Glutamatergic neuronal activity regulates angiogenesis and blood-retinal barrier maturation via Norrin/β-catenin signaling

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SUMMARY

Interactions among neuronal, glial and vascular components are crucial for retinal angiogenesis and blood-

retinal barrier (BRB) maturation. Although synaptic dysfunctions precede vascular abnormalities in many

retinal pathologies, how neuronal activity, specifically glutamatergic activity, regulates retinal angiogenesis

and BRB maturation remains unclear. Using *in vivo* genetic studies in mice, single cell RNA sequencing

and functional validation, we show that deep plexus angiogenesis and paracellular BRB maturation are

delayed in *Vglut1$^{-/-}$* retinas, where neurons fail to release glutamate. In contrast, deep plexus angiogenesis

and paracellular BRB maturation are accelerated in *Gnat1$^{-/-}$* retinas, where constitutively depolarized rods

release excessive glutamate. Norrin mRNA expression and endothelial Norrin/β-catenin activity are

downregulated in *Vglut1$^{-/-}$* retinas, and upregulated in *Gnat1$^{-/-}$* retinas. Pharmacological activation of

endothelial Norrin/β-catenin signaling in *Vglut1$^{-/-}$* retinas rescued defects in deep plexus angiogenesis and

paracellular BRB integrity. Our findings demonstrate that glutamatergic neuronal activity regulates retinal

angiogenesis and BRB maturation by modulating Norrin/β-catenin signaling.

INTRODUCTION

The crosstalk among neuronal, glial, and vascular components is essential, not only for proper angiogenesis, but also for the establishment of the inner blood-retinal barrier (BRB) in the developing retina (Klaassen et al., 2013). Retinal angiogenesis is tightly coordinated with the maturation of the BRB properties by endothelial cells (ECs), through the presence of tight-junctions (TJ) that limit paracellular permeability between ECs, specialized transporters to facilitate bidirectional transport of nutrients, and suppression of transcytosis that reduces transcellular EC permeability (Chow and Gu, 2015; Zhao et al., 2015). Although multiple signaling pathways operating in ECs, pericytes (PCs), neuronal or glial cells have emerged as critical regulators of retinal angiogenesis and BRB maturation [reviewed in (Biswas et al., 2020)], it is unclear how distinct types of neuronal synaptic activities influence these processes, and whether neurotransmitters act directly on ECs to mediate their effects. This is highly significant since early loss of neurovascular coupling, impaired response of photoreceptors to light, gradual neurodegeneration, gliosis and neuroinflammation are found prior to any obvious vascular pathologies in diabetic retinopathy and other retinal disease (Abcouwer and Gardner, 2014; Pardue et al., 2014; Umino and Solessio, 2013). Moreover, it has been postulated that diabetes-induced changes in neurons and glial cells lead to vascular defects (Feit-Leichman et al., 2005); yet, the underlying mechanisms remain elusive.

Distinct types of neuronal activity are present in the postnatal mouse retina during angiogenesis and BRB maturation **(Figure 1A)**. From birth to postnatal day (P) 10, starburst amacrine cells propagate a spontaneous cholinergic wave (Bansal et al., 2000; Feller et al., 1996; Zhou, 1998). The cholinergic wave then gradually subsides and a spontaneous glutamatergic wave emerges from P10 to P14 (Bansal et al., 2000; Blankenship et al., 2009; Tiriac et al., 2018; Weiner et al., 2019). The majority of neuronal activity in the mouse retina from P14 onwards is mediated by light-dependent glutamatergic synaptic activity of photoreceptors, and photoactivation of intrinsically-photosensitive retinal ganglion cells (ipRGCs) [reviewed in (Biswas et al., 2020)]. However, light activation of photoreceptors has been observed as early

as P8 (Bonezzi et al., 2018; Tiriac et al., 2018). The superficial vascular plexus develops between P0-P8 (Stahl et al., 2010) over the ganglion cell layer (GCL) synchronous with neural activity from the cholinergic wave and photoactivation of ipRGCs. In contrast, the deep plexus (P8-P12) angiogenesis in the outer plexiform layer (OPL) (Stahl et al., 2010) and BRB maturation span both cholinergic and glutamatergic spontaneous waves, glutamatergic synaptic activity of photoreceptors as well as photoactivation of ipRGC [reviewed in (Biswas et al., 2020)]. Few studies have addressed how neuronal activity regulates retinal angiogenesis and BRB maturation in the developing retina. Photoactivation of both Opn4^{+} (Rao et al., 2013) and Opn5^{+} (Nguyen et al., 2019) RGCs regulates angiogenesis in the retina. Pharmacological blockade of cholinergic wave before P8 delays deep plexus angiogenesis and BRB maturation, suggesting an important role for cholinergic activity in these processes (Weiner et al., 2019). However, the role of glutamatergic neuronal activities in retinal angiogenesis and BRB maturation remains unclear, although this is the predominant activity when most of the vascular development and maturation occurs in the retina.

The Norrin/β-catenin signaling is critical for retinal angiogenesis and BRB maturation by inducing stabilization and nuclear translocation of β-catenin. Genetic elimination of Norrin (ligand), Frizzled-4, Lrp5/6, Tspan12 (receptors) and β-catenin in the mouse retina delays superficial vascular plexus angiogenesis, induces loss of the deep plexus (Junge et al., 2009; Luhmann et al., 2005; Xia et al., 2010; Ye et al., 2009; Zuercher et al., 2012) and BRB integrity (Paes et al., 2011; Wang et al., 2012). How Norrin expression is regulated in the retina remains unclear. Using *in vivo* anatomical and functional characterizations of the vasculature, as well as single-cell transcriptomic analyses and validation studies, we show that deep plexus angiogenesis and paracellular BRB maturation are delayed in *Vglut1*^{-/-} retinas that have reduced synaptic release of glutamate from photoreceptors and bipolar cells (Blankenship et al., 2009). In contrast, deep plexus angiogenesis is accelerated and paracellular BRB matures precociously in *Gnat1*^{-/-} retinas, where rod photoreceptors remain constitutively depolarized due to the absence of the G protein subunit α Transducin 1, critical for phototransduction (Calvert et al., 2000; Schroeder et al., 2018).

These phenotypes are not due to abnormalities in neurovascular unit (NVU) assembly, aberrant

specification of neuronal or glial subtypes, or changes in neuronal metabolic demand. Importantly, Norrin

mRNA expression in the inner nuclear layer (INL), and as a consequence endothelial Norrin/β-catenin

signaling, are downregulated in *Vglut1*^{-/-} retinas, and upregulated in *Gnat1*^{-/-} retinas. Pharmacological

activation of endothelial Norrin/β-catenin signaling in *Vglut1*^{-/-} retinas rescues defects in both deep plexus

angiogenesis and paracellular BRB integrity. Our study elucidates a critical mechanism by which

glutamatergic neuronal activity regulates retinal angiogenesis and BRB maturation by modulating Norrin/β-

catenin signaling in the developing retina. These findings have important implications for development of

potential interventions in various neurovascular pathologies.

RESULTS

Deep plexus angiogenesis is delayed in the *Vglut1*^{-/-} retina.

Photoreceptors release glutamate in the outer plexiform layer OPL in the dark and suppress

glutamate release upon photon capture (Okawa et al., 2008). The synaptic release of glutamate is dependent

on vGluT1, a vesicular glutamate transporter (Sherry et al., 2003). Consequently, *Vglut1*^{-/-} mice have

reduced synaptic release of glutamate from photoreceptors and bipolar cells **(Figure 1B, C)**(Blankenship

et al., 2009). To understand if extracellular glutamate levels affect retinal angiogenesis, we compared the

vascular growth in both the superficial and deep plexuses between wild-type (WT) and *Vglut1*^{-/-} retinas.

Since the central retina is developmentally more mature than the peripheral retina, we analyzed these two

regions separately **(Figure 1D)**. Although the vascular coverage of the retina in the superficial plexus was

similar in both genotypes by P8 and P10 **(Figure 1E-G)**, the vascular coverage of the retina in the deep

plexus and its branch-point density were reduced significantly in the *Vglut1*^{-/-} retina at P10 and P12 **(Figure**

1H-M). By P14, however, the vascular coverage of the retina in the deep plexus was similar between the

two genotypes, although the branch-point density of the *Vglut1*^{-/-} deep plexus still remained significantly

lower than the WT **(Figure 1H-M)**. Importantly, these vascular deficit patterns were consistent in both the central and peripheral retina of *Vglut1*$^{-/-}$ mice (**Figure 1I-M**).

To understand the molecular mechanisms underlying these vascular phenotypes, we performed single-cell RNA-sequencing analyses (scRNA-seq) of retinal CD31^{+} ECs purified from dissociated P10 WT and *Vglut1*$^{-/-}$ retinas by fluorescence-activated cell sorting (FACS; **Figure S1A, B)**. The purity of ECs was confirmed by uniform expression of EC markers [*Pecam1* (CD31) and *Cdh5* (VE-Cadherin)] in the entire population, and absence of mural cell [*Pdgfrb* (PDGFRβ) and *Des* (Desmin)] and astrocyte [*Gfap* and *Pdgfra*] markers **(Figure S1C)**. ECs isolated from P10 WT and *Vglut1*$^{-/-}$ retinas clustered separately on the Uniform Manifold Approximation and Projection (UMAP) plot based on differences in their transcriptomic signatures **(Figure 2A; Tables S1, S2)**. Gene ontology (GO) analyses of the differentially expressed genes (DEGs) between the two genotypes revealed that pathways involved in angiogenesis, blood vessel morphogenesis and cell proliferation were downregulated in P10 *Vglut1*$^{-/-}$ compared to WT retinal ECs **(Figure 2B; Tables S3, S4, S7)**, consistent with the phenotypic data (**Figure 1**). In contrast, pathways involved in cellular and protein metabolic processes were upregulated in P10 *Vglut1*$^{-/-}$ compared to WT retinal ECs **(Figure 2C; Tables S3, S4, S6)**. Expression levels of several pro-angiogenic genes [e.g. *Ptprb*, *Aplnr, Unc5b* etc.], including two effectors of Norrin/β-catenin pathway [*Ctnnb1* (β-catenin) and *Lef1*] were downregulated significantly in P10 *Vglut1*$^{-/-}$ compared to WT retinal ECs **(Figure 2D, F; Table S3)**. In contrast, the majority of genes enriched in the deep plexus tip cells (D-tip cells) compared to the superficial plexus tip cells (S-tip cells) [e.g. *Bsg*, *Rgcc*, *Plxnd1*, *Cdkn1a*, *Pde4b*, *Prcp*], as well as those enriched in D-tip cells compared to all ECs [e.g. *Lamb1*, *Pcdh17*, *Adm*] (Zarkada et al., 2021) were upregulated in P10 *Vglut1*$^{-/-}$ compared to WT retinal ECs **(Figure 2E, G; Table S4)**, indicative of a delay in angiogenic processes at the transcriptome level. To validate these molecular findings, we labeled proliferating cells with Ki67 in both WT and *Vglut1*$^{-/-}$ retinas to assess whether endothelial stalk cell proliferation was downregulated in *Vglut1*$^{-/-}$ retinal ECs **(Figure 2H)** (Siemerink et al., 2013) . Consistent with the scRNAseq

data, there was a significant reduction in the number of proliferating Ki67$^+$ ECs in P12 *Vglut1$^{-/-}$* retinal deep

plexus compared to the WT **(Figure 2I, J)**, while the number of apoptotic ECs (cleaved Caspase-3$^+$) was

not significantly different **(Figure 2J)**. These findings suggest that the delayed angiogenesis in *Vglut1$^{-/-}$*

retinal deep plexus is due, in part, to reduced EC proliferation. In addition, consistent with the scRNA-seq

data, we observed numerous Dll4$^+$ tip cells (Hellstrom et al., 2007; Suchting et al., 2007) in the leading edge

of the *Vglut1$^{-/-}$* deep plexus at P12, while the WT deep plexus was completely vascularized at this stage

(Figure 2K, L). These data demonstrate that angiogenesis (EC proliferation) in the retinal deep, but not

superficial, plexus, is delayed with a larger number of tip cells when there is no extracellular glutamate

release by neurons in the *Vglut1$^{-/-}$* retinas.

Paracellular BRB maturation is impaired in the *Vglut1$^{-/-}$* retina.

Next, we asked if diminished glutamate release from photoreceptors and bipolar cells affects BRB

maturation. We injected intravenously biocytin-tetramethylrhodamine (biocytin-TMR, 870 Da) tracer in

WT and *Vglut1$^{-/-}$* mice at P10 and P14 and quantified its leakage in the retina as a functional readout of the

paracellular BRB maturation **(Figure 3A)**(Biswas et al., 2022; Mazzoni et al., 2017). There was a

significantly higher biocytin-TMR leakage (area and intensity) in the *Vglut1$^{-/-}$* compared to the WT retinas

at both time points **(Figure 3B-G)**. Importantly, these patterns were consistent in both the central and

peripheral retina, and the superficial and deep plexuses. Consistent with a delay in BRB maturation, our

scRNA-seq analyses showed that expression levels of most genes that promote BRB maturation were

downregulated in P10 *Vglut1$^{-/-}$* compared to WT retinal ECs, including tight junction-associated genes

[*Cldn5* (Claudin-5) and *Tjp1* (ZO-1)], transporters [*Slc7a5* (Lat1), *Slc2a1* (Glut1) etc.,] and effectors of

Norrin/β-catenin pathway [*Ctnnb1* and *Lef1*] **(Figure 3H, I; Table S5)**. Surprisingly, expression levels of

Ocln (Occludin; tight junction protein), vBM proteins (Collagen IV, Laminin), BBB transcription factors

(e.g. *Foxq1*, *Foxf2*, *Zic3* etc.), or caveolar-related transport (*Cav-1*, *Cav-2*, *Cavin-1*, *Mfsd2a*) were

unaffected in P10 *Vglut1$^{-/-}$* retinal ECs **(Tables S2, S5)**.

We validated if endothelial expression of tight junction proteins was reduced in the *Vglut1⁻/⁻* retina

by labeling the retinas with Claudin-5 and ZO-1. Consistent with the scRNA-seq data, there was a

significant reduction in Claudin-5 and ZO-1 protein localization to EC junctions in the P14 *Vglut1⁻/⁻*

compared to the WT retina (**Figure 3J-M**). These patterns were consistent in both the superficial and deep

plexuses (**Figure 3L, M**). Importantly, these phenotypes were not caused by abnormalities in the NVU

assembly, as mural cell (PDGFRβ⁺), glial endfeet (Aquaporin-4; Aqp-4⁺) and vascular basement membrane

(vBM; Laminin and Collagen IV) coverage of retinal blood vessels were similar between the two genotypes

(Figure S2).

We asked whether the lack of glutamate release by neurons affects also the transcellular BRB

maturation. We injected intravenously albumin-Alexa594 (MW= 60kDa), a protein that crosses the BRB

primarily through a transcellular route (Mazzoni et al., 2017) into P10 WT and *Vglut1⁻/⁻* mice and assessed

its extravasation into the retina. The tracer was largely confined within the blood vessels in both genotypes,

and its intensity in the parenchyma was very low and identical between the genotypes **(Figure S3A, B)**. In

addition, there was no difference in endogenous serum IgG leakage between P10 WT and *Vglut1⁻/⁻* retinas

(Figure S3C). These functional studies are consistent with the scRNAseq data showing no change in the

expression of *Mfsd2a*, required for suppression of transcellular BRB permeability (Chow and Gu, 2017),

between the two genotypes **(Table S2)**. In addition, immunofluorescence analysis showed no difference in

retinal EC expression of Caveolin-1, a transmembrane protein responsible for endothelial transcytosis

(Biswas et al., 2020; Gu et al., 2014), between the two genotypes **(Figure S3D, E).** Finally, PLVAP

expression, a component of the diaphragms of EC fenestrae normally found in the immature BRB (Bosma

et al., 2018) **(Figure S3F)**, was absent in ECs from both genotypes despite a slight downregulation of *Plvap*

mRNA in P10 *Vglut1⁻/⁻* retinal ECs by scRNA-seq **(Figure 3H; Table S5)**. Together, these data demonstrate

that there is a delay in the paracellular, but not transcellular, BRB maturation in both the superficial and

deep plexuses in retinas with decreased extracellular glutamate **(Figure S3G)**.

BRB maturation is accelerated in the absence of the cholinergic wave due to an early onset of

glutamatergic activity.

192   During development, the cholinergic wave persists beyond P10 in the *Vglut1^{-/-}* retina lacking

glutamatergic neuronal activity (Blankenship et al., 2009). Conversely, the glutamatergic wave begins

earlier (P8) than usual in the *Chrnb2^{-/-}* retina where the cholinergic wave is abolished (Bansal et al., 2000).

It has been recently reported that pharmacological blockade of cholinergic waves before P8 delays deep

plexus angiogenesis and BRB maturation, suggesting an important role for cholinergic activity to promote

these processes in the developing retina (Weiner et al., 2019). However, our phenotypic analysis of the

Vglut1^{-/-} retinal vasculature implies that the cholinergic wave by itself is not sufficient to induce paracellular

BRB maturation since it is very delayed in the *Vglut1^{-/-}* retina through P14 (**Figure 3**). To test this

hypothesis, we examined paracellular BRB integrity in the *Chrnb2^{-/-}* retina where cholinergic wave is

abolished and glutamatergic wave begins earlier (P8) than usual (Bansal et al., 2000) **(Figure 4A)**. There

was less biocytin-TMR leakage in the parenchyma **(Figure 4B-D),** and increased Claudin-5 coverage of

blood vessels **(Figure 4E, F)** in the P10 *Chrnb2^{-/-}* retina compared to the WT, consistent with the idea that

the earlier onset of glutamatergic wave promotes a precocious BRB maturation in the *Chrnb2^{-/-}* retina. These

data demonstrate that the glutamatergic neuronal activity, but not the cholinergic wave, is the primary driver

of paracellular BRB maturation in the developing retina.

Deep plexus angiogenesis is accelerated and paracellular BRB is precociously mature in the *Gnat1^{-/-}*

retina.

210   Phototransduction is a complex cascade, dependent in part on the G protein subunit α Transducin 1

211   (*Gnat1*). *Gnat1^{-/-}* rod photoreceptors remain constitutively depolarized (Calvert et al., 2000; Schroeder et

al., 2018) with a consequent increase in glutamate release from rods **(Figure 5A, B)**. To understand how excess glutamate release by rod photoreceptors affects retinal angiogenesis, we compared the vascular growth of the retinal superficial and deep plexuses between the WT and *Gnat1*^{-/-} retinas. While the vascular coverage of the retina in the superficial plexus was similar between the two genotypes by P10 **(Figure 5C, D)**, both the vascular coverage of the retina by the deep plexus, and its branch-point density were significantly increased in the *Gnat1*^{-/-} retina at this stage **(Figure 5E-J)**. However, the angiogenesis phenotype was transient, and by P14 there was no difference between the two genotypes **(Figure 5F, G, I, J; Figure S4A)**. Importantly, these patterns were similar in both the central and peripheral retina. Consistent with the accelerated deep plexus angiogenesis phenotype seen in the P10 *Gnat1*^{-/-} retina, there was an increased EC proliferation (Ki67^{+} ECs) in the P10 mutant compared to the WT deep vascular plexus **(Figure 5K, L)**.

Next, we asked whether excess glutamate release by rod photoreceptors affects paracellular BRB maturation. Measurements of biocytin-TMR leakage area and fluorescence intensity showed a reduction in tracer leakage in *Gnat1*^{-/-} compared to the WT retinas in the central and peripheral retinas and the superficial and deep plexuses at P10 and P14 **(Figures 5M-O; S4B-D)**. Consistent with the functional data, there was a significant increase in Claudin-5 protein localization at BRB tight junctions in the P10 *Gnat1*^{-/-} retina compared to the WT **(Figure 5P-R)**. Importantly, these patterns were uniform in both the superficial and deep plexuses. These data demonstrate that retinal deep plexus angiogenesis is accelerated and paracellular BRB integrity is precociously mature when there is excess glutamate released by the rods.

It is possible that differences in the specification of neuronal subtypes or Müller glia in either *Vglut1*^{-/-} or *Gnat1*^{-/-} retinas may be responsible for the vascular phenotypes related to angiogenesis and BRB maturation seen in these mutants. To address this issue, we immunolabelled and quantified the number of retinal neurons and Müller glia. There was no significant difference in the number of ganglion cells [NeuN[+]

(Buckingham et al., 2008; Hajdu et al., 2019)], amacrine (except for a slight reduction in the *Vglut1*^{-/-} retina)

and horizontal cells [Calbindin[+] (Usui et al., 2015)], photoreceptors [measured by outer nuclear layer (ONL)

thickness] among the three genotypes **(Figure S5A-I)**. Similarly, the number of Müller glia, measured by

Sox9 labeling (Poche et al., 2008; Serjanov et al., 2018) was similar among WT, *Vglut1*^{-/-} and *Gnat1*^{-/-}

retinas **(Figure S5J, K).** Therefore, the angiogenesis and BRB phenotypes seen in *Vglut1*^{-/-} and *Gnat1*^{-/-}

retinas are not caused by defects in neuronal and glial cell type specification.

Neurons and Müller glia in the inner nuclear layer of the retina respond to altered levels of

extracellular glutamate.

To understand how extracellular glutamate concentration affects retinal angiogenesis and

paracellular BRB maturation, we first asked whether glutamate can act directly on retinal ECs. Our scRNA-

seq analyses of P10 and P14 WT retinal ECs revealed that neither ionotropic (*Grin1*, *Grin2b*, *Grin2d*,

Gria1), nor metabotropic (*Grm3*, *Grm5*, *Grm6*, *Grm7*, *Grm8*) glutamate receptor subunits are expressed in

retinal ECs at these time points **(Figure S6A).** Thus, the action of glutamate is unlikely to be directly on

retinal ECs. Analysis of a previously published scRNAseq database of all cell types from the P14 retina

(Macosko et al., 2015) showed that ionotropic and metabotropic glutamate receptor subunits are expressed

primarily by the inner nuclear layer (INL) neurons and Müller glia **(Figure S6B)**, suggesting that

extracellular glutamate could act on INL neurons and Müller glia.

To examine whether altered levels of extracellular glutamate are sensed by Müller glia in *Vglut1*^{-/-}

and *Gnat1*^{-/-} retinas, we measured the expression levels of glutamine synthetase (GS) - an enzyme that

coverts glutamate to glutamine -, and Glutamate Aspartate Transporter [GLAST, or excitatory aminoacid

transporter 1 (EAAT-1)] - a glutamate transporter. These proteins are upregulated in Müller glia when

exposed to excess extracellular glutamate (Shen et al., 2004; Taylor et al., 2003). GS and GLAST protein

expression levels, measured by the mean fluorescence intensity, were downregulated in *Vglut1*^{-/-}, and

upregulated in *Gnat1*$^{-/-}$ retinas, compared to the WT levels **(Figure 6A-D)**. To determine whether altered

levels of extracellular glutamate are sensed by neurons in *Vglut1*$^{-/-}$ and *Gnat1*$^{-/-}$, we measured the expression

levels of Glutamate Transporter 1 [GLT-1, or excitatory aminoacid transporter 1 (EAAT-2)], a glutamate

transporter expressed primarily in retinal neurons (Harada et al., 1998), with expression regulated by the

extracellular glutamate (Russo et al., 2013). GLT-1 expression in INL neurons was downregulated in the

Vglut1$^{-/-}$, and upregulated in the *Gnat1*$^{-/-}$ retinas, compared to the WT **(Figure 6E-F)**. These findings

confirm that altered levels of extracellular glutamate, present in either *Vglut1*$^{-/-}$ or *Gnat1*$^{-/-}$ retinas, are sensed

by Müller glia and INL neurons. Importantly, altered levels of extracellular glutamate do not trigger Müller

cell gliosis in *Vglut1*$^{-/-}$ and *Gnat1*$^{-/-}$ retinas, as there was no upregulation of GFAP expression [a marker of

gliosis; (Hippert et al., 2015; Lee et al., 2021)] in Müller glia processes spanning multiple retinal layers

(**Figure S5L**). However, normal GFAP expression was detected in retinal astrocytes over the GCL

(colocalized with PDGFRα) in all genotypes **(Figure S6L, M)**.

Next, we asked whether alterations in neuronal metabolic demand may trigger the vascular

phenotypes in *Vglut1*$^{-/-}$ and *Gnat1*$^{-/-}$ retinas. We examined expression levels of hexokinase-2 (HK2) and

pyruvate kinase M-2 (PKM2), two key glycolytic enzymes that are readouts of neuronal metabolism (Cheng

et al., 2020), by Western blotting. The levels of these enzymes were similar in both P10 WT, *Gnat1*$^{-/-}$ and

Vglut1$^{-/-}$ retinas **(Figure S7A-L)**. Thus, alterations in extracellular glutamate levels caused by genetic

perturbations in the release of glutamate by neurons do not affect neuronal metabolic demand in the retina.

Extracellular glutamate levels affect Norrin expression by retinal neurons and Müller glia and

endothelial Norrin/β-catenin signaling.

Our scRNA-seq analyses revealed that expression levels of two Norrin/β-catenin signaling effectors

(*Ctnnb1* and *Lef1*) promoting angiogenesis and BRB maturation were downregulated in P10 *Vglut1*$^{-/-}$

compared to WT retinal ECs **(Figures 2D; 3H)**. Among seven key transcription factors (*Foxf2*, *Foxl2*,

Foxq1, *Lef1*, *Ppard*, *Zfp551* and *Zic3*) required for BBB maturation (Hupe et al., 2017), only *Lef1* was

downregulated significantly in P10 *Vglut1*$^{-/-}$ retinal ECs, suggesting a very specific effect on Norrin/β-

catenin signaling. To address changes in Norrin/β-catenin signaling, we examined *Norrin* (*Ndp*) mRNA

expression in *Vglut1*$^{-/-}$ and *Gnat1*$^{-/-}$ retinas by fluorescent *in situ* hybridization (FISH). *Ndp* mRNA

expression was drastically reduced in the INL layer of P10 *Vglut1*$^{-/-}$ retinas compared to the WT; in contrast,

its expression was highly upregulated in the INL of P10 *Gnat1*$^{-/-}$ retinas compared to the WT **(Figure 6G,**

H). The upregulation of *Ndp* persisted in the INL of *Gnat1*$^{-/-}$ retinas through P14 **(Figure S7M)**. Consistent

with our observations, analysis of a previously published scRNAseq database (Macosko et al., 2015)

demonstrated that INL neurons (horizontal cells and a subset of amacrine and bipolar cells) and Müller glia

express high levels of *Norrin* mRNA and glutamate transporters [*Slc1a2* (GLT-1) and *Slc1a3* (GLAST)]

respectively (Macosko et al., 2015) **(Figure 6I)**. Taken together, these transcriptional data and the response

of the INL cells (neurons and Müller glia) to extracellular glutamate (i.e, changes in GS, GLAST, GLT-1

protein levels) in the *Vglut1*$^{-/-}$ and *Gnat1*$^{-/-}$ retinas (**Figure 6**), suggest that glutamate could directly act on

Müller glia and INL neurons to induce *Norrin* mRNA expression.

Next, we examined the activation of Norrin/β-catenin signaling pathway in *Vglut1*$^{-/-}$ and *Gnat1*$^{-/-}$

retinal ECs. We immunolabeled P14 WT, *Vglut1*$^{-/-}$ and *Gnat1*$^{-/-}$ retinal sections with Lef1 (an effector of

Norrin/β-catenin signaling) and quantified the number of Lef1$^+$ ECs in both the superficial and deep

plexuses. There were significantly fewer Lef1$^+$ ECs in the *Vglut1*$^{-/-}$ retina and significantly higher in the

Gnat1$^{-/-}$ retina compared to the WT **(Figure 7A, B)**. Interestingly, our scRNA-seq data suggest that none

of the downstream targets of VEGF-A signaling [*Nr4a2*, *Egr3*, *Igfbp3*, *Hlx1*, *Crem*, *Per1*, *Mef2c*, *Ccrl1*,

Thbd, *Ndrg1*, *Dnajb9*, *Mycn*; (Schweighofer et al., 2009)] were altered in *Vglut1*$^{-/-}$ retinal ECs **(Table S2)**.

Therefore, angiogenesis and BRB phenotypes in *Vglut1*$^{-/-}$ and *Gnat1*$^{-/-}$ retinas are likely driven by altered

Norrin/β-catenin signaling.

Activation of endothelial Norrin/β-catenin signaling restores angiogenesis and BRB deficits in *Vglut1⁻/⁻* mice.

If angiogenesis and BRB phenotypes in *Vglut1⁻/⁻* and *Gnat1⁻/⁻* retinas are driven by altered Norrin/β-catenin signaling, we hypothesized that activating Norrin/β-catenin signaling in retinal ECs should rescue angiogenesis and BRB phenotypes in *Vglut1⁻/⁻* retinas. To test this hypothesis, we injected intraperitoneally either BIO [(2Z,3E)-6-bromoindirubin-3-acetoxime, BIO-Acetoxime] that activates Wnt (Norrin)/β-catenin signaling by inhibiting GSK-3β, or MeBIO [1-methyl-BIO], an analog of BIO with minimal activity against GSK-3β (Corada et al., 2019) in WT and *Vglut1⁻/⁻* mice. There were significantly fewer Lef1⁺ ECs in the MeBIO-treated *Vglut1⁻/⁻* retina compared to the MeBIO-treated WT retina; however, BIO-treatment significantly increased the number of Lef1⁺ ECs in the *Vglut1⁻/⁻* retina compared to the MeBIO-treated *Vglut1⁻/⁻* retina **(Figure S8)**. Importantly, we did not observe any Lef1⁺ nuclei outside the vasculature with either treatment. These data confirm that BIO-treatment activated Norrin/β-catenin signaling specifically in *Vglut1⁻/⁻* retinal ECs. Measurement of vascular coverage in the deep plexus revealed that while vascular coverage was significantly lower in the MeBIO-treated *Vglut1⁻/⁻* retina compared to the MeBIO-treated WT retina, BIO-treatment significantly increased vascular coverage by the deep plexus in the *Vglut1⁻/⁻* retina nearly to the MeBIO-treated WT retinas **(Figure 7C-E)**. Similarly, measurement of Biocytin-TMR leakage area and intensity revealed that while tracer leakage was significantly higher in the MeBIO-treated *Vglut1⁻/⁻* retina compared to the MeBIO-treated WT retina, BIO-treatment significantly decreased tracer leakage in the *Vglut1⁻/⁻* retina nearly to the MeBIO-treated WT levels **(Figure 7F-I)**. Thus, activation of endothelial Norrin/β-catenin signaling was sufficient to rescue angiogenesis and BRB phenotypes in the *Vglut1⁻/⁻* retina. These data strongly suggest that glutamate released by neurons regulates retinal angiogenesis and paracellular BRB integrity by modulating Norrin expression in retinal neurons and Müller glia and endothelial Norrin/β-catenin signaling.

DISCUSSION

Structural and functional abnormalities in neurons or glial cells precede vascular pathologies in multiple CNS neurological diseases with prominent vascular involvement, including those in the retina. For example, in diabetic retinopathy there is an early loss of neurovascular coupling, impaired response of photoreceptors to light, gradual neurodegeneration, gliosis and neuroinflammation before any observable vascular pathologies (Abcouwer and Gardner, 2014; Pardue et al., 2014; Umino and Solessio, 2013). Moreover, the early phases of either age-related macular degeneration, or retinitis pigmentosa, characterized by changes in synaptic activity and metabolic deficits in Müller glia (Jones et al., 2016a; Jones et al., 2016b; Pfeiffer et al., 2016), may also affect blood vessel function leading to neurodegeneration. Although vascular pathologies, including aberrant angiogenesis and BRB breakdown, are found in diabetic retinopathy and proliferative vitreoretinopathy that cause acquired adult blindness, as well as retinopathy of prematurity which leads to blindness in premature infants (Chan-Ling and Stone, 1992; Klaassen et al., 2013; Liegl et al., 2016; Prokofyeva and Zrenner, 2012), the molecular mechanisms that link neuronal or glial abnormalities with vascular deficits remain elusive. Our studies elucidate a critical missing step that links glutamatergic neuronal activity with vascular development and maturation in the retina, that may also be highly relevant for several retinal disease. Below, we discuss: a) the role of glutamate in angiogenesis and barriergenesis, b) the signaling pathways that function downstream of glutamate to promote these processes, and c) the relevance for the disease.

Glutamate is the predominant neurotransmitter in the retina during vascular development and in adulthood (Boccuni and Fairless, 2022). In our study, we used three mouse models: a) $Vglut1^{-/-}$, where retinal photoreceptors and bipolar cells fail to release glutamate into the synaptic cleft, b) $Gnat1^{-/-}$, where depolarized rod photoreceptors release excess glutamate into the synaptic cleft, and c) $Chrnb2^{-/-}$, where cholinergic wave is abolished but glutamatergic wave begins at P8 instead of P10 to address its role in angiogenesis and barriergenesis. We found that deep plexus angiogenesis and paracellular BRB maturation

in the retina are critically linked to the extracellular glutamate levels. These processes are delayed in *Vglut1*⁻

⁻ retinas, where neurons fail to release glutamate. In contrast, deep plexus angiogenesis and paracellular

BRB maturation are accelerated in *Gnat1*⁻/⁻ retinas, where constitutively depolarized rods release excessive

glutamate. Although the deep plexus angiogenesis, which occurs from P8-P12, was affected in all mutant

mouse models, the superficial plexus angiogenesis (P0-P8) was largely unperturbed. This is likely because

the superficial plexus is fully formed by P8, before the onset of glutamatergic neuronal activity in the mouse

retina. This developmental time course can also explain why treatment with 2-amino-4-phosphonobutyrate,

a compound that blocks glutamatergic wave, from P3- P7 did not affect retinal angiogenesis in a previous

study (Weiner et al., 2019), because the treatment was performed before the onset of glutamatergic wave in

the developing mouse retina. Similarly, we found that the transcellular, but not paracellular BRB, was also

not affected in the *Vglut1*⁻/⁻ retina. This is consistent with previous studies showing that transcellular BRB

in the mouse retina is fully mature by P10 (Chow and Gu, 2015), whereas paracellular BRB does not fully

mature until P18 (Mazzoni et al., 2017). Thus, it is conceivable that glutamatergic neuronal activity kicks

in too late to affect the maturation of the transcellular BRB, but has enough time to influence the maturation

of the paracellular BRB.

Interestingly, *Vglut1*⁻/⁻ retina lacking glutamatergic neuronal activity shows persistent cholinergic

wave beyond P10 (Blankenship et al., 2009). Since deficits in the deep plexus angiogenesis and paracellular

BRB integrity persist in the *Vglut1*⁻/⁻ retina throughout P14, these data suggest that the cholinergic wave is

not sufficient to promote deep plexus angiogenesis and paracellular BRB maturation. In contrast,

paracellular BRB is precociously mature in the *Chrnb2*⁻/⁻ retina where cholinergic wave is abolished and

glutamatergic wave begins earlier (P8) than usual (Bansal et al., 2000). Overall these data indicate that

glutamatergic neuronal activity, but not the spontaneous cholinergic activity, is the primary driver to

promote paracellular BRB maturation. We were not able to extend our studies beyond P14 in *Vglut1*⁻/⁻ mice

as the pups die around P15 (Fremeau et al., 2004). Notably, the vascular phenotypes, albeit opposite, were

more severe in the *Vglut1*$^{-/-}$ retina compared to the *Gnat1*$^{-/-}$ retina. This is likely because glutamate release

is abolished from both bipolar cells and photoreceptors (rods and cones) in the *Vglut1*$^{-/-}$ retina (Blankenship

et al., 2009). In contrast, only depolarized rod photoreceptors release excess glutamate in the *Gnat1*$^{-/-}$ retina

(Calvert et al., 2000; Schroeder et al., 2018). This may likely explain why the vascular phenotypes are less

prominent in the P10 *Gnat1*$^{-/-}$ retina, and possibly why the angiogenic phenotype (but not BRB phenotype)

in the *Gnat1*$^{-/-}$ retina normalizes to wild-type levels by P14.

How does extracellular glutamate trigger angiogenesis and BRB maturation in the developing

retina? It is possible that the vascular phenotypes in *Vglut1*$^{-/-}$ and *Gnat1*$^{-/-}$ retinas could be due to alterations

in either neuronal numbers which have been shown to affect retinal angiogenesis by changing the level of

available pro-angiogenic factor VEGF-A (Okabe et al., 2014). However, we did not observe any significant

differences in neuronal numbers between WT, *Vglut1*$^{-/-}$ and *Gnat1*$^{-/-}$ retinas, with the exception of a slight

decrease in amacrine cells in the *Vglut1*$^{-/-}$ retina. These data suggest that angiogenesis and BRB phenotypes

in *Vglut1*$^{-/-}$ and *Gnat1*$^{-/-}$ retinas are not caused by alterations in neuronal numbers. Metabolic demand of

retinal neurons also modulates angiogenesis (Joyal et al., 2016; Sapieha et al., 2008; Usui et al., 2015).

However, the expression levels of HK2 and PKM2, two key glycolytic enzymes that are readouts of

photoreceptor cell metabolism (Cheng et al., 2020), were unaffected in both P10 *Vglut1*$^{-/-}$ and *Gnat1*$^{-/-}$

retinas compared to the WT, in spite of the prominent vascular phenotypes in these mutant retinas at this

developmental stage. These data suggest that angiogenesis and BRB maturation abnormalities seen in

retinas with altered extracellular levels of glutamate are not due to alterations in neuronal numbers and

neuronal metabolic demand.

Our data demonstrate that Norrin mRNA expression and endothelial Norrin/β-catenin activity are

downregulated in *Vglut1*$^{-/-}$ retinas, and upregulated in *Gnat1*$^{-/-}$ retinas between P10-P14, and therefore are

likely regulated by the extracellular glutamate concentration. Consistent with these findings our scRNA-

seq analyses showed that expression levels of effectors of Norrin/β-catenin pathway [*Ctnnb1* and *Lef1*] are downregulated in *Vglut1*^{-/-} retinal ECs. However, Norrin mRNA is expressed in the retina before P10 (Ye et al., 2009), and perturbation of Norrin/β-catenin signaling delays superficial plexus angiogenesis as early as P5 (Wang et al., 2012; Ye et al., 2009), well before the onset of glutamatergic neuronal activity. Therefore, early (P5-P8) Norrin mRNA expression in the retina, which is critical for superficial plexus angiogenesis, is likely regulated by a glutamate-independent mechanism (Macosko et al., 2015). Our data in conjunction with a previous study (Macosko et al., 2015) also suggest that Norrin mRNA is expressed by several cell types in the developing retina including Müller glia as well as INL neurons (horizontal cells and subsets of amacrine and bipolar cells). Further studies will elucidate the relative contribution of Müller glia- or INL neurons-derived Norrin for the deep plexus angiogenesis and paracellular BRB maturation in response to extracellular glutamate. Importantly, pharmacological activation of endothelial Norrin/β-catenin signaling was sufficient to rescue both deep plexus angiogenesis and paracellular BRB integrity in the *Vglut1*^{-/-} retina, consistent with the idea that Wnt/β-catenin signaling functions downstream of extracellular glutamate to promote deep plexus angiogenesis and barriergenesis. Our scRNA-seq data also show a slight downregulation of *Unc5b* in *Vglut1*^{-/-} retinal ECs. Unc5b has been shown to modulate Wnt/β-catenin signaling in CNS ECs (Boye et al., 2022), suggesting the possibility that the cross-talk between these two pathways may be affected in *Vglut1*^{-/-} retinal ECs. Interestingly, none of the downstream targets of VEGF-A signaling was affected in *Vglut1*^{-/-} retinal ECs at the transcriptome level. Thus, VEGF-A signaling pathway does not appear to be regulated by glutamate release in the developing retina.

Taken together our data suggest a new mechanism by which glutamatergic neuronal activity regulate retinal angiogenesis and BRB maturation in the developing retina **(Figure 8)**. We propose that extracellular glutamate, released either during spontaneous glutamatergic wave or due to light-dependent glutamatergic synaptic activity of photoreceptors from P8 onwards, signals to Müller glia and INL neurons. Glutamate signaling induces Norrin mRNA and protein expression and secretion by Müller glia and INL neurons.

Norrin, in turn, activates endothelial Norrin/β-catenin signaling in ECs which promotes angiogenesis in the

deep plexus and paracellular BRB maturation in both superficial and deep plexuses of the retina (**Figure**

8). Our genetic data in *Vglut1*^{-/-} (no glutamate release into the synaptic cleft), *Gnat1*^{-/-} (excess glutamate

release into the synaptic cleft) and *Chrnb2*^{-/-} (early onset of glutamatergic wave), and the pharmacological

rescue of *Vglut1*^{-/-} phenotypes by activation of the endothelial Wnt/β-catenin signaling are consistent with

the proposed model that extracellular glutamate levels control angiogenesis and barriergenesis. Although,

the exact mechanism of how glutamate mediates these effects are not fully clear, our single cell RNAseq

data together with the published datasets (Macosko et al., 2015) suggest that glutamate cannot act directly

on ECs as they do not express either ionotropic or metabotropic glutamate receptor subunits or glutamate

transporters. The published transcriptional data of the glutamate receptor and transporter expression

(Macosko et al., 2015) and our analysis of the response of the INL cells (neurons and Müller glia) to

extracellular glutamate (i.e, changes in GS, GLAST, GLT-1 protein levels) in the *Vglut1*^{-/-} and *Gnat1*^{-/-}

retinas, suggest that glutamate could directly act on Müller glia and INL neurons to induce *Norrin* mRNA

expression. These cells express subsets of ionotropic or metabotropic glutamate receptors and glutamate

transporters that make them exquisite sensors of extracellular glutamate levels. In addition, Norrin mRNA

is predominantly expressed by the INL cells during vascular development and maturation. Future studies

will address in more detail the molecular mechanisms by which glutamate affects Norrin expression by the

INL cells. Our findings, not only extend our understanding of the molecular mechanisms by which vascular

development and homeostasis occurs in the CNS [reviewed in (Biswas et al., 2020)] including the role that

neuronal activity plays in these processes both in the cortex (Lacoste et al., 2014) and retina (Nguyen et al.,

2019; Rao et al., 2013; Weiner et al., 2019), but also have important implication to identify potential

interventions to treat CNS neurovascular pathologies, including those in the retina such as diabetic

retinopathy, or age-related macular degeneration.

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AUTHOR CONTRIBUTIONS

Conceptualization: S.B., W.J.B., D.A.; Methodology: S.B., D.A., G.B.; Software: S.S.; Validation: S.B., G.B; Formal analysis: S.B., S.S., G.B., P.A.; Investigation: S.B., S.S., G.B.; Resources: W.J.B., D.A.; Data curation: S.B., S.S., G.B.; Writing - original draft: S.B., D.A.; Writing - review & editing: S.B., S.S., W.J.B., D.A.; Visualization: S.B.; Supervision: D.A., Project administration: D.A., Funding acquisition: W.J.B., D.A.

DECLARATION OF INTEREST

The authors declare no competing or financial interests.

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Detailed methods are provided in the online version of this paper and include the following:

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KEY RESOURCES TABLE

Reagent or resource	Source	Identifier
Primary antibodies		
Rat monoclonal anti-CD31	BD Biosciences	Cat #553370, RRID:AB_394816
FITC rat monoclonal anti-mouse CD31	BD Pharmingen	Cat #553372, RRID:AB_394818
APC rat monoclonal anti-mouse CD31	BD Pharmingen	Cat #551262, RRID:AB_398497
Rabbit monoclonal anti-Ki67	Abcam	Cat #ab16667, RRID:AB_302459
Rabbit monoclonal anti-Cleaved Caspase-3	Cell Signaling Technology	Cat #9664S, RRID:AB_2070042
Goat polyclonal anti-DLL4	R & D Systems	Cat #AF1389, RRID:AB_354770
Rabbit polyclonal anti-Claudin-5	ThermoFisher Scientific	Cat #34-1600, RRID:AB_2533157
Mouse monoclonal anti-ZO-1	ThermoFisher Scientific	Cat #33-9100, RRID:AB_2533147
Rabbit polyclonal anti-SOX9	Millipore Sigma	Cat #ABE571, Lot #2535307
Mouse monoclonal anti-Glutamine synthetase	Millipore Sigma	Cat #MAB302, RRID:AB_2110656
Rabbit monoclonal anti-EAAT1 (GLAST)	Abcam	Cat #ab181036, RRID:AB_2885103

Rabbit polyclonal anti-EAAT2 (GLT-1)	Abcam	Cat #ab41621, RRID:AB_941782
Rabbit polyclonal anti-GFAP	Millipore Sigma	Cat #AB5804, RRID:AB_2109645
Rat monoclonal anti-CD140a (PDGFRα)	BD Biosciences	Cat #558774, RRID:AB_397117
Rabbit monoclonal anti-LEF1	Cell Signaling Technology	Cat# 2230s, RRID:AB_823558
Goat polyclonal anti-PDGFRβ	R & D Systems	Cat #AF1042, RRID:AB_2162633
Rabbit polyclonal anti-Laminin	Millipore Sigma	Cat #L9393, RRID:AB_477163
Rabbit polyclonal anti-Collagen IV	Abcam	Cat #ab6586, RRID:AB_305584
Rabbit polyclonal anti-Aquaporin-4	Millipore Sigma	Cat #A5971, RRID:AB_258270
Rabbit polyclonal anti-Caveolin-1	Abcam	Cat #ab18199, RRID:AB_444314
Rabbit polyclonal anti-PLVAP	Proteintech	Cat #14452-1-AP, RRID:AB_2166100
Mouse monoclonal anti-NeuN	Millipore Sigma	Cat #MAB377, RRID:AB_2298772
Rabbit polyclonal anti-Calbindin	Millipore Sigma	Cat #AB1778, RRID:AB_2068336

Mouse monoclonal anti-PKCα	Santa Cruz Biotechnology	Cat #sc-8393, RRID:AB_628142
Rabbit monoclonal anti-Hexokinase II	Abcam	Cat #ab209847, RRID:AB_2904621
Rabbit monoclonal anti-Pyruvate kinase M2	Cell Signaling Technology	Cat #4053, RRID:AB_1904096
Mouse monoclonal anti-GAPDH	Proteintech	Cat #60004-1-Ig, RRID:AB_2107436
Chemicals, peptides, and recombinant proteins		
Biocytin-TMR (5-(and-6)-tetramethylrhodamine biocytin)	ThermoFisher Scientific	Cat #T12921
Bovine Serum Albumin (BSA), AlexaFluor 594 conjugate	ThermoFisher Scientific	Cat #A13101
Fluorescein-labeled *Griffonia* (*Bandeiraea*) *Simplicifolia* Lectin I (GSL I, BSL I)	Vector Laboratories	Cat #FL-1101, RRID:AB_2336490
6-BIO ((2*Z*,3*E*)-6-bromoindirubin- 3-acetoxime, BIO-Acetoxime)	Calbiochem	Cat #361551
MeBIO (1-methyl-BIO)	Calbiochem	Cat #361556
Propidium iodide	ThermoFisher Scientific	Cat #P1304MP
CD16/CD32 Fc block	BD Pharmingen	Cat #553141
Experimental Models: Organisms/Strains		

Vglut1⁺ᐟ⁻ (C57/BL6J background)	Gift from Dr. Robert H. Edwards (Fremeau et al., 2004)	N/A
Gnat1⁺ᐟ⁻ (C57/BL6J background)	Gift from Dr. William J. Brunken (Calvert et al., 2000)	N/A
Chrnb2⁺ᐟ⁻ (C57/BL6J background)	Gift from Dr. Marina Picciotto (Bansal et al., 2000)	N/A
Oligonucleotides		
Vglut1-WT forward: 5'CCAAGCAAGGTTAAGCCTAG3'	IDT	N/A
Vglut1-WT reverse: 5'GGTGAATTTGGAAAAGAGC3'	IDT	N/A
Vglut1-KO forward: 5'TCGCAGCGCATCGCCTTCTA3'	IDT	N/A
Vglut1-KO reverse: 5'GCCACACGTTTCTTCTGAGG3'	IDT	N/A
Gnat1-WT forward: 5'GCCATCATCTACGGCAACACTCTGC3'	IDT	N/A
Gnat1-WT reverse: 5'GCCGGCGGAATTGAGCTGGTA3'	IDT	N/A

Gnat1-KO forward: 5'GCCGGTGAATCCGGGAAGAGC 3'	IDT	N/A
Gnat1-KO reverse: 5'GGGCTGCTAAAGCGCATGCTC 3'	IDT	N/A
Chrnb2-WT forward: *5'*CGGAGCATTTGAACTCTG AGCAGTGGGGTCGC3'	IDT	N/A
Chrnb2-WT reverse: 5'CTCGCTGACACAAGGGCT GCGGAC3'	IDT	N/A
Chrnb2-KO forward: *5'*CACTACGTCTGAACG TCGAAAACCCG3'	IDT	N/A
Chrnb2-KO reverse: 5'CGGGCAAATAATATC GGTGGCCGTGG3'	IDT	N/A
Softwares and algorithms		
ImageJ/Fiji	NIH	https://imagej.net/software/fiji/downloads
Zen microscopy software	ZEISS	https://www.zeiss.com/microscopy/en/products/software/zeiss-zen.html#packages

Seurat	Seurat	https://satijalab.org/seurat/
Tidyverse	Tidyverse	https://www.tidyverse.org
DAVID	DAVID bioinformatics resources	https://david.ncifcrf.gov
Prism 9	GraphPad	https://www.graphpad.com/ scientific-software/prism/
Other		
RNA *in situ* probe for mouse *Ndp* (Norrin)	(Mazzoni et al., 2017)	N/A
RNA *in situ* probe for full-length mouse *Apcdd1*	(Mazzoni et al., 2017)	N/A
C57B6 wild-type P14 retina by drop-seq (single-cell RNA-sequencing database)	(Macosko et al., 2015)	https://singlecell.broadinstitute.org/single_cell/study/SCP 301/c57b6-wild-type-p14-retina-by-drop-seq

RESOURCE AVAILABILITY

Lead contact

Further information and requests for resources and reagents should be directed to the lead contact, Dritan

Agalliu (da191@cumc.columbia.edu).

Materials availability

This study did not generate new unique reagents.

Data and code availability

All data are available in the manuscript and the supplementary information. The codes used in this study

have been previously published and are freely available (see Key Resources Table). Any additional

information required to reanalyze the data reported in this study will be available upon request.

EXPERIMENTAL MODEL AND SUBJECT DETAILS

Mice

All animal usage and protocols were approved by the Institutional Animal Care and Use Committee

(IACUC) at Columbia University Irving Medical Center. Experimental procedures were optimized to

minimize animal stress and the number of animals used for experiments. Mice were maintained on 12

light/12 dark cycle. Both sexes (males and females) were used for experiments and analyses. All mice were

maintained in C57/BL6J background. The *in vivo* BRB permeability assays were performed either at P10

or P14. Generation of *Vglut1*$^{-/-}$ mice was described before (Fremeau et al., 2004). These mice were bred as

heterozygous and gave birth in Mendelian ratios. Age-matched littermate WT and *Vglut1*$^{-/-}$ mice were used

for experiments (*Vglut1*$^{-/-}$ mice die around P15). Generation of *Gnat1*$^{-/-}$ mice was described before (Calvert

et al., 2000). These mice were bred as heterozygous and gave birth in Mendelian ratios. Age-matched

littermate WT and *Gnat1*$^{-/-}$ mice were used for experiments. Note that *Gnat1*$^{-/-}$ mice a viable and fertile.

Generation of *Chrnb2*$^{-/-}$ mice was described before (Bansal et al., 2000). These mice were bred as *Chrnb2*$^{+/-}$

and gave birth in Mendelian ratios. Age-matched littermate WT and *Chrnb2*$^{-/-}$ mice were used for

experiments. Note that *Chrnb2*$^{-/-}$ mice a viable and fertile.

METHOD DETAILS

Immunofluorescence

Unless otherwise specified, isolated tissues (retina, brain and liver) were fixed in 4% PFA for 2

hours for immunostaining. The exceptions were retinal flat-mount staining for Laminin, in which cases

retinas were fixed for 10 minutes in 2% PFA. For retinal flat-mounts, tissues were washed with 1X PBS

following PFA fixation and blocked overnight in blocking buffer (5% goat or donkey serum, 0.3% Triton

X-100 in 1× PBS) at 4°C. Samples were then incubated with primary antibodies in antibody-diluting

solution (5% goat or donkey serum; 0.01% Triton X-100 in 1X PBS) for 48h at 4°C, washed, and incubated

with secondary antibodies for 24 h. For radial section staining, samples were washed in 1 × PBS,

cryoprotected in 30% sucrose overnight, embedded in optimal cutting temperature compound (Tissue-Tek;

Torrance, CA, USA), and sectioned at a thickness of 12 μm. Tissue sections were blocked for 2 h at room

temperature followed by primary antibody incubation overnight at 4°C. Following 1X PBS washes, sections

were incubated with secondary antibodies for 4 h at room temperature. Samples were imaged in room

temperature using a Zeiss LSM700 confocal microscope [ZEISS 20X air (Objective Plan-Apochromat

20x/0.8 M27; numerical aperture: 0.8) or 40X water (Objective C-Apochromat 40x/1.2 W autocorr M27;

numerical aperture: 1.2) objectives; ZEN image acquisition software] and analyzed using Fiji software.

Western blotting

Retinas were collected from mice after perfusion with PBS. Six retinas from three mice were

combined for each sample. Collected tissue was homogenized in lysis buffer containing protease and

phosphatase inhibitors using a Dounce homogenizer followed by sonication. Protein concentration was

assayed by BCA (Bio-Rad) and resolved on SDS-PAGE. Protein levels in P10 retinas were measured by

fluorescent western blot analysis [4-15% or 7.5% Mini-PROTEAN TGX gels (Bio-Rad)] and quantitation

was performed using the LICOR system, as previously described. Fluorescent quantification of protein

levels was performed using the Odyssey SA infrared imaging system. Values are displayed as protein levels

corrected with GAPDH (loading control) and normalized to the WT values.

Antibodies

Primary antibodies used were rat anti-CD31 (BD Biosciences, Cat #553370, 1:250), rabbit anti-Ki67

(Abcam, Cat #ab16667, 1:500), rabbit anti-cleaved Caspase-3 (Cell Signaling Technology, Cat #9664S,

1:500), Goat anti-DLL4 (R & D Systems, Cat #AF1389, 1:200), rabbit anti-Claudin-5 (ThermoFisher

Scientific, Cat #34-1600, 1:500), rabbit anti-SOX9 (Millipore Sigma, Cat #ABE571, 1:500), mouse anti-

Glutamine Synthetase (Millipore Sigma, Cat #MAB302, 1:500), rabbit anti-EAAT1 (Abcam, Cat

#ab181036, 1:250), rabbit anti-EAAT2 (Abcam, Cat #ab41621, 1:250), rabbit anti-GFAP (Millipore Sigma,

Cat #AB5804, 1:500), rat anti-CD140a (BD Biosciences, Cat #558774, 1:100), rabbit anti-LEF1 (Cell

Signaling Technology, Cat #2230s, 1:100), goat anti-PDGFRβ (R & D Systems, Cat #AF1042, 1:250),

rabbit anti-Laminin (Millipore Sigma, Cat #L9393, 1:500), rabbit anti-Aquaporin-4 (Millipore Sigma, Cat

#A5971, 1:250), rabbit anti-Caveolin-1 (Abcam, Cat #ab18199, 1:500), rabbit anti-PLVAP (Proteintech,

Cat #14452-1-AP, 1:250), mouse anti-NeuN (Millipore Sigma, Cat #MAB377, 1:500), rabbit anti-

Calbindin (Millipore Sigma, Cat #AB1778, 1:250), mouse anti-PKCα (Santa Cruz Biotechnology, Cat #sc-

8393, 1:1000), rabbit anti-Hexokinase II (Abcam, Cat #ab209847, 1:1000), rabbit anti-Pyruvate Kinase M2

(Cell Signaling Technology, Cat #4053, 1:1000), mouse anti-GAPDH (Proteintech, Cat #60004-1-Ig,

1:50000), FITC rat anti-mouse CD31 (BD Pharmingen, Cat #553372, 1:200), and APC rat anti-mouse

CD31 (BD Pharmingen, Cat #551262, 1:200). Secondary antibodies used were: goat anti-rat Alexa Fluor

594 (A11007), goat anti-rabbit Alexa Fluor 594 (A11012), goat anti-rat Alexa Fluor 488 (A11006), goat

anti-rabbit Alexa Fluor 488 (A11034), donkey anti-rat Alexa Fluor 594 (A21209), donkey anti-rabbit Alexa

Fluor 594 (A32754), donkey anti-rat Alexa Fluor 488 (A21208), donkey anti-rabbit Alexa Fluor 488

(A21206), donkey anti-rat Alexa Fluor 647 (A48272), donkey anti-rabbit Alexa Fluor 647 (A32795),

donkey anti-goat Alexa Fluor 594 (A32758) and donkey anti-goat Alexa Fluor 488 (A11055) (all 1:250;

ThermoFisher Scientific). IRDyes 680 and 800 (1:20000; LI-COR) were used as secondary antibodies for

Western blot.

In situ hybridization

Both alkaline phosphatase and fluorescent *in situ* hybridization of retinal sections using antisense mRNA

probe for full-length mouse *Apcdd1* and *Ndp* (Norrin) were performed as described before (Mazzoni et al.,

2017). The samples were imaged using either a ZEISS Axio Imager (alkaline phosphatase) or a ZEISS

LSM700 confocal (fluorescent) microscope and analyzed using Fiji software.

Barrier permeability assays

Mice were anesthetized using isoflurane and injected with either 1% Biocytin-5(and-6-)-

Tetramethylrhodamine (biocytin-TMR: ThermoFisher Scientific, Cat #T12921) or 1% Bovine Serum

Albumin (BSA) - AlexaFluor 594 conjugate (albumin-Alexa594: ThermoFisher Scientific, Cat #A13101).

After 40 minutes in circulation, mice were re-anesthetized and perfused with 1X PBS via the cardiac route.

Retinas and livers were isolated and fixed in 4% PFA for 2 hours prior to immunostaining with FITC-

conjugated Lectin. Since blood vessels in the liver do not have a barrier, Biocytin-TMR or Albumin-594

fluorescence levels in the livers of corresponding animals were used as internal controls for measurement

of biocytin-TMR and albumin-Alexa594 fluorescence levels in the retinas as described (Biswas et al., 2022;

Mazzoni et al., 2017).

Retinal endothelial cell isolation

P10 WT and *Vglut1*^{-/-} as well as P14 WT mice were anesthetized using isoflurane and perfused for 4 minutes

with ice-cold sterile 1X PBS. The eyes were enucleated and retinas were dissected in Earl's balanced salt

solution (EBSS). Retinas were dissociated in a single-cell suspension using a published protocol

(Vanlandewijck et al., 2018). Once the retinas were dissociated into single cells, it was resuspended in 200

ml of CD16/CD32 Fc block (BD Pharmingen, Cat #553141, 1:200 in FACS buffer) and incubated at

room temperature for 15 minutes. The samples were washed with 2 ml of FACS buffer, with 100 ml kept

aside for use as unstained and fluorescence minus one (FMO) controls. The cells were then resuspended in

200 ml of anti-mouse CD31 [either FITC rat anti-mouse CD31 (BD Pharmingen, Cat #553372, 1:200) or

and APC rat anti-mouse CD31 (BD Pharmingen, Cat #551262), 1:200 in FACS buffer)] antibody to label

ECs, covered in aluminum foil and incubated on ice for 60 mins. Following antibody labeling, the samples

were washed twice with 2 ml of FACS buffer and resuspended in 400 ml of propidium

iodide (Thermofisher, Cat. #P1304MP; 1/10,000 in FACS buffer). Gates for the surface stain were set using

the unstained and FMO controls, and either CD31-APC$^+$ or CD31-FITC$^+$ ECs were sorted out using the

BD FACSAria Flow Cytometer (Columbia Stem Cell Initiative Flow Cytometry Core) for single-cell RNA-

sequencing.

Single-cell RNA-sequencing (scRNA-seq) analysis

Total of 1104 ECs for P10 WT retinas and 1046 ECs for P10 *Vglut1$^{-/-}$* retinas were analyzed for differential

gene expression analyses (**Table S1**). The 10x Genomics Chromium platform (Yuan et al., 2018; Yuan and

Sims, 2016) was used to generate low-depth data (~2000 genes/cell), and was processed using the Cell

Ranger analysis pipeline to align reads and generate feature-barcode matrices. The Seurat R package (Hao

et al., 2021) was implemented to read the output of the Cell Ranger pipeline and merge cells from all the

samples (WT and mutant) into a single R object. The standard pre-processing workflow for scRNAseq data

was carried out in Seurat, which consisted of the selection and filtration of cells based on quality control

metrics (e.g., number of unique genes detected in each cell > 200, total number of molecules detected within

a cell > 1,000 and < 50,000, percentage of reads within a cell that map to the mitochondrial genome < 20,

etc.), data normalization and scaling, and the detection of highly variable features. Next, linear

dimensionality reduction (PCA) was performed on the scaled data using the previously determined highly

variable features, an alternative heuristic method ('Elbow plot') was implemented to determine the

'dimensionality' of the dataset, and cells were clustered by applying the weighted shared nearest-neighbor

graph-based clustering method using the first 20 PCs (Menon, 2018). Lastly, the 20 PCA dimensions were

further reduced into two-dimensional space using the non-linear dimensional reduction technique, uniform

manifold approximation and projection for dimension reduction (UMAP), to visualize and explore the

scRNA-seq dataset and each of its unique EC clusters. From the gene signatures that are uniquely present

in mutant ECs compared to WT ECs, and validated by fluorescent in situ hybridization and/or

immunofluorescence. Gene ontology (GO) enrichment analysis was performed using DAVID

bioinformatics database to elucidate significantly up- and downregulated pathways in mutant ECs.

BIO and MeBIO treatment

The *in vivo* injections of 6-BIO ((2*Z*,3*E*)-6-bromoindirubin- 3-acetoxime, BIO-Acetoxime; Calbiochem,

Cat #361551) and control MeBIO (1-methyl-BIO; Calbiochem, Cat #361556) were performed as previously

published (Corada et al., 2019). Pups were anesthetized with 1% isoflurane. Intraperitoneal injections of

BIO and MeBIO were performed at a concentration of 5 mg/kg/day in sterile PBS from P6 to P8. Injected

pups were re-anesthetized and perfused with 1X PBS to harvest tissues for analyses at P10.

QUANTIFICATION AND STATISTICAL ANALYSIS

Image quantification

For retinal flat-mounts, each measurement was made in at least 3 quadrants per sample. The measurements

were done separately in the central (near the optic nerve-head) and peripheral (near the edge) retina. For

sections, at least three sections were imaged per sample. In each case, multiple representative images were

acquired and averaged. To measure vascular area and branch point density, area positive for CD31 or Lectin

was measured from each image in Fiji software (National Institutes of Health) using signal masking. Branch

point numbers were normalized to unit area (1 mm^2). To measure number of proliferative or apoptotic ECs,

the number of Ki67$^+$ or cleaved Caspase-3$^+$ ECs, respectively, were normalized to unit CD31$^+$ vascular area

(1 mm^2). The area of Biocytin-TMR leakage was done separately in the central and peripheral retina. The

intensity of biocytin-TMR and albumin-Alexa594 outside of retinal vessels was measured as described

(Mazzoni et al., 2017). Biocytin-TMR and albumin-Alexa594 signal intensities in the retina and cerebella

were normalized to those of livers. For vascular area positive for Claudin-5 and Caveolin-1, area positive

for Lectin was selected from each image in Fiji software using signal masking, followed by measuring the

percentage of Lectin$^+$/Claudin-5$^+$ or Lectin$^+$/Caveolin-1$^+$ in corresponding images. To measure the number

of ganglion (NeuN$^+$), amacrine, horizontal (Calbindin$^+$) and bipolar cells (PKCα^+), the number of cells were

normalized to the length of either ganglion cell layer (GCL; for ganglion cells) or inner nuclear layer (INL;

for amacrine, horizontal and bipolar cells). To measure the number of photoreceptors, the thickness of the

outer nuclear layer (ONL) was quantified as a function of photoreceptor number. To measure the number

of Müller glia, the number of Sox9$^+$ cells were normalized to the length of INL. To measure the relative

expression of GS and GLAST, the M.F.I were calculated for each field and data was presented as values

normalized to the number of Sox9$^+$ Müller glia. To measure *Ndp* expression, mean fluorescence intensity

(M.F.I) of *Ndp* in the INL was calculated with histogram analysis in Fiji software and normalized to the

WT values. For Lef1$^+$ EC quantification, the number of Lef1$^+$ ECs was normalized to unit CD31$^+$ or Lectin$^+$

vascular area (1 mm^2). For western blots, values are displayed as target protein levels corrected with

GAPDH (loading control) and normalized to the WT values using Odyssey SA infrared imaging system.

Statistical analysis

Retinas from 3-5 different animals (for *in vivo* experiments) were used for statistical analysis. For western

blots, retinas from 3 animals/genotype were combined into one sample, and 4 samples/genotype was used

for quantification. To test for statistical significance of any differences, unpaired Student's t test was

performed using GraphPad Prism. A value of $P < 0.05$ was considered statistically significant. For scRNA-

seq analysis, we considered transcripts with adjusted p value < 0.05, and >1.2-fold ($\log_2$fc > 0.25 and $\log_2$fc

< -0.25) difference in expression as significant. For GO analysis, Gene sets with false discovery rate (FDR)

< 0.01 were considered significant.

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FIGURES AND FIGURE LEGENDS

Figure 1. Deep plexus angiogenesis is delayed in the *Vglut1*⁻/⁻ retina. A) Timeline of the neuronal activity

[cholinergic and glutamatergic waves and glutamatergic synaptic activity of photoreceptors

(phototransduction)] and angiogenesis (superficial, deep and intermediate plexuses) in the postnatal WT

retina (P1-P22). **B, C)** Schematic diagram of glutamate release from bipolar cells and photoreceptors in WT

(**B**) and *Vglut1*⁻/⁻ (**C**) retinas. *Vglut1*⁻/⁻ photoreceptors and bipolar cells fail to release glutamate into the

synaptic cleft. **D)** Schematic diagram of distinct developmental regions in the retina. Central retina is

developmentally more mature than peripheral retina. **E)** Representative images of the superficial plexus

from P8 WT and *Vglut1*$^{-/-}$ retinal flat-mounts stained for CD31 (green; EC marker). **F, G)** Dotted bar graphs

of the vascular coverage of the superficial plexus in P8 and P10 WT and *Vglut1*$^{-/-}$ central (**F**) and peripheral

(**G**) retina (n=3 mice/genotype). **H, K)** Representative images of the deep plexus from P10 and P14 WT

and *Vglut1*$^{-/-}$ retinal flat-mounts visualized with CD31 staining (green). **I, J, L, M)** Dotted bar graphs of the

vascular coverage (**I, L**) and branch point density (**J, M**) of the deep plexus in P10, P12 and P14 WT and

Vglut1$^{-/-}$ central (**I, J**) and peripheral (**L, M**) retina (n=4 mice/genotype). Scale bars = 62 μm. Statistical

analyses were done with Students t-test: *$p<0.05$, **$p<0.02$, NS = not significant. Error bars: Mean ±

S.E.M.

Figure 2. Aberrant angiogenic transcriptomic signatures are present in *Vglut1*^{-/-} ECs from single cell RNA-sequencing (scRNA-seq). A) UMAP (uniform manifold approximation and projection for dimension reduction) projection shows separation of P10 WT and *Vglut1*^{-/-} retinal ECs based on their transcriptomic signatures. **B, C)** Gene ontology (GO) analyses of P10 WT and *Vglut1*^{-/-} retinal ECs show top downregulated (**B**) and upregulated (**C**) pathways. **D, E)** Dot plot of expression levels for angiogenesis (**D**) and tip cell (**E**) genes in P10 WT and *Vglut1*^{-/-} retinal ECs. The dot size indicates the percent of the

population expressing each marker; the color scale indicates the average level of gene expression. Genes

enriched in deep plexus tip cells (D-tip cells) compared to superficial plexus tip cells (S-tip cells) are shown

in red. Genes enriched in deep plexus tip cells (D-tip cells) compared to all ECs are shown in purple. **F, G)**

Feature plots of representative angiogenesis (**F**) and tip cells (**G**) genes in P10 WT and *Vglut1$^{-/-}$* retinal ECs.

H) Schematic of a vascular sprout consisting of leading tip cells and proliferative stalk cells. **I)**

Representative images of the deep plexus from P12 WT and *Vglut1$^{-/-}$* retinal flat-mounts stained for Ki67

(green) and CD31 (purple). **J)** Measurements of Ki67^{+} (proliferative) or cleaved Caspase3^{+} (apoptotic) ECs

in P12 WT and *Vglut1$^{-/-}$* retinal deep plexus (*n=4*). **K)** Representative images of the deep plexus from P12

WT and *Vglut1$^{-/-}$* retinal flat-mounts stained for CD31 (green). The dotted line shows the border of the

vascular front in the *Vglut1$^{-/-}$* retina. **L)** Representative images of the deep plexus from P12 WT and *Vglut1^{-}*

$^{/-}$ retinal flat-mounts stained for CD31 and Dll4. Arrowheads point to Dll4^{+} tip cells in the *Vglut1$^{-/-}$* retina.

Scale bars = 41 μm. Students t-test: **<0.02, NS = not significant. Error bars: Mean ± S.E.M.

Figure 3. Paracellular BRB maturation is impaired in *Vglut1⁻ᐟ⁻* retina. A) Schematic of biocytin-TMR

paracellular leakage through impaired tight junctions at the BRB; the leaked biocytin-TMR is taken up by

neurons. vBM = vascular basement membrane. **B, C, D)** Representative images of the superficial **(B, C)**

and deep **(D)** plexuses of P10 and P14 WT and *Vglut1⁻ᐟ⁻* retinal flat-mounts labeled with Lectin (green) 40

minutes after intravenous injection of biocytin-TMR, followed by PBS perfusion. **E, F, G)** Measurements

of the area **(E, F)** and fluorescence intensity **(G)** of leaked biocytin-TMR in P10 and P14 WT and *Vglut1⁻ᐟ⁻*

retinal flat-mounts (n=4). BRB formation is impaired in *Vglut1⁻/⁻* retina. **H)** Dot plot of expression levels

for BRB genes in P10 WT and *Vglut1⁻/⁻* retinal ECs. The dot size indicates the percent of the population

expressing each marker; the color scale indicates the average level of gene expression. **I)** Feature plots of

representative BRB genes in P10 WT and *Vglut1⁻/⁻* retinal ECs. **J)** Representative images of the superficial

and deep plexuses of P14 WT and *Vglut1⁻/⁻* retinal flat-mounts stained for Claudin-5 (Cldn5; purple) and

Lectin (green). Empty arrowheads point to Lectin⁺ blood vessels devoid of Claudin-5 at tight junctions. **K)**

Representative images of the superficial and deep plexuses in P14 WT and *Vglut1⁻/⁻* retinal flat-mounts

stained for ZO-1 (Tjp1, purple) and Lectin (green). Empty arrowheads point at Lectin⁺ blood vessels devoid

of ZO-1 localization to tight junctions. **L, M)** Measurement of Claudin-5 (**L**) and ZO-1 (**M**) coverage of

blood vessels in P14 WT and *Vglut1⁻/⁻* retinas (n=4 mice / genotype). Scale bars = 41 μm. Students t-test:

*<0.05, **<0.02. Error bars: Mean ± S.E.M.

Figure 4. Paracellular BRB matures precociously in the *Chrnb2⁻ᐟ⁻* retina. A) Schematic diagram illustrating that glutamatergic wave begins earlier (P8) than usual (P10) in the *Chrnb2⁻ᐟ⁻* retina where cholinergic wave is abolished. **B)** Representative images of superficial and deep plexuses of P10 WT and *Chrnb2⁻ᐟ⁻* retinal flat-mounts labeled with Lectin (green) 40 minutes after intravenous biocytin-TMR injection, followed by PBS perfusion. **C, D)** Measurements of the area (**C**) and fluorescence intensity (**D**) of leaked biocytin-TMR in P10 WT and *Chrnb2⁻ᐟ⁻* retinal flat-mounts (n=4 mice / genotype). **E)** Representative images of the superficial and deep plexuses of P10 WT and *Chrnb2⁻ᐟ⁻* retinal flat-mounts

945   stained for Claudin-5 (purple) and Lectin (green). Empty arrowheads point at Lectin$^+$ blood vessels devoid

946   of Claudin-5 localization to tight junctions. **F)** Measurement of Claudin-5 coverage of blood vessels in P10

947   WT and *Chrnb2$^{-/-}$* retinas (n=3 mice / genotype). Scale bars = 41 μm. Students t-test: **<0.02. Error bars:

948   Mean ± S.E.M.

Figure 5. Deep plexus angiogenesis and paracellular BRB maturation are accelerated in the *Gnat1-/-*

retina. A, B) Schematic diagrams of glutamate release from rod photoreceptors in WT (**A**) and *Gnat1-/-* (**B**)

retinas. *Gnat1-/-* rod photoreceptors (depolarized) release excess glutamate into the synaptic cleft. **C)**

Representative images of the superficial plexus in P10 WT and *Gnat1-/-* retinal flat-mounts stained for

Lectin (green). **D)** Measurements of vascular coverage of the superficial plexus in P10 WT and *Vglut1-/-*

central and peripheral retina (n=3 mice / genotype). **E, H)** Representative images of the deep plexus in P10

WT and *Gnat1*^{-/-} retinal flat-mounts stained for Lectin (green). **F, G, I, J)** Measurements of vascular

coverage (**F, I**) and branch point density (**G, J**) of the deep plexus in P10 and P14 WT and *Gnat1*^{-/-} central

(**F, G**) and peripheral (**I, J**) retina (n=4 mice / genotype). **K)** Representative images of the deep plexus in

P10 WT and *Gnat1*^{-/-} retinal flat-mounts stained for Ki67 (purple) and CD31 (green). **L)** Measurements of

Ki67[+] ECs in P10 WT and *Gnat1*^{-/-} retinal deep plexus (n=4 mice / genotype). **M)** Representative images

of superficial and deep plexuses of P10 WT and *Gnat1*^{-/-} retinal flat-mounts labeled with Lectin (green) 40

minutes after intravenous injection of biocytin-TMR (purple), followed by PBS perfusion. **N, O)**

Measurements of the area (**N**) and fluorescence intensity (**O**) of leaked biocytin-TMR in P10 WT and *Gnat1*^{-/-}

retinal flat-mounts (n=4 mice / genotype). **P, Q)** Representative images of the superficial (**P**) and deep

(**Q**) plexuses in P10 WT and *Gnat1*^{-/-} retinal flat-mounts stained for Claudin-5 (purple) and Lectin (green).

P' and Q' are magnified images of the corresponding boxed areas. Empty arrowheads point at Lectin[+] blood

vessels devoid of Claudin-5 localization to tight junctions. **R)** Measurement of Claudin-5 coverage of blood

vessels in P10 WT and *Gnat1*^{-/-} retinas (n=4 mice / genotype). Scale bars: **C, E, H** = 62 μm and **K, M, P,**

Q = 41 μm. Students t-test: *<0.05, **<0.02, NS = not significant. Error bars: Mean ± S.E.M.

Figure 6. Expression of glutamine synthetase, glutamate transporters and Norrin are downregulated in *Vglut1*-/- retinas and upregulated in *Gnat1*-/- retinas. A, B) P14 WT, *Vglut1*-/- and *Gnat1*-/- retinal sections were stained for glutamine synthetase (GS) (**A**), and the mean fluorescence intensity (M.F.I) in the INL was quantified (**B**) for each genotype (n=4 mice / genotype). **C, D)** P14 WT, *Vglut1*-/- and *Gnat1*-/-

retinal sections were stained for GLAST (**C**), and the M.F.I in the INL was quantified (**D**) for each genotype

(n=4 mice / genotype). **E, F)** P14 WT, *Vglut1*^{-/-} and *Gnat1*^{-/-} retinal sections were stained for GLT-1 (**E**),

and the M.F.I in the INL was quantified (**F**) for each genotype (n=4 mice / genotype). **G)** Fluorescent *in*

situ hybridization of P10 WT, *Vglut1*^{-/-} and *Gnat1*^{-/-} retinal sections with an antisense probe against *Ndp*

(Norrin), followed by staining with DAPI. Norrin is expressed throughout the INL. **H)** Quantification of

the M.F.I of *Ndp* in the INL of P10 WT, *Vglut1*^{-/-} and *Gnat1*^{-/-} retinal sections (n=4 mice / genotype). **I)**

Expression profiles of *Ndp*, *Slc1a3* (GLAST) and *Slc1a2* (GLT-1) in the P14 WT retina from an existing

scRNA-seq database (Macosko et al., 2015). *Ndp* mRNA is expressed predominantly by the horizontal cells

and Müller glia in the INL (small subsets of amacrine and bipolar cells also express *Ndp*). In the INL,

Slc1a3 is primarily expressed by Müller glia and astrocytes, whereas *Slc1a2* is expressed in retinal neurons

as well as Müller glia. GCL: ganglion cell layer, INL: inner nuclear layer, ONL: outer nuclear layer. Scale

bars = 41 μm. One-way ANOVA: **<0.02, NS = not significant. Error bars: Mean ± S.E.M.

Figure 7. Upregulation of Norrin/β-catenin signaling rescues vascular deficits of the *Vglut1⁻ᐟ⁻* retina.

A, B) P14 WT, *Vglut1⁻ᐟ⁻* and *Gnat1⁻ᐟ⁻* retinal sections were stained for Lef1 (green), CD31 (purple) and DAPI (blue; **A**), and the number of Lef1⁺ ECs was quantified (**B**) for each genotype (n=4 mice / genotype). **C-E)** MeBIO (control)- or BIO (activates Norrin/β-catenin signaling)-treated P10 WT and *Vglut1⁻ᐟ⁻* retinas were stained with Lectin [green; (**C**) low and (**D**) high magnification], and vascular coverage of the peripheral deep plexus was quantified (**E**) for each treatment (n=4 mice / genotype). **F)** Representative

images of flat mount MeBIO- or BIO-treated P10 WT and *Vglut1⁻ᐟ⁻* retinas 40 minutes after intravenous injection of biocytin-TMR and perfusion with PBS. P10 *Vglut1⁻ᐟ⁻* retinas treated with MeBIO (control) have high leakage of biocytin-TMR in the retina. P10 *Vglut1⁻ᐟ⁻* retinas treated with BIO have low leakage of biocytin-TMR in the retina similar to P10 WT retinas. **G**) Representative images (higher magnification) of flat mount MeBIO- or BIO-treated P10 WT and *Vglut1⁻ᐟ⁻* retinas 40 minutes after intravenous injection with biocytin-TMR (purple) and stained for lectin (green). **H, I**) Quantification of biocytin-TMR leakage area (**H**) and fluorescence intensity (**I**) were quantified for each treatment (n=5 mice / genotype). GCL: ganglion cell layer, INL: inner nuclear layer. Scale bars **A, D, G** = 41 μm, **C, F** = 200 μm. One-way ANOVA: ****<0.02**. Error bars: Mean ± S.E.M.

Figure 8. Glutamatergic neuronal activity regulates retinal angiogenesis and BRB maturation through Norrin/β-catenin signaling. Glutamate is taken up into synaptic vesicles by vGluT1 (*Vglut1*), and is released into the synaptic cleft by neurons, either during spontaneous glutamatergic wave (from bipolar cells), or light-dependent glutamatergic synaptic activity of photoreceptors in the retina. The inhibition of glutamate release from rods after light exposure is regulated by Transducin (*Gnat1;* purple line). The released glutamate signals to Müller glia and inner nuclear layer (INL) neurons including horizontal,

amacrine and bipolar cells. As a result, Müller glia and INL neurons upregulate *Norrin* mRNA and protein

expression and likely its secretion; however, the relative contribution from Müller glia and INL neurons on

extracellular Norrin levels in this process is unclear. Glutamate-dependent secretion of Norrin activates

endothelial Norrin/β-catenin signaling, which in turn promotes deep plexus angiogenesis and the

paracellular BRB maturation in both the superficial and deep plexuses of the retina. INL: inner nuclear

layer.