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# Organization and emergence of a mixed GABA-glycine retinal circuit that provides inhibition to mouse ON-sustained alpha retinal ganglion cells

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# SUMMARY

In the retina, amacrine interneurons inhibit retinal ganglion cell (RGC) dendrites to shape retinal output. Amacrine cells typically use either GABA or glycine to exert synaptic inhibition. Here, we combined transgenic tools with immunohistochemistry, electrophysiology, and 3D electron microscopy to determine the composition and organization of inhibitory synapses across the dendritic arbor of a well-characterized RGC type in the mouse retina: the ON-sustained alpha RGC. We find mixed GABA-glycine receptor synapses across this RGC type, unveiling the existence of "mixed" inhibitory synapses in the retinal circuit. Presynaptic amacrine boutons with dual release sites are apposed to ON-sustained alpha RGC postsynapses. We further reveal the sequence of postsynaptic assembly for these mixed synapses: GABA receptors precede glycine receptors, and a lack of early GABA receptor expression impedes the recruitment of glycine

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AUTHOR CONTRIBUTIONS

M.H. and R.S. designed research. A.S., B.N.E., A.B., C.G., W.-Q.Y., D.B., R.S., and M.H. performed research. A.S., B.N.E., A.B., C.G., W.-Q.Y., D.B., and M.H. analyzed data. U.R. contributed new reagents. A.S., R.S., and M.H. wrote the paper.

SUPPLEMENTAL INFORMATION

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DECLARATION OF INTERESTS

The authors declare no competing interests.

receptors. Together our findings uncover the organization and developmental profile of an additional motif of inhibition in the mammalian retina.

#### **Graphical abstract**



# In brief

Sawant et al. show the occurrence of mixed GABA-glycine synapses across the dendrites of a well-characterized retinal output neuron, where GABA and glycine are released from distinct presynaptic vesicles putatively by a widefield interneuron. Emergence of receptors at these synapses is temporally offset during development with GABA receptors recruiting glycine receptors.

# INTRODUCTION

A common feature of neural circuits is the tight interplay between excitation and inhibition that sculpts both spontaneous and evoked activity (Isaacson and Scanziani, 2011). In sensory systems such as the retina and olfactory sensory neurons, circuit inhibition can lead to feature selectivity such as direction selectivity (Wei and Feller, 2011), orientation selectivity (Antinucci and Hindges, 2018), and approach sensitivity (Münch et al., 2009) and can also regulate the behavioral response of an organism (e.g., odor-evoked inhibition of sensory neurons can itself evoke attraction-avoidance behaviors; Cao et al., 2017). The composition and organization of inhibitory motifs have thus been a topic of active investigation across circuits. A common circuit principle is the rich diversity of interneurons that can provide

synapse-specific inhibition across specific compartments of a principal neuron (e.g., basket versus chandelier interneuronal input across pyramidal neuron; Thomson and Jovanovic, 2010) or contribute to specific neural computations (e.g., in the retinal circuit, where AII and A17 interneurons specifically process dim-light signals; Hoon et al., 2014; Wässle, 2004). Interneuronal diversity is most appreciated in the inner mammalian retina (Helmstaedter et al., 2013; MacNeil and Masland, 1998), where the functional characteristics, connectivity, and organizational principles (pre- and postsynaptic specializations) remain unknown for the vast majority of amacrine cell (AC) interneurons. ACs shape the output responses of retinal ganglion cells (RGCs), which ferry visual information from the retina to higher brain centers (Hoon et al., 2014; Masland, 1988; Nirenberg and Meister 1997; Wässle, 2004). ACs mediate postsynaptic inhibition on the soma and/or dendrites of RGCs either via the neurotransmitter GABA or glycine, and in general GABA-releasing ACs extend dendritic arbors over a wider spatial extent than glycinergic ACs (Koulen et al., 1996; Wässle et al., 1998; Zhang and McCall, 2012). Added to the diversity of ACs is the diversity of RGC types (Baden et al., 2016; Sanes and Masland, 2015; Völgyi et al., 2009), with only a few RGC types well characterized in terms of their roles in visual processing and their retinal synaptic connectivity.

In this study, we focused on inhibitory postsynapses across a well-characterized murine RGC type called the ON-sustained alpha RGC (henceforth referred to as "ONa"). The ONa exhibits a sustained depolarizing response to light increments across luminosities (Krieger et al., 2017) and is the RGC type most sensitive to dim-light signals, carrying single-photon visual information to higher brain areas (Smeds et al., 2019). The excitatory circuit for the ON $\alpha$  has been delineated, and it is known which bipolar cell type (type 6) provides the majority of excitatory input and how these excitatory inputs regulate ONa visual responses (Schwartz et al., 2012). Previous work has shown that GABAA receptors and glycine receptor alpha-1 subunit-containing (GlyRa1) synapses mediate postsynaptic inhibition on ONa (Koulen et al., 1996; Majumdar et al., 2007). However, the molecular composition and developmental profile of inhibitory synapses providing postsynaptic inhibition across ONa RGCs remain undetermined. We combined murine transgenic tools with single-cell electrophysiology and serial electron microscopy (EM) to determine the molecular composition of inhibitory synapses across ONas and the synaptic mechanism of GABA and glycine release from ACs onto ONas and uncovered the identity of an "ON" laminating AC type that provides inhibitory input to ONa. We further probed the development of inhibitory synapses across ONa and uncovered a key role of early GABAA receptors for establishment of ONa inhibitory synapses. Together our findings have revealed an additional motif of retinal inhibition on a well-characterized RGC type that revises our understanding of how specific inhibitory circuits are organized to regulate visual processing in the mammalian retina.

# RESULTS

#### GABA and glycine receptors colocalize on ONa RGC dendrites

The ONa receives both dim and bright light information via rod and cone photoreceptors, respectively (Figure 1A). Rod and cone photoreceptor signals reach the ONa through well-

characterized parallel pathways that ultimately converge at cone bipolar cell terminals, which make glutamatergic synapses onto ONa dendrites (Figure 1A; see also Hoon et al., 2014; Wässle, 2004). To determine the composition of inhibitory, GABA, and glycinergic synapses across the ONa dendritic arbor that mediate postsynaptic inhibition onto this cell, we used a specific mouse transgenic line (Thy1-YFPH) in which a subset of RGCs are fluorescently labeled. The ONa is one of the RGC types labeled in this line (Bleckert et al., 2013, 2014) and can be unambiguously identified by its characteristic morphology and dendritic lamination pattern (Bleckert et al., 2013, 2014; Krieger et al., 2017). Adult Thy1-YFPH retinas were co-labeled with antibodies against GABA<sub>A</sub> and GlyRa1 receptor subunits, as previous studies have shown that mouse ONas get input from both GABA and glycinergic ACs through GABA<sub>A</sub> and GlyR $\alpha$ 1 receptors, respectively (Koulen et al., 1996; Majumdar et al., 2007; Wässle et al., 1998). To determine which GABA<sub>A</sub> receptor type is expressed across ONa arbors, we co-labeled retinas with antibodies against GlyRa1 and either a3 subunit-containing GABAA receptors (GABAAa3; Figure 1) or a1 subunitcontaining GABAA receptors (GABAAa1; Figure S1). These two GABAA receptor types were selected because they are most likely to provide inhibition on ONa arbors, as  $GABA_A \alpha 1$ -,  $GABA_A \alpha 2$ -, and  $GABA_A \alpha 3$ -containing  $GABA_A$  receptors are the main GABA<sub>A</sub> receptor types present at distinct non-overlapping synapses in the inner retinal synaptic layer (Wässle et al., 1998) and because GABAAa2 receptors are specifically localized to a non-ONa RGC inhibitory circuit (Greferath et al., 1995). Very few GABAAa1 receptor puncta were found to be distributed across ONa dendrites (Figure S1A), confirming that this receptor type is not a prominent component of GABAergic inhibition across ONas. In corroboration, when we quantified expression of GABAAa1 across ONa dendrites, we observed negligible percentage occupancy of GABA<sub>A</sub> $\alpha$ 1 across ON $\alpha$  arbors (volume of receptor pixels relative to volume of ONa arbor; Figure S1B). In contrast, GABAAa3 puncta were abundantly localized across the ONa arbor, where they were closely associated with GlyRa1 puncta (Figure 1B). The observation of colocalized GABAAa3 and GlyRa1 receptor clusters within the ONa dendritic arbor was striking, as previous studies of GABA and glycine receptor distribution in the inner synaptic layer of the mouse and rat retina have reported a non-overlapping distribution pattern of these receptor subtypes (mouse retina, Frazao et al., 2007; rat retina, Sassoè-Pognetto et al., 1995). We next quantified the percentage colocalization between the GlyRa1 puncta within the ONa RGCs and the GABA<sub>A</sub> $\alpha$ 3 receptor signal (see STAR Methods for details) and determined ~55% of true colocalization between these receptor types (true colocalization = total colocalization – random colocalization after 90° flip of GABAAa3 channel; Figure 1C; Figure S1C). Thus, our analyses revealed that ~55% of ONa RGC GlyRa1 receptor-containing postsynapses also have GABAAa3 receptors. Together our observations revealed the GABAA receptor type that is expressed across ONas and also uncovered a population of "mixed" GlyRa1-GABA<sub>A</sub>a3 postsynapses across the mouse ONa.

#### Mechanism of GABA-glycine neurotransmitter release onto ONa RGC dendrites

Given our observation of mixed GlyRa1-GABA<sub>A</sub>a3 postsynapses across the ONa, the next question we addressed was, what is the presynaptic mechanism of GABA and glycine release onto the ONa? Figure 2A illustrates four possible scenarios by which GABA and glycine release from AC boutons could activate mixed GlyRa1-GABA<sub>A</sub>a3 receptors: (I)

presynaptic terminals with synaptic vesicles containing (and co-releasing) both GABA and glycine, (II) presynaptic terminals with a mixed pool of distinct synaptic vesicles containing either GABA or glycine, (III) presynaptic terminals apposed to mixed GlyRa1-GABA<sub>A</sub>a3 receptors with dedicated pools of synaptic vesicles filled with either GABA or glycine, and (IV) two different presynaptic AC terminals releasing GABA and glycine at close proximity. To differentiate between these possibilities, we performed whole-cell patch-clamp recordings from ONa RGCs (Figure 2B) and analyzed the amplitude and frequency of miniature inhibitory postsynaptic currents (mIPSCs) in the presence of glutamate receptor blockers (NBQX and D-AP5) and tetrodotoxin (TTX) to block the voltage-gated sodium channels. We reasoned that if GABA and glycine were co-released from the same presynaptic vesicle (Figure 2A, scenario I), upon application of the GABAA receptor blocker GABAzine (exemplar mIPSC trace with and without GABAzine in Figure 2C), we would see a decrease in overall amplitude of ONa mIPSCs and no change in the frequency of ONa mIPSC events. In contrast, if GABA and glycine were released through distinct presynaptic vesicles (Figure 2A, scenarios II-IV), we would see a decrease in the frequency of ONa. mIPSCs and no change in the amplitude of ONa mIPSC events after GABAzine application. Upon quantifying ONa mIPSC amplitude (Figure 2D) and frequency (Figure 2E) of events before versus after GABAzine application, we observed a significant reduction in mIPSC event frequency but not amplitude after GABAzine application (Figures 2D and 2E). We next repeated the same mIPSC experiment in the presence of the glycine receptor blocker strychnine (Figure S2) and again observed a significant reduction in mIPSC frequency but no change in mIPSC amplitude after strychnine application (Figures S2B and S2C).

Inhibitory input on ONa RGCs can be mediated by both spiking and non-spiking ACs (Park et al., 2018). Thus, to account for all spontaneous inhibitory synaptic release on ONa RGCs, we performed recordings from ONas without TTX (but in the presence of glutamate receptor blockers) and analyzed the amplitude and frequency of these spontaneous inhibitory postsynaptic currents (sIPSCs) before and after application of GABAzine (Figure S3). Consistent with the mIPSC recordings, we observed a significant reduction in sIPSC event frequency after application of GABAzine without any change in sIPSC amplitude (Figures S3D and S3E). Of note, previous sIPSC recordings pooled across all mouse alpha RGC types mention no noticeable effect of GABAzine application (Majumdar et al., 2007). However, our recordings specifically from ONa RGCs show a robust effect of GABAzine on sIPSC event frequency (Figure S3E; average  $\pm$  SEM: control, 17.81  $\pm$  0.16; +GABAzine,  $9.46 \pm 1.02$ ; p = 0.000297). We also analyzed the distribution of both the rise time and decay time of ONa RGC mIPSC (Figures S2D and S2E) and sIPSC (Figures S3F and S3G) events and observed a unimodal (see also STAR Methods) distribution in the control condition (before GABAzine) and after GABAzine application (Figures S2 and S3). This precluded us from separating mIPSC and sIPSC events into GABAergic or glycinergic events on the basis of their kinetics. Taken together, our results from both the mIPSC and sIPSC experiments suggest that GABA and glycine are not co-released from the same presynaptic vesicle onto the ONa arbor.

#### GABA-glycine co-transmission could be mediated by ON-laminating widefield ACs

Our recordings from ONa RGCs preclude co-release of GABA and Glycine from the same presynaptic vesicle and point to three possible presynaptic arrangements for ONa mixed GABA and glycine synapses (scenarios II–IV). To identify which is the prevalent scenario and gain insight into the ultrastructural arrangement of AC synaptic boutons across the ONa, we performed serial block face scanning EM (SBFSEM) and reconstructed the ultrastructural arrangements of inhibitory synapses across the ONa RGC. The Thy1-YFPH line was used to locate an ONa, and near infrared branding (NIRBing; see Bishop et al., 2011; Bleckert et al., 2013; Della Santina et al., 2016) was used to create fiduciary marks surrounding the ONa to enable localization and reconstruction at the EM (Figure 3A). The ONa RGC some and proximal dendritic arbors were reconstructed and all sites of inhibitory input identified and annotated (Figure 3B; see STAR Methods for criteria of synapse annotation). We observed two distinct arrangements of presynaptic AC boutons apposed to sites of inhibitory input across the ONa arbor. One class contained a single synaptic vesicle pool clustered across the synaptic sites, whereas the second class contained two or more clusters of synaptic vesicles at distinct sites apposed to a single postsynaptic thickening (site) akin to our expectations from scenario III (Figures 3C-3C''). We thereafter classified inhibitory synapses as "single" (one pool of synaptic vesicles), "dual" (two distinct synaptic vesicle pools/release sites, verified across two or three consecutive EM planes), triple (with three pools of synaptic vesicles), or, rarely observed, quadruple (with four pools), and we quantified the number of these inhibitory synapse types across the proximal ONa RGC arbor (Figure 3D). We observed that ~60% of inhibitory synapses across the ONa have a single release pool, and about ~40% of inhibitory synapses across the ONa have a presynaptic bouton with multiple distinct synaptic vesicle release sites (Figure 3D). The presence of a single presynaptic bouton containing multiple release sites apposed to an ONa synapse would favor scenario III (i.e., a single AC releasing GABA and glycine from distinct release sites). To determine whether this arrangement of inhibitory synapses was restricted to the proximal dendritic arbor of the ONa as observed in our NIRBing SBFSEM dataset (Figures 3A–3D) or whether a similar distribution could be observed across a wider region of the ONa dendritic arbor, we used the k0725 SBFSEM dataset (Briggman lab; Ding et al., 2016) to trace and fully reconstruct all of the ONa dendritic arbor (see STAR Methods for details) included within the volume of this EM stack. We mapped all the inhibitory synapses across the ONa arbor within the k0725 dataset (Figure 3E) and quantified its distribution. Once again, we classified inhibitory synapses as "single" or "dual" on the basis of the number of synaptic vesicle pools apposed to a postsynaptic site. We observed dual synapses distributed across both proximal and distal segments of the ONa dendritic arbor (Figure 3E) and a similar proportion of inhibitory synapses with single (~60%; Figure 3F) and multiple (~40%; Figure 3F) release sites, consistent with our quantifications of the synapse distribution along the proximal ONa RGC dendritic arbor (Figure 3D). Of note in our determination of the ultrastructural arrangements of AC boutons apposed to ONa arbors both in the NIRBed and in the k0725 dataset, we did not observe any postsynaptic site with two closely arranged presynaptic boutons (i.e., scenario IV arrangements). Together our observations revealed the ultrastructural arrangement of AC terminals apposed to inhibitory synapses across the ONa and uncovered that about 40% of

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inhibitory input onto the ONa arrives through AC boutons with multiple synaptic vesicle release sites.

To uncover the morphological identity of ACs that provide input onto the ONa at dual release sites, which could be suggestive of GABA and glycine release at distinct sites, we reconstructed profiles of ACs providing inhibitory input to the ONa using the k0725 dataset. In this dataset, we could reconstruct three ACs and trace the neurites that provide input to ONa at dual synaptic vesicle release sites all the way back to the soma at the inner nuclear layer (Figure 4). All three ACs thus identified were widefield ACs that laminated in the "ON" plexus coincident with the arborization of the ONa. We thus refer to this AC type as ON-laminating widefield ACs (ON-WACs). Of note, all three examples of reconstructed ON-WACs showed no dendritic processes at other laminae of the inner plexiform layer. All three ON-WACs provided the majority of inhibitory input onto the ONa arbor at boutons with dual synaptic vesicle release sites (Figures 4A-4C). Given the extent of the dataset, we could reconstruct only one portion of the dendritic arbor for the second ON-WAC (Figures 4B-4B''). On average, all three reconstructed ON-WACs provided ~40 inhibitory synapses with dual synaptic vesicle release sites onto the ONa arbor. Upon analyses of the ON-WAC->ONa RGC synaptic bouton diameter, we observed that ON-WAC presynaptic boutons with dual release sites were significantly larger than those with a single release site (Figure S4A). We next determined the identity of all ON-WAC output (inhibitory) synapses to RGCs (both ONa and other/non-ONa RGC types), bipolar cells and other ACs (Figures S4B–S4D). We found that of the total ON-WAC->RGC output synapses, the majority were to the ONa RGC (~69%; Figure S4B). The ONa RGC also received the majority of the ON-WAC->RGC synapses with dual synaptic vesicle release sites (~60%; Figure S4B). When considering the ON-WAC output synapses across all inner retinal cell types (RGCs, other ACs, and bipolar cells), the ONa RGC received the majority of the ON-WAC output synapses with dual synaptic vesicle release sites (~54%), and other ACs received the majority of the ON-WAC output synapses with a single synaptic vesicle release site (~77%; Figures S4C and S4D). Thus, ONa RGCs are the main RGC postsynaptic partner for ON-WACs and ON-WACs preferentially synapse onto ONa RGCs with multiple release sites. Taken together, our observations uncovered the identity of an inhibitory input onto the ONa that occurs through ON-WACs via presynaptic boutons with primarily dual synaptic vesicle release sites.

#### GABA<sub>A</sub> receptors localize prior to glycine receptors across ONa RGC dendrites

To determine the timeline of ONa inhibitory synapse organization, we next immunolabeled for GABA<sub>A</sub>a3 and GlyRa1 synapses and determined the expression of these receptor subtypes across ONa dendrites at four developmental time points (Figure 5): postnatal day 8 (P8), P12, P16, and P21. As eye opening in rodents is around P14, our selection includes two time points before and two time points after eye opening. Our experiments were performed in the *Thy1*-YFPH mouse line to enable visualization of ONa RGCs and to isolate receptor signal specifically within the ONa (Figure 5). At P8, only GABA<sub>A</sub>a3 receptor signal was observed within the ONa dendritic arbor, and negligible GlyRa1 signal could be detected across ONa cells at this time point (Figure 5A). From P12 till P21, both GABA<sub>A</sub>a3 and GlyRa1 were robustly expressed within ONa RGCs (Figure 5A). We also immunolabeled for the inhibitory postsynaptic scaffolding protein gephyrin within

developing ONas (Figure 5B). Gephyrin is known to scaffold all glycine receptors and a subset of retinal GABAA receptors primarily those containing GABAAa2 or GABAAa3 receptor subunits (Sassoè-Pognetto et al., 1995; Sassoè-Pognetto and Wässle, 1997). We found robust gephyrin expression within ONa arbors as early as P8 and maintenance of this expression profile all through circuit formation (till P21; Figure 5B). Next we quantified the expression level of each synaptic marker (GABAAa3, GlyRa1, and gephyrin) within P8, P12, P16, and P21 ONa dendrites by determining the volume occupancy of each marker normalized to the RGC dendritic volume (percentage occupancy; Figure 5C). At P8, both  $GABA_A \alpha 3$  and gephyrin are present at comparable amounts within ON $\alpha$  dendrites, with no detectable GlyRa1 expression (Figure 5C). By P12, GlyRa1 expression within ONa dendrites reaches its mature levels, and GABA<sub>A</sub> $\alpha$ 3 levels at P12 also significantly increase compared with P8 levels (Figure 5C). Gephyrin maintains its expression levels within ONa RGCs across time points, and the ONa GABAAa3/GlyRa1 expression ratio remains relatively constant from P12 to P21. Taken together, our observations show that the scaffolding protein gephyrin is present within ONo.s at mature amounts as early as 1 week after birth and that GABAA receptor expression precedes GlyR expression across the ONa. RGC.

# Early GABA<sub>A</sub> $\alpha$ 3 receptor expression is necessary for recruiting GlyR $\alpha$ 1 and organizing inhibitory synaptic sites across the ON $\alpha$ RGC

Our observation of early GABA<sub>A</sub> $\alpha$ 3 expression within ON $\alpha$  RGCs (Figure 5) indicates that GABAAa3 might play a role for the developmental organization of mixed GABAA-GlyR synapses across the ONa arbor. To test this possibility and the dependence of ONa GlyRa1 expression on the presence of early GABAAa3, we used a GABAAa3-knockout (a3KO) mouse (Yee et al., 2005) and determined the expression of GlyRa1 receptors across a3KO ONa RGCs (Figure 6). To visualize ONa RGCs in the a3KO, we crossed the a3KO line into the Thy1-YFPH transgenic background. GlyRa1 synaptic puncta were drastically downregulated across a3KO ONa RGCs (Figure 6A), with significantly less total GlyR receptor puncta, dendritic GlyR puncta, and somatic GlyR puncta in a3KO ONas compared with control (Figure 6B). Of note, the total number of GlyR puncta remaining within a3KO ONas was ~45% of the control level (Figure 6B: littermate control total GlyRa1 puncta within  $ONa = 1,564.25 \pm 254.67$ , a3KO total GlyRa1 puncta within  $ONa = 709 \pm 88.1$ ). As ~55% of GlyRa1 puncta within ONas are colocalized with GABA<sub>A</sub>a3 (Figure 1C), this would mean that the fraction of ONa GlyRa1 that is lost in the a3KO represents the fraction associated with GABAAa3 at mixed synaptic sites. To determine if the loss of GlyRa1 receptors in the a3KO was specific to the mixed synapses across the ONa arbor, we next determined the GlyRa1 expression on two other alpha RGC types, OFF sustained and OFF transient, that are known to receive robust glycinergic input (Murphy and Rieke, 2006) and that express GlyRa1 receptors across their dendritic arbors (Zhang et al., 2014). We observed comparable GlyRa1 distribution across the dendritic arbors of both OFFsustained and OFF-transient RGCs in a 3KO retinas compared with control (Figure S5). Of note, the GlyRa1 synaptic sites across the OFF RGCs do not appear colocalized with GABAAa3 receptor clusters (Figure S6), providing further evidence that only mixed GABAAa3-GlyRa1 synaptic clusters are impaired in the a3KO. Taken together our

observations underscore a selective disruption of GABA<sub>A</sub> $\alpha$ 3 -GlyR $\alpha$ 1 mixed synapses across the  $\alpha$ 3KO ON $\alpha$  RGCs.

We further compared the distribution of excitatory postsynapses across a 3KO and littermate control ONa RGCs by biolistic expression of the glutamatergic postsynaptic scaffolding protein PSD-95, known to recognize sites of glutamatergic input across the arbors of these RGCs (Schwartz et al., 2012). We observed comparable distribution of PSD-95 puncta across a 3KO and control ONa RGC arbors (Figure S7A), verifying that excitatory input onto a 3KO RGC remains unperturbed.

To determine the presence of remaining GABAA receptor subunits across a3KO ONa RGCs, we next determined the expression of GABAAY2 receptor subunits across a3KO ONas compared with control. We used the *Thy1*-YFP $\gamma$ 2 transgenic line to visualize  $GABA_A\gamma^2$  receptor expression across RGCs (Bleckert et al., 2013) and crossed this line into the a3KO background. GABA<sub>A</sub>a3 receptors are known to co-assemble with GABA<sub>A</sub> $\gamma$ 2 subunits in the retina (Greferath et al., 1995) and GABAAa3 receptor puncta on ONa RGC dendrites colocalize with  $GABA_A\gamma 2$  and gephyrin puncta (Figure 7A). In the  $\alpha 3KO$ ,  $GABA_A\gamma^2$  receptor expression within ONa RGCs is dramatically reduced compared with control (Figures 7B and 7D), confirming the absence of any functional  $GABA_A$  receptors across the dendritic arbors of a3KO ONas. In further support, the other GABAA receptor type normally present at minimal amounts across ONa RGC arbors (GABAAa1; Figure S1) is not upregulated across a3KO ONa RGCs (Figures S7B and S7C). Finally, we assessed the levels of gephyrin across a3KO ONas by labeling for gephyrin and quantifying the amount of gephyrin in a 3KO and control ONa RGCs (Figures 7C and 7D). The number of gephyrin puncta across a3KO ONa RGCs was comparable with control amounts, unveiling that the mechanisms controlling gephyrin recruitment to ONa RGC synapses are not regulated by GABAAa3. Together our observations in the a3KO revealed that the molecular organization of inhibitory synapses across the ONa RGCs is disrupted in the absence of early GABA<sub>A</sub> $\alpha$ 3 expression, such that both GABA<sub>A</sub> and glycine receptors are not accrued and clustered correctly at inhibitory synaptic sites across GABAAa3 deficient ONa RGCs, but the scaffolding protein gephyrin remains at these sites independent of the absence of clustered inhibitory receptors.

# DISCUSSION

Inhibition in the retina is mediated by GABAergic and glycinergic ACs, ~50% of retinal inhibition is mediated by GABAergic ACs, and ~50% is mediated by glycinergic ACs (Hoon et al., 2014; Wässle, 2004; Wässle et al., 2009). Morphological studies have categorized these two AC subsets as occupying distinct non-overlapping synaptic sites in the retinal synaptic layer (Koulen et al., 1996), unlike inhibitory synapse organization in the brainstem and spinal cord, where postsynaptic sites with colocalized GABA and glycine receptors are often observed (Frazao et al., 2007; Todd et al., 1996) and presynaptic interneurons correlease both inhibitory neurotransmitters (Jonas et al., 1998). Here we identified an inhibitory circuit onto a well-characterized mammalian RGC that is composed of mixed GABA-glycine receptor synapses (i.e., the same postsynapse containing both GABA<sub>A</sub> $\alpha$ .3 and GlyR $\alpha$ 1 receptors). Combining electrophysiology and SBFSEM, our data reveal that the

inhibitory neurotransmitters GABA and glycine are not co-released from the same synaptic vesicle but rather released via distinct synaptic vesicles at release sites within a single presynaptic AC bouton. Tracing the processes of AC types that provide inhibitory input at dual release sites onto the ONa arbor, we uncovered three examples of ON-WACs with similar morphology. Tracking the developmental profile of inhibitory synapses across ONa dendrites revealed that the GABA<sub>A</sub>a3 receptor localizes at ONa synapses prior to the emergence of GlyRa1 receptors. The early GABA<sub>A</sub>a3 receptor accumulation is critical for recruitment of GlyRa1 at ONa "mixed" synapses, as GlyRa1 receptor sites are significantly downregulated across the ONa arbor in the a3KO retina compared with control. The GABA<sub>A</sub>a3. Together our findings reveal the existence of a mixed GABA-glycinergic circuit in the mammalian retina, trace the profile of a putative GABA-glycine co-releasing AC type, and determine the molecular assembly and organizational inter-dependence of this synapse type.

#### A selective "mixed" GABA-glycine inhibitory circuit in the mammalian retina

The enormous diversity among retinal ACs has precluded a complete anatomical and functional characterization of ACs. But previous studies on the organization of retinal inhibitory synapses have often reported distinct localization of GABAergic and glycinergic postsynaptic sites (Frazao et al., 2007; Koulen et al., 1996; Wässle et al., 1998) and a nonoverlapping expression pattern of GABA and glycinergic presynaptic markers (Haverkamp and Wässle, 2000). Only a recent high-throughput single-cell RNA sequencing study showed the presence of an AC population that was positive for both GABA synthetic enzymes and the transporter expressed by glycinergic ACs (Yan et al., 2020). Our findings are in keeping with this observation, as the mixed GABA<sub>A</sub>a3-GlyRa1 inhibitory circuit we find is a subset (~55% of all ONa GlyR synapses) of all the retinal inhibitory synapses. Our findings also shed light on the receptor composition of inhibitory synapses distributed across the ONa. We find three distinct populations of inhibitory synapses that mediate postsynaptic inhibition on the ONa RGC: mixed GABAAa3-GlyRa1 synapses, GlyRa1-only synapses, and GABAAa3-only synapses. Previous studies have shown the expression of GlyRa1 receptors on ONa RGCs (Majumdar et al., 2007; Wässle et al., 1998), presence of GlyRmediated inhibitory postsynaptic currents in ONa RGCs (Majumdar et al., 2007), and their potential contribution toward spike output (Murphy and Rieke, 2006). The A8 glycinergic amacrine of the mouse retina has been shown to provide inhibitory input to ONa RGCs through GlyRa1-containing synapses (Lee et al., 2015), and a GABAergic CRH (corticotropin-releasing hormone)-expressing AC has been shown to provide inhibitory input onto the ONa primarily for the duration of positive contrast stimulus (Park et al., 2018). Thus, on the basis of our observations and previous studies, one can presume that the CRH GABAergic ACs provide inhibitory input to ONas at GABAAa3-containing synapses. ONa RGCs exhibit a sustained action potential firing response to light increments (Krieger et al., 2017; Murphy and Rieke, 2006) over a wide dynamic range of visual input spanning both dim- and bright-light stimuli (Grimes et al., 2014). In addition to a robust excitatory glutamatergic drive from ON bipolar cells (Schwartz et al., 2012), ONa RGCs have been shown to receive inhibitory input during both positive and negative contrast stimuli (i.e.,

during light onset and offset) (Park et al., 2018; van Wyk et al., 2009), and this inhibitory input is mediated by both GABA<sub>A</sub> and glycine receptors (Majumdar et al., 2007; Murphy and Rieke, 2006; Park et al., 2018). Our data reveal the identity of an ON-WAC that could provide inhibitory input to ONas at dual release sites with putative mixed GABA-GlyRs. Future studies elaborating the light-evoked responses of the ON-WAC are needed to determine its functional properties, although its lamination profile would suggest that it has a depolarizing response to light onset ("ON" response), and it could thus provide inhibitory input to ONas during positive contrast stimuli.

Our findings of colocalized GABAAa3 and GlyRa1 receptor sites across the ONa represent mixed GABA-glycine postsynapses in the retinal circuit. Colocalization of GABA and glycine receptors is, however, not uncommon among spinal cord and brainstem circuits (Frazao et al., 2007; Gamlin et al., 2018; Todd et al., 1996). In the avian auditory brainstem, mixed GABA-GlyR synapses have faster response kinetics than inhibitory synapses containing only GABARs (Kuo et al., 2009), and GABA can speed up GlyR-mediated synaptic currents (Lu et al., 2008), thereby refining the temporal window of inhibition at these synapses. Thus, co-transmission of GABA and glycine could be a means for enhancing the temporal resolution of inhibition in the mature auditory system (Lu et al., 2008). Mixed GABA and GlyR synaptic sites can also serve roles during development of brainstem circuits. For example, in developing abducens motor neurons, co-release of GABA and glycine increases reliability and optimizes inhibition of motor neuron function (Russier et al., 2002). But a purely developmental role of mixed GABAA-GlyR synapses on the ONa is unlikely given the continued presence of this mixed circuit in the mature retina. Additional studies that assess the functional properties of ONa RGCs upon selective disruption of GABAR synapses, GlyR synapses, and mixed GABAR-GlyR synapses are needed to determine the contribution of each of these inhibitory motifs on regulating the output of ONas. As ONa RGCs are critical components of the dim-light visual circuit ferrying singlephoton signals to higher visual centers (Smeds et al., 2019), unveiling how postsynaptic inhibition and the underlying circuit components modulate ONa signaling is crucial to understand the retinal substrates for dim light vision.

#### GABA<sub>A</sub>a3 as an early developmental recruiter of GlyRa1 to retinal mixed synapses

Across the CNS, GABA<sub>A</sub> $\alpha$ 3 receptors are often expressed during early periods of development (Bosman et al., 2002; Laurie et al., 1992; Liu and Wong-Riley, 2004). In the adult, GABA<sub>A</sub> $\alpha$ 3 receptors occupy a rather restricted distribution representing 10%–20% of expressed GABA<sub>A</sub> receptors (Fritschy and Mohler, 1995; McKernan and Whiting, 1996; Pirker et al., 2000). In monoaminergic neurons of the CNS, GABA<sub>A</sub> $\alpha$ 3 receptors are the main GABA<sub>A</sub> receptor subtype (Fritschy and Mohler, 1995). Consequently, the  $\alpha$ 3KO mouse shows behavioral signatures of functional hyperactivity in the midbrain dopaminergic system, which leads to a deficit in sensorimotor gating (Yee et al., 2005). Of note, lack of GABA<sub>A</sub> $\alpha$ 3 is not compensated by upregulation of other major GABA<sub>A</sub> receptor subunits (i.e., GABA<sub>A</sub> $\alpha$ 1, GABA<sub>A</sub> $\alpha$ 2, GABA<sub>A</sub> $\beta$ 2/3, or GABA<sub>A</sub> $\gamma$ 2) (Yee et al., 2005). Another brain region where GABA<sub>A</sub> $\alpha$ 3 receptors are predominant is the nucleus reticularis thalami (Fritschy and Mohler, 1995; Pirker et al., 2000). Analyses of GABA<sub>A</sub> $\alpha$ 3 deficiency in this region as well revealed that nucleus reticularis thalami neurons do not replace GABA<sub>A</sub> $\alpha$ 3

with other GABA<sub>A</sub> (a1, a2, or a5) receptor types (Studer et al., 2006). In these neurons, GABA<sub>A</sub> $\alpha$ 3 and GABA<sub>A</sub> $\gamma$ 2 are clustered together, similar to co-clustered GABA<sub>A</sub> $\alpha$ 3- $\gamma$ 2 receptors across ONa RGCs. In neurons of the nucleus reticularis thalami, lack of GABA<sub>A</sub> $\alpha$ 3 leads to a disruption in GABA<sub>A</sub> $\gamma$ 2 clustering (Studer et al., 2006), similar to our observations of a severe attenuation in GABA<sub>A</sub> $\gamma$ 2 puncta across a3KO ONa RGCs. In contrast, although GABAAa3 and GABAAy2 deficiency impaired the clustering of gephyrin in a3KO nucleus reticularis thalami neurons (Studer et al., 2006), the gephyrin distribution across a3KO ONa RGCs remained unchanged in terms of both its distribution and its density. One possibility for this observation could be the very early expression of gephyrin across ONa RGCs compared with the timeline of GABAA and GlyR expression. As gephyrin expression levels across the ONa reach mature levels as early as P8, it seems likely that gephyrin does not require the presence of either GABAA or GlyR receptors for its postsynaptic localization and could be upstream to the role of GABAAa3 for the organization and formation of ONa inhibitory synapses. In contrast to gephyrin, however,  $GABA_A \alpha 3$  and GlyR expression levels along ON $\alpha$  dendrites reach mature levels around the time of eye opening, and GABA<sub>A</sub> $\alpha$ 3 expression precedes emergence of GlyR $\alpha$ 1 receptors. Thus, early GABAAa3 might play an instructive role for the recruitment and clustering of GlyRa1 at ONa mixed GABA<sub>A</sub>a3-GlyRa1 synapses. Our observation that the proportion of GlyRa1 lost in a3KO ONa RGCs could represent the mixed GABAAa3-GlyRa1 synapse fraction reaffirms this organizational role of early  $GABA_A\alpha 3$  receptors. Of note, the organizational role of GABAAa3 during retinal circuit assembly is circuit specific, as inhibitory microcircuits (containing mixed GABAAa3-GlyRa1 synapses) impinging on the ONa RGC are selectively altered, and GlyRa1 synapses distributed across other RGC types such as OFF RGCs are not impaired upon GABAAa3 deficiency. Future studies are necessary to delineate the functional consequences of lost mixed GABAAa3-GlyRa1 synapses on the response properties of ONa RGCs.

#### ON-WACs as a presynaptic interneuronal partner to ONa RGCs

The ON-WACs reconstructed in our study provide inhibitory input onto the ONa predominantly at synapses with dual synaptic vesicle release sites. Interestingly, the glutamatergic (excitatory) input that the ONa RGC receives through type 6 bipolar cells (Schwartz et al., 2012) is at multisynaptic sites (Morgan et al., 2011), which could underlie the robust excitatory drive provided by type 6 bipolar cells to ONa RGCs (Schwartz et al., 2012). The input from ON-WAC multi-release sites onto ONa RGCs could thus represent the inhibitory counterpart to the type 6 bipolar cell->ONa excitatory synapse. Of note, thalamic afferents also use multi-release site presynaptic boutons for synapsing onto cortical interneurons to guarantee reliable transmission (Bagnall et al., 2011). Thus, the multi-release site appositions between the ON-WACs->ONa RGCs could be a "fail-safe" mechanism of synaptic inhibition.

The morphology of the ON-WAC resembles the type 53 AC type determined by Helmstaedter et al. (2013) during their connectomic reconstructions of the inner retina. The functional role of the ON-WAC remains to be determined, and future studies capitalizing on new AC transgenic lines would be needed to target this cell type for electrophysiology. Of note, a recent study profiling the AC population found ACs in the inner nuclear layer

positive for both the glycinergic AC marker glycine transporter-1 and the GABA synthetic enzyme (glutamic acid decarboxylase) (Yan et al., 2020). The ON-WAC profiles unveiled in our study do have somata in the inner nuclear layer and could thus likely be the same AC population as observed in the profiling study. Future studies are needed to find AC-specific transgenic lines that label ON-WACs and then perform immunolabeling to show that these cells are positive for both GABA and glycinergic markers.

Mixed synaptic circuits of the CNS (i.e., synapses using more than one neurotransmitter system) can use pre- or postsynaptic segregation or specialization mechanisms. Golgiinhibitory interneurons of the cerebellar granular layer can mediate GABAergic inhibition of granule cells and glycinergic inhibition of unipolar brush cells because of the differential expression of GABARs and GlyRs in a target-specific manner and not by segregation of the inhibitory neurotransmitters across presynaptic terminals (Dugué et al., 2005). In contrast, the ON-WACs identified in our study could potentially use a model in which GABA and glycine are released at distinct sites along the presynaptic terminal boutons, as suggested by our EM observation of dual synaptic vesicle release sites of ON-WAC boutons. Other ACs have been reported to co-release different neurotransmitters: the starburst ACs co-release acetylcholine and GABA through distinct presynaptic vesicle pools (Lee et al., 2010), and the dopaminergic ACs co-release dopamine and GABA from synaptic vesicles that can express transporters for both neurotransmitters leading to co-enrichment and simultaneous release (Hirasawa et al., 2012). Given that the same vesicular transporter can enrich both GABA and glycine within presynaptic vesicles (Wojcik et al., 2006), future EM studies using postembedding immunogold labeling for the two inhibitory neurotransmitters are needed to determine if GABA-containing vesicles and glycine-containing vesicles are differentially enriched at segregated ON-WAC release sites. Thus, our results showing the presence of mixed GABA-glycine inhibitory circuits in the retina will motivate future studies that further explore the structural and functional properties of this motif of retinal inhibition and how it is recruited to support retinal processing.

# STAR \* METHODS

#### **RESOURCE AVAILABILITY**

**Lead contact**—Further information and requests for resources and reagents should be directed to and will be fulfilled by the Lead Contact, Mrinalini Hoon (mhoon@wisc.edu).

Materials availability—This study did not generate new unique reagents.

**Data and code availability**—The datasets supporting the current study have not been deposited in a public repository because of extremely large file sizes but are available from the Lead Contact on request.

#### EXPERIMENTAL MODEL AND SUBJECT DETAILS

All experiments were performed in accordance with the guidelines of the Institutional Animal Care and Use Committee of the University of Wisconsin-Madison and the National Institutes of Health. Animals of both sexes were used for experiments. *Thy1*-YFPH mice

(Bleckert et al., 2014; Feng et al., 2000) were used at P8, P12, P16, P21 and adult (> 1.5months) time-points. This line was crossed into the GABA<sub>A</sub> $\alpha$ 3 knockout transgenic line (Yee et al., 2005) and age-matched adult (> 1.5 month) littermate control and knockout animals were used for all the GABA<sub>A</sub> $\alpha$ 3 knockout analyses. To visualize GABA<sub>A</sub> $\gamma$ 2 receptor sites across the RGC arbors, the *Thy1*-YFP $\gamma$ 2 mice (Bleckert et al., 2013) were utilized and crossed into the GABA<sub>A</sub> $\alpha$ 3 knockout background to assess GABA<sub>A</sub> $\gamma$ 2 puncta across RGCs in age-matched adult (> 1.5 month) littermate control and GABA<sub>A</sub> $\alpha$ 3 knockout animals. For experiments involving biolistics, 1.2–1.5 month old *Thy1*-GABA<sub>A</sub> $\gamma$ 2YFP × GABA<sub>A</sub> $\alpha$ 3 knockout and age-matched littermate control animals were used (Figure 7) and 1.2–1.5 month old age-matched GABA<sub>A</sub> $\alpha$ 3 knockout-littermate control animals were used for PSD-95 transfections (Figure S7). All electrophysiology experiments were carried out on 1.5 month old wild-type animals (C57B6/J; Jackson Labs).

## METHOD DETAILS

**Immunohistochemistry**—Animals were euthanized with Isoflurane, decapitated, and enucleated. Retinas were dissected in cold oxygenated mouse artificial cerebrospinal fluid (mACSF, pH 7.4) containing (in mM): 119 NaCl, 2.5 KCl, 2.5 CaCl<sub>2</sub>, 1.3 MgCl<sub>2</sub>, 1 NaH<sub>2</sub>PO<sub>4</sub>, 11 glucose, and 20 HEPES. During retina dissections note was taken of retinal location and orientation (Wei et al., 2010). Whole-mount immunolabelings were performed on retinas that were flattened on a filter paper (Millipore, HABP013). Flat-mounted retinas were fixed for 15 mins in 4% paraformaldehyde (in mACSF). After rinses in phosphate buffer (PBS), the retinas were pre-incubated in blocking solution containing 5% donkey serum and 0.5% Triton X-100 (in PBS) followed by incubation with primary antibodies in blocking solution over 3-4 nights at 4°C. Primary antibodies used were directed against: GFP (1:1000, chicken, Abcam), GABAAa3 (1:3000, guinea pig, J.M. Fritschy), GABAAa1 (1:5000, guinea pig, J.M. Fritschy), GlyRa1 (1:500, mouse monoclonal mAb2b, Synaptic Systems) and gephyrin (1:1000, mouse monoclonal clone 3B11, Synaptic systems). Secondary antibody incubation was carried out overnight in PBS using anti-isotypic Alexa Fluor (1:1000, Invitrogen) or DyLight conjugates (1:1000, Jackson Immunoresearch). Retinas were subsequently mounted on slides using Vectashield mounting medium (Vector Labs).

**Biolistic transfections**—Gold particles (1.6 µm diameter, Bio-Rad) were coated with DNA plasmids encoding either tdTomato or postsynaptic density protein 95 fused to cyan fluorescent protein (PSD95-CFP) under the control of the cytomegalovirus (CMV) promoter (Bleckert et al., 2013; Okawa et al., 2019). The particles were biolistically delivered to whole-mount retinas using a Helios gene gun (Bio-Rad). Transfected retinas were subsequently incubated in mACSF solution in a humid oxygenated chamber at 33°C for a period of 24–26 hours. Post-incubation, retinas were fixed for 20 mins in 4% PFA and after washes in PBS were either mounted and coverslipped directly or processed for immunohistochemistry as described in the previous section.

**Image acquisition and analysis**—Image were acquired using a Leica laser scanning confocal microscope (Leica TCS LSP8), or an Olympus FV1000 confocal microscope. All image stacks were acquired using a 63x oil immersion objective (NA 1.4) with an

approximate voxel size of  $0.1 \ \mu m \times 0.1 \ \mu m \times 0.4 \ \mu m$  (X-Y-Z resolution). Given the gradient in ONa RGC dendritic arbors across the nasal-temporal axis of the retina (Bleckert et al., 2014), these regions were avoided when collecting ONa RGC data across transgenic retinas to ensure comparable dendritic field sizes across the different retinas and genotypes. Raw images were subsequently median-filtered using ImageJ (FIJI, NIH) and visualized using Amira image analyses software (Thermo Fisher Scientific). For extracting synaptic signal specifically within ONa RGCs, the soma and dendrites of ONa RGCs were masked in 3D using the *LabelField* function in Amira. Thereafter the *Arithmetic* function was utilized to multiply a synaptic protein channel with the RGC mask.

For estimating colocalization between GlyRa1 and GABAAa3 puncta, the GlyRa1 signal within the ONa RGC was first isolated and each individual puncta was masked in 3D to create regions of interest (ROIs) encompassing the entire puncta volume (across image planes). These delineated ROIs specifically marked GlyRa1 receptor puncta volume in 3D within the ONa RGC. A custom written MATLAB code (Mathworks, USA) was thereafter used to ascertain colocalization between the demarcated GlyRa1 puncta and the GABAAa3 channel. The GABA<sub>A</sub> $\alpha$ 3 receptor channel was first thresholded as described in Hoon et al., 2017 and Sinha et al., 2017 to exclude any background (noise) signals. To threshold the GABAAa3 signal, a plot of all GABAAa3 pixels was considered and a threshold 3 standard deviations above the noise peak was selected (for more details see Hoon et al., 2017 and Sinha et al., 2017). The proportion of GlyRa1 puncta (ROI) that also contained the thresholded GABAAa3 signal within their 3D volume was next calculated. A GlyRa1 puncta was deemed as "colocalized" if the thresholded GABA<sub>A</sub> $\alpha$ 3 signal occupied more than 20% volume of all pixels representing the GlyRa1 punctum. Analyzing the proportion of GlyRa1 ROI that were colocalized (i.e., volume overlap with GABAAa3) yielded a % colocalization. To assess random interactions, the GABAAa3 channel was flipped 90 degrees and a % colocalization determination was made similar to the procedure outlined above (see also Sinha et al., 2017 for additional details). As our analyses routine considers the entire 3D volume of the GlyRa1 we are also accounting for scenarios where the two receptor puncta are offset and incorporates postsynaptic scenarios where the GABA<sub>A</sub> $\alpha$ 3 and GlyRa1 clusters are partially overlapping and apposed to dual release presynapses as observed in the ONa electron microscopy data and synaptic arrangements shown in scenarios III-IV (Figure 2A).

For estimation of % receptor occupancies across the dendritic arbors of ONa RGCs, the dendrites of the RGCs were masked in 3D using Amira and multiplied with the receptor channel to isolate the receptor signal within the RGC dendrites (as described above). A threshold was thereafter applied to the receptor channel (3 standard deviations above the channel noise peak, see Hoon et al., 2017; Sinha et al., 2017 for more details) to eliminate background noise pixels and quantify volume of 'detected' receptor pixels within the RGC dendritic mask. The volume of the receptor pixels was expressed relative to the RGC dendritic volume for determination of the % receptor occupancy. This method ensured normalization across RGC dendritic sizes.

For quantifying the number of synaptic puncta within the soma and dendrites of ONa RGCs, the soma and dendrites of an individual ONa RGC were at first masked out (using

Amira as described above) and the synaptic channel signal specifically within these structures was isolated. ROIs delineating each receptor cluster (puncta) were thereafter generated for the clusters along the ONa RGC dendrite and within the soma. These masks were imported into MATLAB and a custom written code extracted the soma centroid location, total dendritic volume, puncta size, puncta number, and puncta centroid location. Receptor puncta within soma or dendrite were thereafter ascertained to calculate puncta number and density estimates.

**Electron microscopy**—The *Thy1*-YFP line was used to visualize the ONa RGC for branding its location with fiduciary marks using the technique of Near-infrared branding (NIRB) (Bishop et al., 2011; Bleckert et al., 2013). The retina was processed for generating electron microscopy blocs using the protocol and steps outlined in Della Santina et al., 2016. Fiduciary marks were used to identify the location of the ONa RGC at the electron microscope level. A Zeiss 3 View serial block face scanning electron microscope was used to image the retinal region with the ONa RGC in a  $3\times 2$  montage (tiles approximately  $50\times 50$  $\mu$ m; 8000×8000 pixels per tile and z section thickness of 50nm) centered on the NIRBed ONa RGC to capture the soma and the proximal dendritic arbors. Image stacks were visualized and aligned using TrakEM2 plugin of Fiji (ImageJ, NIH). The ONa RGC was reconstructed and all inhibitory synapses annotated to determine distribution of these sites across the proximal dendritic arbor. Amira was used for visualization and display. For analyses of the synaptic distribution across a wider dendritic field of an ONa RGC and for tracing of connected presynaptic partners, the k0725 dataset was obtained through the Briggman Lab (courtesy of Dr. Kevin Briggman) and visualized using the KNOSSOS software (Max Planck Institute for Medical Research in Heidelberg, Germany). Skeletons of cells were exported into Amira using MATLAB codes from the Briggman Lab and locations of soma and synapses were depicted as spheres. Acquisition parameters and sample preparation details of the k0725 dataset is described in Ding et al., 2016.

In the k0725 dataset, the ONa RGC was identified by its characteristic dendritic lamination in the retinal inner plexiform layer. This was done by masking potential RGCs and comparing their dendritic lamination with skeletons of ON Starburst ACs (SACs) provided by the Briggman lab (Ding et al., 2016) as ONa RGC dendrites should laminate below the ON SAC arbors (Krieger et al., 2017). Only one ONa RGC was thus identified based on our criterion. As the soma of this cell was not completely within the boundaries of the dataset, synaptic information for the cell was acquired from analyses of all of its dendritic arbors within the volume of the stack.

Inhibitory synapses were identified by the presence of a pool of synaptic vesicles clustered along a release site and apposed to a thickened pre- and postsynaptic membranes as previously described (Gray, 1969). Synapses were only confirmed when 2–3 consecutive image planes displayed these ultrastructural features. Single and multiple release sites were confirmed by scrutinizing synaptic vesicle clustering across 2–3 consecutive image planes. The synaptic distribution was ascertained by this analysis procedure for both the NIRBed ONa RGC as well as the ONa RGC arbors in the k0725 dataset. Presynaptic boutons with multiple release sites resembled the ultrastructure of thalamic afferents->cortical interneuron synapses (Bagnall et al., 2011). To quantify the distance between two vesicle clusters in a

multi-release presynaptic bouton, we quantified the distance between the centers of the two vesicle pools and averaged this measure across 2–3 consecutive image planes. On average two vesicle clusters in a multi-release ON-WAC bouton were separated by a distance of  $319.30 \pm 24.73$  nm (n = 58 boutons with dual release sites). Synapses were classified by number of release sites into single or multiple (dual, triple or quadruple) and these categories were non-overlapping. To measure bouton diameter, the EM planes with the largest bouton diameter were considered and for each bouton a diameter average across 2–3 consecutive image planes was calculated.

For identifying and tracing presynaptic amacrine partners in the k0725 dataset, starkly visible (most-prominent) dual release site-containing amacrine boutons were traced to identify and mask presynaptic amacrine interneurons/partners. Upon identification of 3 Widefield ON-laminating Amacrine Cells (ON-WACs), total inhibitory output onto the ONα RGC from each interneuron was quantified using the same procedure as described above. We also determined the output (inhibitory synapses) made by the ON-WACs onto other (non-ONα) ganglion cells, amacrine cell processes and bipolar cell terminals. Retinal bipolar cell terminals were characterized by presence of ribbon sites, amacrine processes were determined by presence of large microtubule-filled dendrites that lack output synapses or accumulation of synaptic vesicles similar to criteria detailed in Gamlin et al. (2020).

Patch-clamp electrophysiology—Retinae from light-adapted wild-type mice were used for electrophysiology experiments. Isolated retina was stored in oxygenated (95% O<sub>2</sub>/5% CO<sub>2</sub>) Ames medium (Sigma-Aldrich, St. Louis, MO) at ~30°C. Isolated retinas were flattened onto poly-l-lysine slides (Sinha et al., 2016), placed in a upright microscope, and perfused with oxygenated Ames solution at a rate of ~5 mL/min. During recordings, retinal neurons were visualized and targeted using infrared illumination (940 nm, Sutter Instrument). ONa RGCs, were targeted based on their relatively big soma size and their light-evoked response characteristics assessed by cell-attached spike recordings (Figures S3A and S3B). A full-field light stimuli (diameter 450 µm) was delivered to the tissue from an LED with peak spectral output at 505 nm at an intensity that caused isomerization of ~1000 opsin molecules per cone per second. Electrophysiological recordings were performed using a MultiClamp 700B amplifier (Molecular Devices) by fire polished borosilicate glass pipettes (3-5 MU; Sutter Instrument) pulled using a DMZ-Zeitz puller (Zeitz Instruments). All voltage traces were sampled at 50 kHz and low pass filtered at 3 kHz. All electrophysiology data were acquired by a MATLAB-based data acquisition software (Symphony-DAS). Voltage-clamp recordings were obtained using pipettes filled with an intracellular solution containing (in mM) the following: 105 CsCH<sub>3</sub>SO<sub>3</sub>, 10 TEA-Cl, 20 HEPES, 10 EGTA, 2 QX-314, 5 Mg-ATP, 0.5 Tris-GTP (~280 mOsm; pH ~7.3 with CsOH). Alexa 594 dye (100–200 microM) was included in the intracellular solution to image the ganglion cells post recording as shown in Figure 2B. Miniature inhibitory postsynaptic currents (mIPSCs) were isolated by including blockers for glutamate receptors - 5 µM NBQX (2,3-Dioxo-6-nitro-1,2,3,4-tetrahydrobenzo[f]quinoxaline-7-sulfonamide disodium salt - AMPA receptor antagonist) and 50 µM D-AP5 (D-(-)-2-Amino-5phosphonopentanoic acid - competitive NMDA antagonist) together with 0.1 µM TTX

(Tetrodotoxin – voltage-gated sodium channel blocker), in the Ames solution. For sIPSC recordings, TTX was excluded from the excitatory blocker cocktail. Inhibitory postsynaptic current measurements were made before and after the application of 20 µM GABAzine (selective GABA<sub>A</sub> receptor blocker) or 2 µM Strychnine (Glycine receptor antagonist). mIPSCs and sIPSCs were detected using a built-in event detection routine in the Neuromatic software (Rothman and Silver, 2018). Events were then analyzed for estimating kinetics, frequency, and amplitude of m/sIPSCs using Neuromatic and self-written routines in Igor Pro (Wavemetrics, USA) and MATLAB (Mathworks, USA). mIPSC recordings were performed at a membrane potential of -70 mV where the inhibitory synaptic currents appear as inward currents. sIPSC recordings were performed at a membrane potential of 10 mV where the inhibitory synaptic currents appear as outward currents. We verified that decay kinetics of sIPSCs are slower at room temperature (Average  $\pm$  SEM for decay time of sIPSC events from 5 ONa RGCs =  $2.89 \pm 0.37$ ) compared to recordings at physiological temperatures (~30°C; decay time distribution in Figure S3; Average  $\pm$  SEM = 1.778  $\pm$  0.164) as suggested for mouse retinal alpha ganglion cells by Majumdar et al., 2007 (Majumdar et al., 2007).

#### QUANTIFICATION AND STATISTICAL ANALYSIS

Statistical details of experiments and comparative analyses including number of cells/ animals analyzed and tests utilized is provided in the Figure legends. Unless otherwise stated plotted graphs represent mean  $\pm$  SEM values.

## **Supplementary Material**

Refer to Web version on PubMed Central for supplementary material.

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# Highlights

- Mixed GABA-glycine synapses are present across ON-sustained ganglion cell dendrites
- GABA and glycine are not co-released from the same presynaptic vesicle
- Widefield amacrine cells synapse with ON-sustained dendrites at dual release sites
- Early expression of GABA receptors recruits glycine receptors at mixed synapses



Figure 1. Mixed GABA-glycine receptor postsynapses are localized across ONα dendrites
(A) Schematic of neural organization in mouse retina. Dim- and bright-light signals are sensed by rod and cone photoreceptors, which synapse onto rod and cone bipolar cells
(BCs). Cone BCs provide direct excitatory input to ONα RGC at the inner plexiform layer, but rod BC signals are ferried to ONα RGC through AII interneurons. The ONα RGC receives inhibitory input from GABA and glycinergic amacrine cells (amacrine).
(B) GABA<sub>A</sub>α3 (green) and GlyRα1 (magenta) receptor puncta within ONα RGC soma and proximal dendrites (blue) as visualized in the *Thy1*-YFP line. Inset shows higher magnification view of selected dendritic segment. White arrows point to three examples of colocalized GABA<sub>A</sub>α3 and GlyRα1 puncta.

(C) Percentage colocalization of GlyRa1 puncta within ONa and GABA<sub>A</sub>a3 receptors. The random estimate was generated by flipping the GABA<sub>A</sub>a3 receptor channel 90° (n = 4 ONa RGCs from three retinas and three animals).



Figure 2. GABA and glycine are not co-released from the same presynaptic release vesicle onto ONa RGCs

(A) Different scenarios as to how "mixed" GABA-glycine synapses could be organized.

(B) An ONa RGC targeted for single-cell electrophysiology and filled with Alexa 594.

(C) Exemplar traces of miniature inhibitory postsynaptic currents (mIPSCs) recorded from

ONa in the presence of NBQX, D-APV, and TTX (control; black trace) and after application of GABAzine (red trace).

(D) Quantification of mIPSC amplitude in control condition and after application of GABAzine.

(E) Quantification of occurrence (frequency) of mIPSCs in control condition and after application of GABAzine. A significant reduction in mIPSC frequency (p = 0.0144) was observed.

A paired two-tailed t test was performed for (D) and (E).

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Figure 3. Inhibitory input with dual synaptic vesicle release sites uncovered by SBFSEM of inhibitory synapses across ONa RGCs  $\,$ 

(A) An ONa in the *Thy1*-YFPH transgenic line after burning of fiduciary marks to locate and reconstruct the cell by SBFSEM.

(B) Three-dimensional (3D) reconstruction of the ONa RGC and proximal dendritic arbor (RGC, cyan-green) with annotated sites of inhibitory synaptic inputs (Inh synapse, red).

(C) Exemplar sections from a region of the ONa dendrite (cyan) with annotated inhibitory synapses containing single (top image) and dual (bottom image) release sites.

(D) (C' and C'') Magnified view of inhibitory synapses on the ON $\alpha$  arbor (cyan) with single (C') and dual (C'') synaptic vesicle release sites. Each synaptic vesicle release site is demarcated with a red line.

(D) Distribution of inhibitory synapses across the ONa as sorted into synapses with single, dual, triple, and quadruple release sites. This distribution was determined from the NIRBed ONa RGC.

(E) Top-down view of the dendritic arbor of an ONa RGC (cyan, reconstructed from k0725 dataset) with all dual synaptic vesicle release sites annotated (yellow). The bottom panel shows a side profile of the ONa with dual inhibitory synaptic sites distributed across both the proximal and distal dendritic arbor.

(F) Distribution of inhibitory synapses across the entire dendritic arbor of the ONa as sorted into synapses with single, dual, triple, and quadruple release sites. This distribution was determined from the ONa reconstructed from the k0725 dataset from Ding et al. (2016).





(A–C) Top-down view of SBFSEM reconstructions of three widefield ON-laminating amacrine cells that provide input onto the ONa dendritic arbor (cyan) at dual synaptic vesicle release sites (yellow). Widefield ON amacrine 1, magenta (A); widefield ON amacrine 2, pink (B); widefield ON amacrine 3, red (C). Bottom panels represent side profile of the amacrine neuron and ONa with dual synaptic sites annotated. (A'–C') Distribution of the number of synapses with single, dual, or triple vesicle release sites the respective widefield ON amacrine cell makes onto the ONa dendritic arbor. (A''–C') Three-dimensional (3D) reconstruction of the widefield ON amacrine cell and the ONa RGC with three example raw EM images demonstrating inhibitory synaptic contact between the respective amacrine and ONa RGC at synapses with two synaptic vesicle release sites. Each synaptic vesicle release site is demarcated with a red line. All reconstructions performed on the k0725 dataset from Ding et al. (2016).



Figure 5. GABAergic synapses are established before glycinergic synapses on the ONa RGC dendritic arbor

(A) ONa RGC co-labeling with GABA<sub>A</sub>a3 and GlyRa1 across time points in the *Thy1*-YFP line (P, postnatal day). GABA<sub>A</sub>a3 (green) and GlyRa1 (magenta) signal within the RGC is overlaid on the RGC channel (blue), followed by a merge of only the receptor signals within the cell.

(B) ONa RGCs co-labeling with gephyrin across development. Gephyrin signal within the cell (yellow) is overlaid on the RGC channel (blue). For (A) and (B), below the full RGC 3D view is a short dendritic segment at higher magnification (regions selected for each stack annotated with a rectangle).

(C) Quantification of the percentage dendritic occupancy of each postsynaptic marker (GABA<sub>A</sub> $\alpha$ 3, green; gephyrin, yellow; GlyR $\alpha$ 1, magenta) within developing ON $\alpha$  RGCs. Number of cells quantified at each time point in parenthesis (the different colors correspond to the number of cells analyzed for the specific synaptic marker). N 3 animals. P8 versus P12 GABA<sub>A</sub> $\alpha$ 3 (p = 0.0135) and P8 versus P12 GlyR $\alpha$ 1 (p = 0.0025) RGC occupancies were significantly different. An unpaired two-tailed t test was performed. Scale bars, 30 µm.

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#### Figure 6. ONa GlyR clusters are downregulated in the ${\rm GABA}_{\rm A}{\rm a}{\rm 3KO}$

(A) Three-dimensional (3D) en face view of an ONa RGC (red) in littermate control (Ctrl; top panel) and GABA<sub>A</sub>a3KO (a3KO; bottom panel) in *Thy1*-YFP × GABA<sub>A</sub>a3KO double-transgenic immunolabeled for glycine receptor al sites (GlyRa1, yellow; insets show higher magnification view of select dendritic segments). Detected GlyRa1 within the soma (magenta) and dendritic arbor (cyan) of the ONa were both downregulated in the a3KO RGC compared with Ctrl.

(B) Quantification of the total number of detected GyRa1 puncta, GlyRa1 puncta within the dendrites, and GlyRa1 puncta within the ONa RGC soma in the a3KO and Ctrl. All fractions of GlyRa1 are significantly reduced in the a3KO compared with Ctrl. Numbers in parentheses are number of cells, number of animals sampled. An unpaired two-tailed t test was performed.



# Figure 7. GABAAA $\gamma 2$ but not gephyrin is downregulated across ONa arbors in the absence of GABAAa3

(A) Dendritic segment of an ON $\alpha$  RGC in the *Thy1*-GABA<sub>A</sub> $\gamma$ 2YFP (green) transgenic line with co-labeling for GABA<sub>A</sub> $\alpha$ 3 (red) and gephyrin (magenta) demonstrating that these postsynaptic proteins are colocalized across ON $\alpha$  inhibitory synapses.

(B) Three-dimensional (3D) en face view of ON $\alpha$  RGCs in littermate control (Ctrl; top panel) and GABA<sub>A</sub> $\alpha$ 3KO ( $\alpha$ 3KO; bottom panel) retina crossed into the *Thy1*-

 $GABA_A\gamma 2YFP$  line. ONa RGCs in the *Thy1*-GABA\_A\gamma 2YFP × GABA\_a 3KO doubletransgenic were visualized by biolistic transfection (*CMV*-tdTomato; red). GABA\_A\gamma 2 receptor puncta detected within the ONa RGC (green) are downregulated in the a 3KO. (C) Co-labeling of ONa (red) in Ctrl (top panel) and a 3KO-*Thy1*-YFP (bottom panel) retina with gephyrin (detected puncta within RGC visualized in green).

(D) Top panel: quantification of total and dendritic  $GABA_A\gamma 2$  puncta within Ctrl and  $\alpha 3KO$  ON $\alpha$  RGCs. Bottom panel: quantification of total and dendritic gephyrin puncta within Ctrl and  $\alpha 3KO$  ON $\alpha$  RGCs. Numbers in parentheses are number of cells, number of animals sampled. An unpaired two-tailed t test was performed.

## KEY RESOURCES TABLE

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Antibodies		
Chicken anti-GFP	Abcam	Catalog # ab13970; RRID: AB_300798
Mouse monoclonal anti-GlyRa1	Synaptic Systems	Catalog # 146111; RRID: AB_887723
Guinea pig polyclonal anti- GABA <sub>A</sub> α1	Fritschy and Mohler 1995	Generated in Jean-Marc Fritschy's Lab
Guinea pig polyclonal anti- GABA <sub>A</sub> a3	Fritschy and Mohler 1995	Generated in Jean-Marc Fritschy's Lab
Mouse monoclonal anti- gephyrin	Synaptic Systems	Catalog # 147111; RRID: AB_887719
Chemicals, peptides, and recombine	nant proteins	
Ames	Sigma	A1420
SR-95531 (GABAzine)	Sigma	S106
TTX	Abcam	120055
Strychnine	Sigma	S8753
Alexa 594	ThermoFisher	A10442
NBQX	Tocris	0373
D-AP5	Tocris	0106
Vectashield antifade mounting medium	Vector Labs	Catalog# H-1000
Experimental models: organisms/s	strains	
Mouse: Thy1-YFPH	R. Wong (Feng et al., 2000)	N/A
Mouse: GABAAa3 knockout	U. Rudolph (Yee et al., 2005)	N/A
Mouse: Thy1-YFP <sub>7</sub> 2	R. Wong (Bleckert et al., 2013)	N/A
Mouse: C57BL/6J	Jackson Labs	JAX Stock No: 000664
Recombinant DNA		
CMV-tdTomato	R. Wong, University of Washington (Morgan et al., 2008)	N/A
CMV-PSD95CFP	Construct modified from PSD95-YFP construct from A.M. Craig, University of British Columbia (Kerschensteiner et al., 2009)	N/A
Software and algorithms		
IGOR Pro	WaveMetrics	https://www.wavemetrics.com/
MATLAB	Mathworks	https://ch.mathworks.com/products/matlab.html
Symphony	Symphony-DAS	https://github.com/symphony-das
ImageJ	NIH	https://imagej.nih.gov/ij/
Amira	ThermoFisher Scientific	https://www.thermofisher.com/global/en/home/industrial/ electron-microscopy/electron-microscopy-instruments- workflow-solutions/3d-visualization-analysis-software/amira- life-sciences-biomedical.html

REAGENT or RESOURCE	SOURCE	IDENTIFIER
KNOSSOS	Max Planck Institute for Medical Research, Heidelberg, Germany	https://knossos.app
Neuromatic	Rothman & Silver, 2018	http://www.neuromatic.thinkrandom.com/