microscopy studies identifying increased $\alpha 4$ but not δ subunit within GABAergic synapses. It is important to note RO 15-4513 has high selectivity for the $\alpha 5$ subunit over other alpha subunits, and is used as a relatively selective marker for $\alpha 5$ -GABA_AR subtypes (415-417). Interestingly,

rapid ethanol tolerance paradigms examining CA1 area slices show increased surface synaptic $\alpha 4$ levels, decreased DZP enhancement of mIPSCs and faster mIPSC kinetics after ethanol withdrawal (219). As the quantitative proteomic data here identified increased expression of the PKC ϵ and PKC γ isoforms (**Table 4**), this suggests a PKC mediated mechanistic link between increased synaptic $\alpha 4$ subunit observed biochemically (**Fig. 24**) and the decrease in tonic inhibition by electrophysiology (**Fig. 25**) after DZP. Future studies examining the synaptic composition of GABA $_A$ Rs *in vivo* will be needed to fully elucidate the role of $\alpha 4$ in DZP insensitivity.

Surprisingly, a similar extrasynaptic to synaptic accumulation was seen with the $\alpha 1$ subunit, which also demonstrated increased overall levels (**Fig. 24**). The majority of BZD-sensitive GABA $_A$ Rs in the brain contain the $\alpha 1$ subunit (418). The DZP sedative response is mediated by the $\alpha 1$ subunit as demonstrated by studies using knock-in mice expressing an $\alpha 1$ subunit H101R mutation, which disrupts BZD binding (366). Increased BZD-sensitive $\gamma 2$ -GABA $_A$ R internalization and trafficking *in vivo* has been implicated with sustained DZP exposure (270). Accordingly, increased expression of PKC γ (**Table 4**) in DZP treated mice may promote increased $\alpha 1$ -GABA $_A$ R internalization, as is seen with ethanol treatment (149). An elevated rate of extrasynaptic endocytosis of $\alpha 1$ receptors may also provide context to the observed reduction in GABA $_A$ R tonic current (**Fig. 25**). Additionally, the increase in total and synaptic GABA $_A$ R $\gamma 2$ subunit levels observed biochemically (**Fig. 24, Fig. 28**) may be an adaptive response to rescue inhibition as a result of augmented endocytosis rates of $\alpha 1$ -GABA $_A$ Rs and lead to incorporation of atypical GABA $_A$ R subtypes ($\alpha 4/\gamma 2$) at synapses.

Enhanced inhibition via DZP-mediated GABA $_A$ R potentiation would likely result in a homeostatic upregulation of excitation to restore E/I balance. Importantly, over the last twenty years, the majority of studies have focused on hippocampal plasticity found following 2 days of

BZD withdrawal, leaving the BZD adapted cortex before drug withdrawal relatively uncharacterized. Due to the many confounds and changes induced with the evolving hyperexcitability of the withdrawal state and the prolonged removal of BZD drugs, the glutamatergic receptor adaptations shown for sedative tolerance here may be distinct from withdrawal studies. For example, NMDAR currents are reduced in two day flurazepam withdrawn rats in the CA1 hippocampus (299, 419), potentially due to reduced GluN2B but not GluN2A receptor levels (420), while AMPAR-mediated miniature excitatory postsynaptic current (mEPSC) amplitude are diminished after one and two-day withdrawal (299, 421). Behaviorally, AMPAR current amplitude and anxiety-like behavior measured in the elevated plus-maze in one-day FZP-withdrawn rats is enhanced (422). GluN2B levels are not decreased after one day of flurazepam withdrawal, suggesting down regulation of NMDAR function does not occur until later (423). Conversely, a single *in vivo* dose of DZP increased the AMPA/NMDA current ratio in ventral tegmental area dopaminergic neurons that lasted up to 72 hours, suggesting brain region and time-dependent plasticity (354).

Here we identify in a seven day DZP treatment sedative tolerance paradigm, where animals are not in a withdrawal state, enhanced cortical NMDAR subunit levels by western blot analysis (**Fig. 26**) and decreased AMPA/NMDA amplitude ratio without changes in AMPA mEPSCs (**Fig. 27**), suggesting selectively increased NMDAR function. In agreement, behavioral data suggests co-administration of the highly potent competitive antagonist NMDAR CPP, but not the AMPAR antagonist GYKI 52466, prevents development of sedative behavioral tolerance after DZP in mice (349). MK801, a non-competitive NMDAR agonist also prevents the development of tolerance to locomotor effects (350) of DZP. These findings are consistent with a generalized role of increased

NMDAR function in tolerance to a number of pharmacological drug classes including opioids (346), ethanol (347) and barbiturates (348).

To gain a more holistic understanding of the mechanisms leading to DZP tolerance, both directly and indirectly related to the changes observed in our biochemical and electrophysiology findings, we performed a quantitative proteomics screen against 500+ key synaptic proteins. We found an enrichment in a number of kinase pathways associated with increased NMDAR function including elevated CaMKII subunit levels (424), PKC isozymes (372, 373) and protein tyrosine kinase 2 beta (383-385). Interestingly, CaMKII inhibition in two-day flurazepam withdrawn rats reverses increased AMPAR single-channel conductance (425). This was later connected to CaMKII α -mediated GluA1 Ser831 phosphorylation in the postsynaptic density of two-day FZP-withdrawn rats without changes in (P)T286 CaMKII α levels (426). This may suggest a general increase in CAMKII levels during both tolerance and withdrawal. This increase in CaMKII appears to occur after prolonged DZP treatment, as a single dose decreased transcript levels of CAMKII α in mice cortex (427), and our lab found decreased association of GABA_ARs with CAMKII α 12h following DZP injection (270).

Interestingly we found both the PKC γ isoform and CaMKII subunits to be increased after seven day DZP treatment. Multiple studies implicate both of these kinases as essential for the generation and maintenance of opioid tolerance and dependence (374, 428-435). PKC activation by 4beta-phorbol-12,13-dibutyrate (PDBu; 100nM, 10 min) in endogenous GABA_ARs of NT2-N neurons caused a rightward shift of the concentration-response curve for DZP positive allosteric enhancement without affecting the maximal response, suggesting decreased allosteric coupling of DZP and GABA sites (436). Our proteomic studies also found elevated PKC ϵ isozyme levels after DZP (**Table 4**), which has been described to reduce GABA_AR sensitivity to ethanol and BZDs *in*

vitro and *in vivo* by acting at a $\gamma 2$ S327 residue (150) and negatively regulates cell surface GABA_ARs levels through the membrane fusion ATPase N-ethylmaleimide-sensitive factor (NSF) (437). Importantly, a significant increase in NSF protein peptides after DZP exposure was also seen (**Table 4**). Both PKC γ and PKC ϵ knock-out mice exhibit altered ethanol potentiation of GABA_AR mediated Cl⁻ flux (438), where chronic ethanol consumption decreases association of PKC γ association with $\alpha 1$ but increases its association with $\alpha 4$ (439). Short (4 h) ethanol exposure induces internalization of $\alpha 1$ -containing GABA_ARs (149) coinciding with an increase in surface levels of the $\alpha 4$ subunit (440) with both adaptations occurring in a PKC γ dependent manner. Notably, PKC γ is recruited to the membrane after opioid exposure (441, 442) and PKC γ kinase mutant mice demonstrate reduced tolerance (374) and blocks delayed pronociceptive sensitivity to opioid agents (375). Herein we observed increased $\alpha 1$ subunit and PKC γ levels after seven days DZP treatment, suggesting an increase in surface GABA_AR populations undergoing drug-induced endocytosis and intracellular trafficking in agreement with our previous findings at earlier DZP treatment time points (270).

We further analyzed our proteomics data by using IPA bioinformatics analysis to determine changes in pathway activation or enrichment. Canonical pathway analysis revealed strong predicted activation of synaptogenesis signaling, synaptic LTP and CREB signaling in neurons pathways (**Fig. 29A**). Individual biological pathway assessment suggested the release of neurotransmitter, development of neurons, and long-term potentiation favored an activated state (**Fig. 29B**). Statistically significant protein peptide changes with the most robust difference between DZP and vehicle animals support these changes including growth cone regulator GAP-43 (377-379), the Ca²⁺-sensors Syt1 and Syt7 that contribute to both presynaptic synaptic vesicle ready releasable pool and postsynaptic trafficking to support LTP (443), piccolo (387), dynamin-

3 (391) and RAB3A (390) and the critical phosphodiesterase enzyme PDE2 (395, 396). The collective bioinformatics and proteomics analysis supports synaptic plasticity, in part through NMDAR pathway upregulation and function.

Here we leverage a comprehensive experimental approach utilizing behavioral testing, biochemistry, quantitative proteomics and electrophysiology to examine the neuronal adaptations occurring in response to DZP tolerance *in vivo*. Our study reveals complex alterations in both inhibitory and excitatory neurotransmission that have similar profiles to ethanol and opiate tolerance. We find an increase in the synaptic levels of $\alpha 1$, $\gamma 2$ and the DZP-insensitive $\alpha 4$ subunit, resistance to DZP potentiation and no change in GABA mIPSC amplitude or frequency. Moreover, an increase in NMDAR levels and function was observed by western blot analysis and by electrophysiology. These changes occurred coincidentally with an increase in the levels of multiple CaMKII subunits and the PKC γ isozyme, known positive regulators of NMDAR function. These results define key aspects of the neuroadaptive signature of a brain with sedative BZD tolerance. Future studies will need to identify if other BZD class drugs with different pharmacokinetic and pharmacodynamics profiles relative to DZP elicit similar changes found here. Moreover, the FDA approved NMDAR inhibitor memantine poses an interesting candidate to inhibit or reverse the DZP induced adaptations, as it has been shown to alleviate some negative side effects resulting from opioid (444) and alcohol intake (445, 446). Advancing our understanding and identifying possible targets for treatments for the neuroadaptations produced by long-term BZD are critical for clinical care considering that during the last two decades prescription dosage and/or length of treatment has steadily risen (323).

5.0 Final Conclusions

A deeper molecular understanding of the factors influencing the pharmacological profile of GABA_ARs is crucial for current clinical practices and future drug development. GABA_AR regulatory mechanisms including trafficking, post-translational modifications and composition directly and dynamically tune receptor activity and function during neuronal scaling. Herein we investigated the compensatory neuroadaptations occurring after initial and prolonged treatment with the highly utilized clinical drug, DZP, where functional and behavioral tolerance to DZP has occurred. This work included the generation and characterization of a novel dual reporter GABA_AR optical tool with multiple imaging based applications. The $\gamma 2^{\text{pH}}$ FAP construct aided our ability to detect elusive trafficking changes in receptors after initial DZP and an *in vitro* epilepsy paradigm, and this tool will remain highly useful for future studies into GABA_AR trafficking regulation. The comprehensive use of advanced imaging techniques, biochemistry and label-free quantitative proteomics revealed a complex array of trafficking and regulatory mechanisms dampening inhibitory synapse function in response to one day DZP exposure. Compromised gephyrin scaffolding, increased internalization and lysosomal targeting of select GABA_AR subtypes, and enhanced $\gamma 2$ -GABA_AR association with intracellular and surface trafficking protein mediators *in vivo* defined this work.

Many classical studies have attempted to solve the molecular fingerprint of a BZD tolerant brain, but conclusive evidence remains undetermined due to differences in research paradigm, brain-region and experimental tool limitations (32). Our work utilized a comprehensive experimental strategy in a behaviorally-validated DZP tolerance model to measure protein level changes in inhibitory and excitatory receptors, functional validation by electrophysiology and a

targeted synaptic proteome screening. These findings revealed alterations in subunit specific synaptic and extrasynaptic GABA_AR localization coupled with a general increase in GABA_AR subunits. Additionally, we identified enhanced NMDAR subunit levels and function, and an upregulation of proteins regulating neuronal remodeling, development, and excitatory synapse strengthening. The use of SRM based quantitative proteomic methods afforded us detection of a number of key kinase mediators altered by DZP including CAMKII and PKC subtypes that have also been determined to be important in the adaptive drug response to ethanol and opiates. Importantly, we identified a unique response profile between early and sustained DZP treatment, including opposing changes in GABA_AR subunit levels and the inhibitory scaffolding protein gephyrin. This work highlights the necessity of multiple experimental approaches and emphasizes the importance of understanding drug effects at different stages of treatment exposure. Current clinical and new GABA_AR modulating therapies will have to strongly consider the short- and long-term consequences of manipulating GABA_AR function and the brains fundamental mechanisms to compensate for robust changes in the E/I balance.

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