



# Cellular Physiology and Pathophysiology of EAAT Anion Channels

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### Specialty section:

This article was submitted to  
Cellular Neurophysiology,  
a section of the journal  
Frontiers in Cellular Neuroscience

**Received:** 15 November 2021

**Accepted:** 13 December 2021

**Published:** 06 January 2022

### Citation:

Kovermann P, Engels M, Müller F and  
Fahlke C (2022) Cellular Physiology  
and Pathophysiology of EAAT Anion  
Channels.  
*Front. Cell. Neurosci.* 15:815279.  
doi: 10.3389/fncel.2021.815279

Excitatory amino acid transporters (EAATs) optimize the temporal resolution and energy demand of mammalian excitatory synapses by quickly removing glutamate from the synaptic cleft into surrounding neuronal and glial cells and ensuring low resting glutamate concentrations. In addition to secondary active glutamate transport, EAATs also function as anion channels. The channel function of these transporters is conserved in all homologs ranging from archaeobacteria to mammals; however, its physiological roles are insufficiently understood. There are five human EAATs, which differ in their glutamate transport rates. Until recently the high-capacity transporters EAAT1, EAAT2, and EAAT3 were believed to conduct only negligible anion currents, with no obvious function in cell physiology. In contrast, the low-capacity glutamate transporters EAAT4 and EAAT5 are thought to regulate neuronal signaling as glutamate-gated channels. In recent years, new experimental approaches and novel animal models, together with the discovery of a human genetic disease caused by gain-of-function mutations in EAAT anion channels have enabled identification of the first physiological and pathophysiological roles of EAAT anion channels.

**Keywords:** excitatory amino acid transporter, glutamate transporter, anion channels, chloride homeostasis, retina, channelopathies

## INTRODUCTION

Glial and neuronal excitatory amino acid transporters (EAATs) ensure low resting neurotransmitter concentrations in the synaptic cleft and prevent glutamate excitotoxicity by transporting glutamate from the synaptic cleft into neuronal and glial cells (Danbolt, 2001; Kanner, 2006). EAATs are prototypical dual function proteins that act as both secondary active glutamate transporters and anion channels (Fairman et al., 1995; Wadiche et al., 1995; Larsson et al., 1996). Whereas, the molecular basis of these two transport functions is now well-understood (Fahlke et al., 2016), we are just starting to appreciate the cellular functions of these glutamate-gated chloride channels in the human body.

About 30 years ago, EAAT anion channel behavior was discovered almost simultaneously in two different experimental systems: cloned transporters in heterologous expression systems and native transporters in retinal preparations. Heterologous expression of EAAT1, EAAT2, and EAAT3 in *Xenopus* oocytes and electrophysiological analysis revealed the existence of a current component carried by anions that is not coupled to electrogenic glutamate transport (Wadiche et al., 1995). Moreover, after identification and characterization of the first three isoforms (Kanai and Hediger, 1992; Pines et al., 1992; Storck et al., 1992), homology cloning of EAAT4 (Fairman et al., 1995) and

EAAT5 (Arriza et al., 1997) revealed the existence of family members that predominantly function as anion channels.

A glutamate-gated anion channel with many of the functional features of EAAT glutamate transporters was first observed on cone photoreceptors of salamander retina (Picaud et al., 1995b; Larsson et al., 1996) and on dendrites of ON-bipolar cells in white perch retina (Grant and Dowling, 1995; Picaud et al., 1995b; Larsson et al., 1996). On cone photoreceptors, this channel allows cells to respond to glutamate that they themselves have released and provides a feedback signal about the concentration of glutamate released into the synaptic cleft (Picaud et al., 1995a). In ON-bipolar cells of white perch retina, chloride conductance mediates an inhibitory input that keeps the cells hyperpolarized in the dark, when photoreceptors release glutamate. The retina-specific mammalian EAAT5 (Arriza et al., 1997; Gameiro et al., 2011; Schneider et al., 2014) closely resembles salamander sEAAT5A (Eliasof et al., 1998) and is, thus, assumed to fulfill similar functions in the mammalian retina. However, until recently, the lack of EAAT5-specific blockers and an EAAT5-knockout animal model have prevented the experimental verification of this hypothesis.

Here we review recent progress in the cellular physiology and pathophysiology of EAAT anion channels.

## EAAT ANION CHANNELS EXHIBIT LOW UNITARY CURRENT AMPLITUDES AND ABSOLUTE OPEN PROBABILITIES

Initially, EAAT anion channels were mainly studied in *Xenopus* oocytes. In this system, EAAT anion currents are small compared with endogenous current components and subtraction procedures are usually needed to identify the EAAT anion channel-specific current (Fairman et al., 1995; Wadiche et al., 1995; Wadiche and Kavanaugh, 1998; Ryan et al., 2004; Cater et al., 2014, 2016). The use of a mammalian cell expression system and more permeable anions permit the direct recording of EAAT anion currents under various conditions. **Figure 1** shows representative EAAT4 anion current recordings from HEK293T cells expressing rat EAAT4. Because of the current convention, inward currents at negative potentials correspond to anion efflux. The currents are small in the absence of Na<sup>+</sup> and glutamate, and the application of Na<sup>+</sup> alone or of Na<sup>+</sup> plus glutamate increases current amplitudes in a dose-dependent manner. EAAT4 anion currents exhibit time- and voltage-dependent changes in current amplitudes that resemble voltage-dependent gating (**Figures 1A–C**) (Kovermann et al., 2010). This “gating” is affected by transporter substrates (Machtens et al., 2011), but also by permeant anion concentrations (**Figures 1D,E**) (Kovermann et al., 2010). Such experiments support the notion that EAAT anion channels need Na<sup>+</sup> ions to be active (Mim et al., 2005; Tao et al., 2006; Grewer et al., 2008). However, glial EAAT anion channels are Na<sup>+</sup> independent in the absence of glutamate (Leinenweber et al., 2011; Divito et al., 2017) and can also be active when

K<sup>+</sup> is the only monovalent cation present (Kortzak et al., 2019).

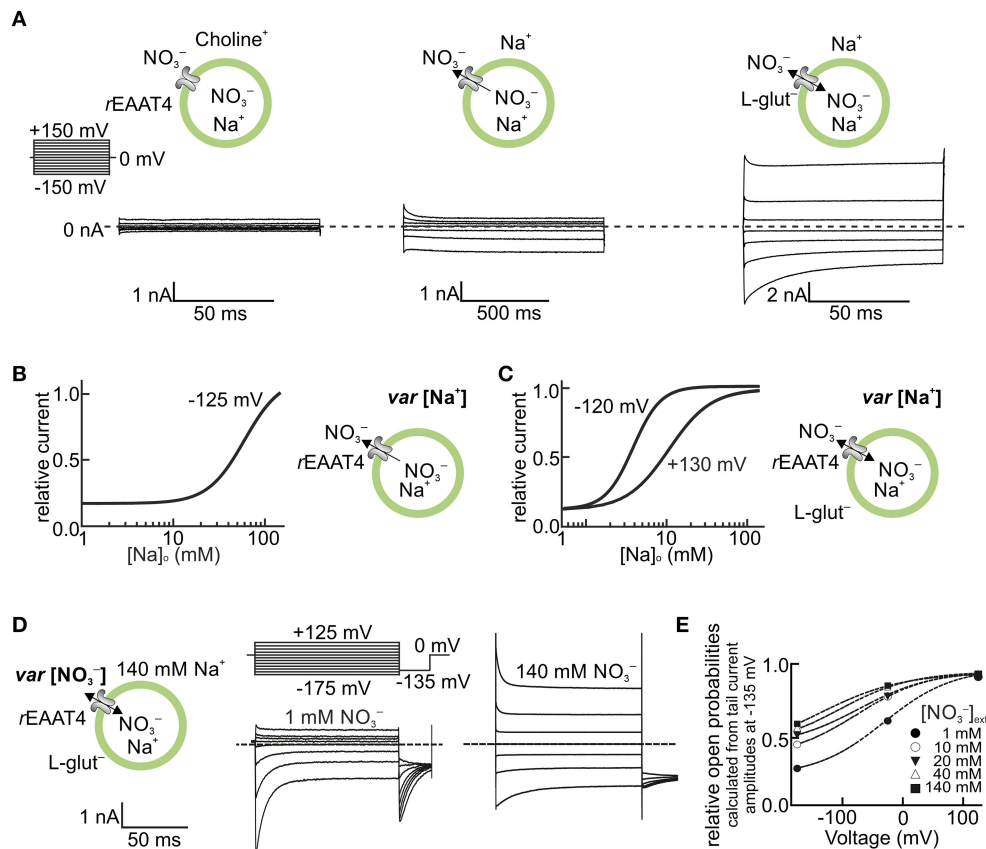
Since EAAT anion currents are large compared with uptake currents and are not coupled to glutamate transport, they were always assumed to be channel mediated. Definitive proof was provided by measurements of unitary current amplitudes *via* noise analysis. Larsson et al. (1996) studied glutamate transporter-associated anion channels on tiger salamander cones using whole-cell patch-clamp recordings. They demonstrated that glutamate transporter-associated current fluctuations are Lorentzian, i.e., generated by the random opening and closing of individual channels. Stationary noise analysis involving the adjustment of anion channel open probabilities by modifying external glutamate provided a single-channel conductance of 0.7 pS at symmetric chloride concentration [Cl<sup>-</sup>] (Picaud et al., 1995b; Larsson et al., 1996). These single-channel amplitudes are too high to be accounted for by carrier-mediated transport. Thus, these data establish channel-like anion conduction by EAAT glutamate transporters.

Noise analysis of mammalian EAAT1–EAAT5 proteins in transfected HEK293T cells provided a unitary conductance of around 1 pS: EAAT5 had the highest single-channel amplitude (Schneider et al., 2014), EAAT4 (Torres-Salazar and Fahlke, 2007) had the lowest, and the high-capacity transporters EAAT1 (Winter et al., 2012), EAAT2 (Schneider et al., 2014), and EAAT3 (Torres-Salazar and Fahlke, 2007) displayed intermediate values. Noise analysis of the EAAT-associated anion channel amplitudes demonstrated identical unitary current amplitudes for various external [glutamate], indicating the existence of a single anion pore that is either open or closed (Kovermann et al., 2010). Absolute open probabilities (determined by comparing EAAT anion and transport currents) turned out to be extremely low, i.e., 0.06 ± 0.01% for EAAT2 (Kolen et al., 2020).

## MOLECULAR DETERMINANTS OF EAAT-ASSOCIATED ANION CHANNEL FUNCTION

EAATs assemble as homo- or heterotrimers (Gendreau et al., 2004; Yernool et al., 2004; Nothmann et al., 2011), with each subunit mediating both transport functions independently of its neighboring subunits (Grewer et al., 2005; Koch et al., 2007; Leary et al., 2007). They are prototypical elevator transporters: each subunit contains a trimerization domain that provides a scaffold for transmembrane movements of the transport domain and has binding sites for all substrates (Yernool et al., 2003; Boudker et al., 2007; Reyes et al., 2009; Verdon and Boudker, 2012; Jensen et al., 2013; Verdon et al., 2014; Guskov et al., 2016; Arkhipova et al., 2019). Substrate transport is based on large-scale (~18 Å) rotational translational movement of the transport domain relative to the static trimerization domain (Crisman et al., 2009; Reyes et al., 2009). For many years, none of the reported structures exhibited a hydrophilic pore-like structure that could be structurally correlated to the EAAT anion pore.

A convincing molecular model of the EAAT anion pore was obtained *via* molecular dynamics simulation of Glt<sub>Ph</sub>



**FIGURE 1** | EAAT anion channels are modulated by transport substrates and permeant anions. **(A–C)**  $\text{Na}^+$  dependence of EAAT4 anion channels heterologously expressed in HEK293T cells. **(A)** Representative whole-cell current recordings of rat EAAT4 with symmetric  $\text{NO}_3^-$  as the permeant anion, in the absence of external  $\text{Na}^+$  and L-glutamate ( $\text{Glu}^-$ ) (left), in the presence of external  $\text{Na}^+$  (middle), and in the presence of external  $\text{Na}^+$  and 5 mM L-glutamate (right, see insets). The  $\text{Na}^+$  concentration dependence of EAAT4 anion channel currents is shown in the absence **(B)** and presence **(C)** of external L-glutamate for high positive and negative voltages (internal  $\text{Na}^+$  concentration in **A,B** was set to  $\sim 114$  mM). **(D,E)** Dependence of EAAT4 anion channel gating on permeant anions. **(D)** Representative whole-cell recordings from rat EAAT4 whole-cell currents with different external concentrations of  $\text{NO}_3^-$  (1–140 mM) (see insets, the internal  $\text{NO}_3^-$  concentration in **C,D** was set to 110 mM). **(E)** Relative open probabilities of rat EAAT4 anion channels at different external concentrations of the permeant anion  $\text{NO}_3^-$ . In the depicted experiments,  $\text{Na}^+$  was replaced by equimolar amounts of choline **(A–C)**, and  $\text{NO}_3^-$  by the impermeant anion D-gluconate **(D,E)**. Relative open probabilities in **E** were calculated from instantaneous tail current amplitudes at  $-135$  mV, as shown in the voltage protocol in **D**. rEAAT4: rat EAAT4. var, varying. This figure is modified and reprinted from Kovermann et al. (2010), with permission.

(Machtens et al., 2015). At the time,  $\text{Glt}_{\text{ph}}$  structures were available for the inward- (Reyes et al., 2009) and outward-facing conformations (Yernool et al., 2004; Boudker et al., 2007; Verdon et al., 2014), as well as for one intermediate state (Verdon and Boudker, 2012). Each of these conformations was tested for possible anion permeation using a computational electrophysiology approach that permitted the observation of ion permeation events under constant voltages (Kutzner et al., 2011). At a  $[\text{NaCl}]$  of 1 M and voltages of around 800 mV, no  $\text{Cl}^-$  permeation event was observed for any of these conformations. However, in simulations starting from various intermediate conformations—either using a published structure (Verdon and Boudker, 2012) or obtained using an essential dynamics approach—lateral movement of the transport domain opened the interface between the trimerization and transport domains. Subsequent wetting caused the formation of an anion-selective

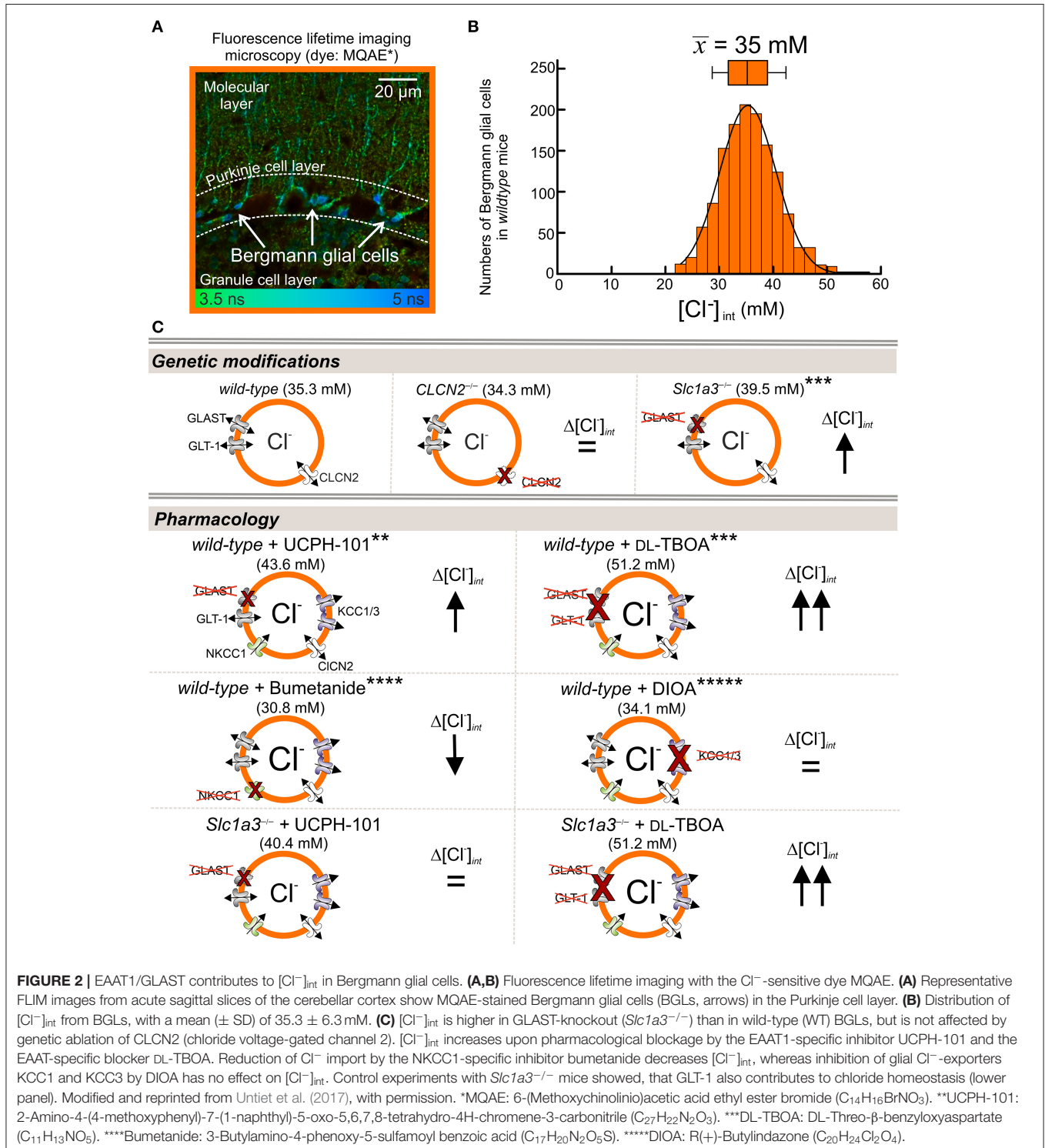
pore with functional properties resembling experimental results for EAAT anion channels.

This novel conformation (named ChC) was experimentally verified using tryptophan-scanning mutagenesis and by combined *in silico* and *in vitro* mutagenesis. Tryptophan fluorescence is collisionally quenched by anions; thus, fluorescence spectroscopy at various anion concentrations permits tryptophan side chains protruding onto the anion permeation pathway to be distinguished from those in other localizations. Predictions of side-chain accessibility to the aqueous medium in different conformations, including the ChC conformation, perfectly matched with iodide ( $\text{I}^-$ ) accessibility for  $\text{Glt}_{\text{ph}}$  mutants with a single tryptophan substitution (Machtens et al., 2015). Computational electrophysiology is well-suited to estimate the effects of amino acid exchange on unitary current amplitudes and anion-to-cation selectivity. An extensive

mutational scan revealed perfect agreement between simulated permeation properties and experimental values, which included unitary current amplitudes determined by noise analysis and anion-cation selectivities obtained from whole-cell recordings under varying anion/cation gradients. These results demonstrate

that the ChC conformation is indeed formed and is responsible for anion conduction in EAATs (Machtens et al., 2015).

Recently, an intermediate conformation of  $\text{Glt}_{\text{ph}}$ , captured *via* crosslinking of an inserted cysteine pair was obtained by cryo-electron microscopy (Chen et al., 2021). The authors used





molecular dynamics simulation to show the formation of a continuous hydration pathway at the interface of transport and trimerization domain. Subsequently, umbrella sampling simulations were used to determine free-energy profiles for pulling  $\text{Cl}^-$  through this aqueous pore. However, no spontaneous permeations were reported, and it is therefore not clear whether this intermediate conformation can conduct anions under physiological chemical/electrical gradients without application of external force. Neither unitary currents nor selectivities between anions or between anions and cation were computed. To experimentally support the role of the novel intermediate conformation in EAAT anion permeation, EAAT1 was mutated at seven position (Chen et al., 2021; #4525). Most of these mutations were already tested by Machtens et al. (2015). Each of the mutation modified reversal potentials of combined EAAT1 transport/anion currents. This analysis does not permit to separate effects of the mutations on glutamate transport, on the likelihood of anion channel opening or on the unitary current amplitude. All tested mutations will also affect the ChC anion conduction pathway, and the used crosslink does not prevent formation of the ChC conformation. Thus, neither experiments nor simulations demonstrate that the novel intermediate conformation is anion-conducting.

At present, it is therefore not possible to assess the functional role of this intermediate conformation. It may represent an additional anion-conductive state under physiological conditions or a translocation intermediate, from which anion channel opening may occur. In contrast, the ChC conformation has been shown to account for EAAT anion conduction with permeation rates and selectivity in full agreement with experimental results and to explain all available mutagenesis results (Machtens et al., 2015).

## EAAT ANION CHANNELS CONTRIBUTE TO CHLORIDE HOMEOSTASIS IN GLIAL CELLS

The association of a missense mutation in *SLC1A3* (encoding the glial glutamate transporter EAAT1) with a case of a human genetic disease (Jen et al., 2005; Winter et al., 2012) was the basis to evaluate the role of EAAT anion channels in glial chloride homeostasis. Glial cells display predominant  $\text{K}^+$  conductance that allows the buffering of  $[\text{K}^+]_i$  in the extracellular space and ensures a stable negative resting potential (Lothman and Somjen, 1975; Futamachi and Pedley, 1976). The  $\text{K}^+$  conductance prevents glial depolarization upon electrogenic glutamate uptake. However, internal  $\text{Cl}^-$  concentrations ( $[\text{Cl}^-]_{\text{int}}$ ) in glial cells are larger than expected from passive distribution (Kimelberg, 1981; Kettenmann et al., 1987; Bevensee et al., 1997; Walz, 2002), and EAAT anion channels might reduce the resting  $[\text{Cl}^-]_{\text{int}}$  via mediating a chloride efflux pathway in parallel to  $\text{K}^+$  efflux through glial  $\text{K}^+$  channels.

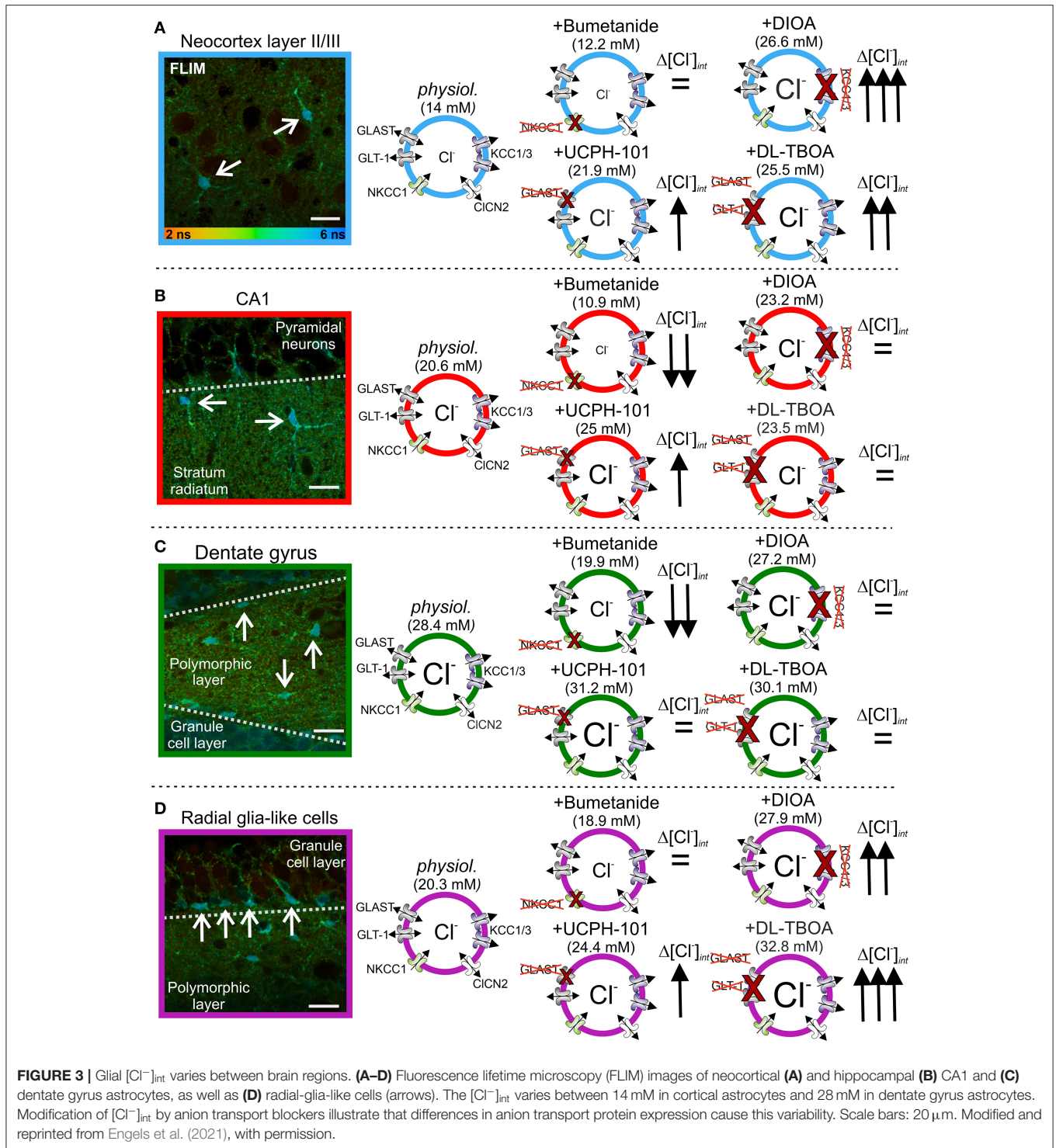
Untiet et al. (2017) measured  $[\text{Cl}^-]_{\text{int}}$  in Bergmann glial cells in acute cerebellar slices using fluorescence lifetime imaging (FLIM) with the  $\text{Cl}^-$ -sensitive dye MQAE. The experiments revealed a mean resting concentration of 35 mM in juvenile

animals (postnatal days P20–P30; **Figures 2A,B**). Blocking the cation–chloride cotransporter NKCC1 decreased  $[\text{Cl}^-]_{\text{int}}$  in Bergmann glial cells, whereas DIOA inhibition of two glial  $\text{K}^+$ – $\text{Cl}^-$  cotransporters, KCC1 and KCC3 (**Figure 2C**), had only minor effects on  $[\text{Cl}^-]_{\text{int}}$ . In *Slc1a3*<sup>−/−</sup> mice lacking the glutamate transporter EAAT1/GLAST, but not in *Clc2*<sup>−/−</sup> mice,  $[\text{Cl}^-]_{\text{int}}$  was increased to 40 mM (**Figure 2C**). Inhibition of EAAT1/GLAST by the highly specific EAAT1 blocker UCPH-101 (Abrahamsen et al., 2013) raised  $[\text{Cl}^-]_{\text{int}}$  to 44 mM in wild-type Bergmann glia, and TBOA blockage of both glial glutamate transporters, EAAT1 and EAAT2, raised  $[\text{Cl}^-]_{\text{int}}$  to around 50 mM. The expression of EAATs is developmentally controlled, and such changes in EAAT expression results in a developmental chloride switch. At P8,  $[\text{Cl}^-]_{\text{int}}$  were comparable to those of juvenile animals after blocking EAAT1 and EAAT2 with TBOA, with  $[\text{Cl}^-]_{\text{int}}$  decreasing to adult levels between P9 and P12. These results demonstrate that EAAT anion channels are major determinants of  $[\text{Cl}^-]_{\text{int}}$  in Bergmann glial cells (Untiet et al., 2017).

Subsequent work on hippocampal and cortical glia revealed that resting  $[\text{Cl}^-]_{\text{int}}$  differs even in highly similar glia types and that the contribution of EAAT anion channels in setting the glial  $[\text{Cl}^-]_{\text{int}}$  is quite variable (**Figure 3**) (Engels et al., 2021).  $[\text{Cl}^-]_{\text{int}}$  varied from 14 mM in cortical astrocytes (**Figure 3A**) to >20 mM in CA1 astrocytes (**Figure 3B**) and radial-glia-like cells (**Figure 3C**), and to 28 mM in dentate gyrus astrocytes (**Figure 3D**). The use of anion transport blockers identified differences in anion transport protein expression as the mechanistic basis of this variability. Whereas, blockage of NKCC1 by bumetanide reduced  $[\text{Cl}^-]_{\text{int}}$  in hippocampal astrocytes (**Figures 3B,C**), no significant change was observed in cortical astrocytes (**Figure 3A**), or radial-glia-like cells (**Figure 3D**). Blockage of KCC1 and KCC3 or of EAAT anion channels substantially increased  $[\text{Cl}^-]_{\text{int}}$  in cortical and CA1 astrocytes and in radial-glia-like cells (**Figures 3A,B,D**), but not in dentate gyrus astrocytes (**Figure 3C**). The experiments showed that EAAT anion channels are involved in the regulation of internal chloride concentrations of certain, but not in all glial cells.

## GLIAL CHLORIDE HOMEOSTASIS IN SLC1A3-ASSOCIATED NEUROLOGICAL DISEASE

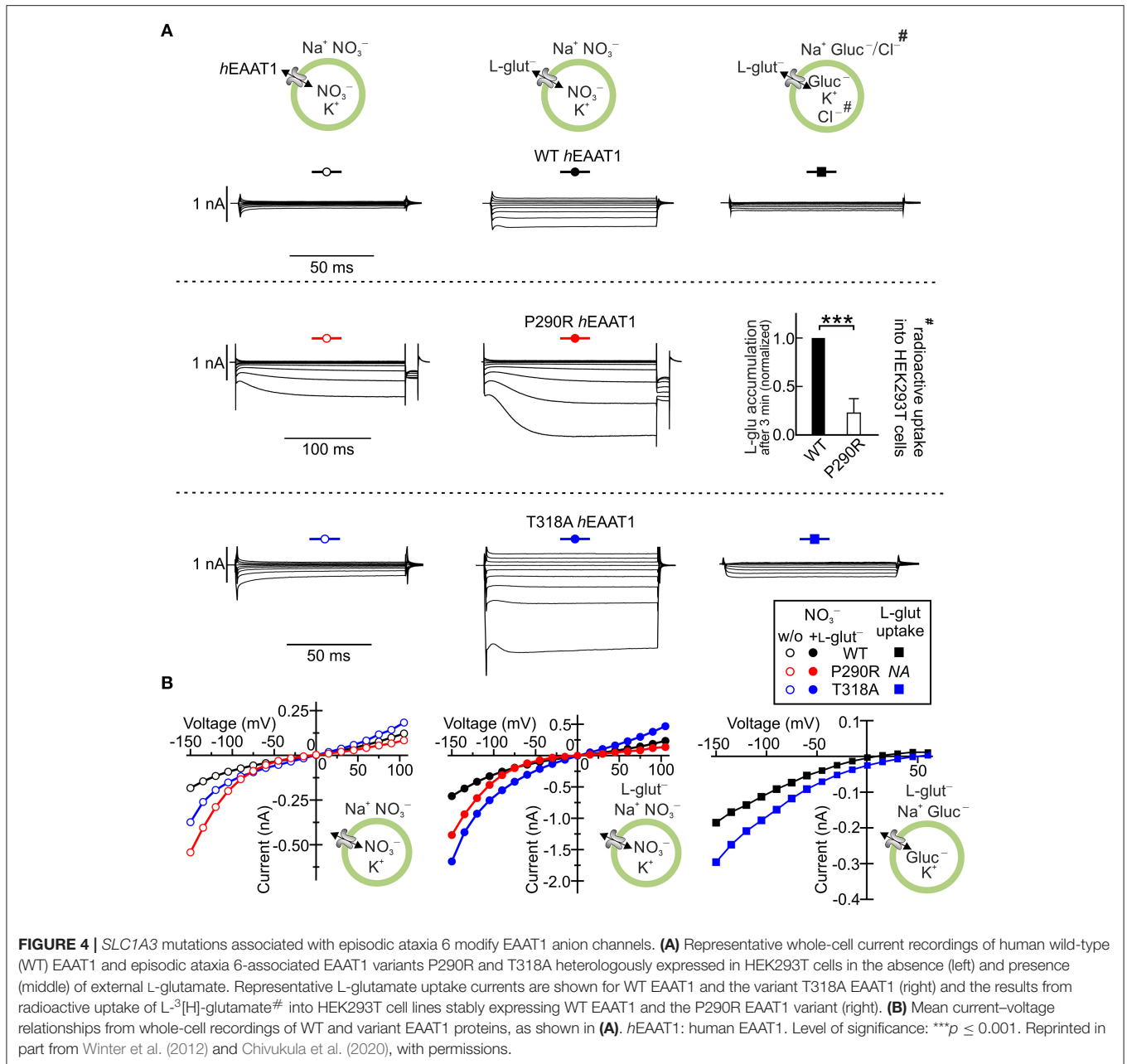
Episodic ataxias are a group of six genetic syndromes characterized by paroxysmal cerebellar incoordination and other neurological symptoms, but differing in their clinical symptoms. Episodic ataxia 6 was first reported in a 10-year-old boy with long ataxia attacks, epilepsy and cerebellar degeneration (Jen et al., 2005), but without myokymia, nystagmus, or tinnitus. The patient was heterozygous for a *SLC1A3* mutation that predicts the substitution of proline by arginine at position 290 in EAAT1. The functional consequences of P290R substitution were evaluated after heterologous expression of the mutant protein in mammalian cells and demonstrated that P290R substitution has opposing effects on the two transport functions of EAAT1:



it reduces glutamate uptake (Jen et al., 2005; Winter et al., 2012) and enhances EAAT1 anion channel activity (Winter et al., 2012) (**Figure 4**). The neurological symptoms of the heterozygous patient were much more pronounced than the neurological phenotype of EAAT1/GLAST (the rodent EAAT1 homolog)-knockout animals (Watase et al., 1998; Stoffel et al.,

2004; Miyazaki et al., 2017), suggesting that the disease is not caused by loss of function of the EAAT1 glutamate transporter.

A heterozygous knock-in mouse (*Slc1a3*<sup>P290R/+</sup>) carrying the disease-causing P290R mutation (Jen et al., 2005) showed ataxia and epilepsy, thus closely resembling the neurological symptoms of the human patient (Kovermann et al., 2020). In



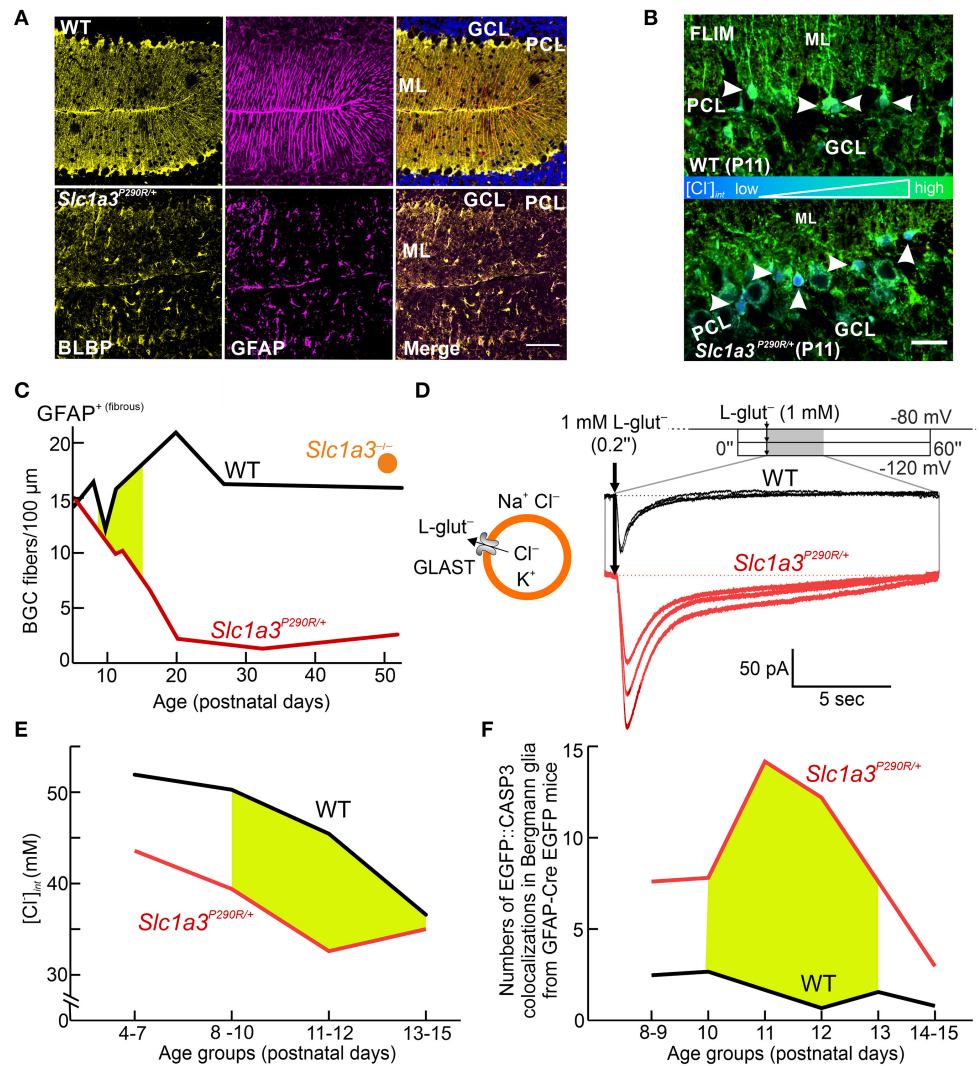
*Slc1a3*<sup>P290R/+</sup> animals, Bergmann glial cells almost completely disappeared between P10 and P20 due to apoptosis. Unaltered numbers of these cells in *Slc1a3*<sup>-/-</sup> animals showed that gain of function of the EAAT1/GLAST anion channel (rather than impaired glutamate transport) causes glial apoptosis (Watase et al., 1998; Stoffel et al., 2004; Miyazaki et al., 2017; Kovermann et al., 2020) (**Figures 5A,B**).

Glutamate-activated Cl<sup>-</sup> currents were increased in electrophysiological recordings from *Slc1a3*<sup>P290R/+</sup> Bergmann glial cells (**Figure 5C**). Since EAAT1 contributes to chloride homeostasis in these cells, [Cl<sup>-</sup>]<sub>int</sub> between P10 and P20 was compared in *Slc1a3*<sup>P290R/+</sup> and wild-type Bergmann glia (Kovermann et al., 2020). FLIM revealed a reduction

in [Cl<sup>-</sup>]<sub>int</sub> by ~20% in *Slc1a3*<sup>P290R/+</sup> Bergmann glia (**Figures 5D,E**), indicating an increased outward Cl<sup>-</sup> flux. Apoptotic events in Bergmann glial cells were significantly increased in mutant animals over the experimental time course (**Figure 5F**), suggesting that increased Cl<sup>-</sup> efflux through P290R EAAT1/GLAST triggers Bergmann glial cell shrinking and apoptosis (Kovermann et al., 2020). Thus, impaired glial chloride homeostasis appears to be a major pathomechanism in episodic ataxia 6.

Functional analysis of other disease-associated *SLC1A3* mutations in heterologous expression systems revealed a variety of alterations in EAAT1 function (Chivukula et al., 2020), indicating that episodic ataxia 6 is not always caused by changes





**FIGURE 5** | Cellular  $\text{Cl}^-$  depletion causes apoptosis in  $\text{Slc1a3}^{\text{P290R/+}}$  Bergmann glial cells. **(A)** Confocal images show the disappearance of Bergmann glial cells (BGCs) in young mice (P20) heterozygous for the P290R mutation in EAAT1/GLAST by immunostaining BGCs for brain lipid-binding protein (BLBP, yellow) and glial fibrillary acidic protein (GFAP, magenta). **(B)** FLIM imaging of cerebellar cortices from wild-type (WT) and  $\text{Slc1a3}^{\text{P290R/+}}$  mice indicates that P290R decreases  $[\text{Cl}^-]_{\text{i}}$ . Arrowheads depict MQAE-filled Bergmann glial cells. GCL, granule cell layer; ML, molecular layer; PCL, Purkinje cell layer. **(C)** Time course of BGC numbers in the cerebella of WT (black),  $\text{Slc1a3}^{\text{P290R/+}}$  (red), and  $\text{Slc1a3}^{-/-}$  (orange) mice shows that loss of BGCs occurs only in P290R mice—not in knockout animals. **(D)** Whole-cell patch-clamp recordings of acute brain slices from WT and  $\text{Slc1a3}^{\text{P290R/+}}$  animals show gain of function of  $\text{Slc1a3}^{\text{P290R/+}}$  anion channels in BGCs from mutant animals upon brief pulses of L-glutamate (L-glut). **(E)**  $[\text{Cl}^-]_{\text{i}}$  is decreased in BGCs from  $\text{Slc1a3}^{\text{P290R/+}}$  mice at all stages of early postnatal development. The age period for BGC loss is shown in yellow. **(F)** Number of cerebellar CASP3 signals in GFAP-EGFP-expressing mice during the second week of life. Reprinted in part and modified from Kovermann et al. (2020), with permission.

in the EAAT1 anion channel function but instead involves a range of functional defects in this transporter. The mutations C186S (RefSeq: NM\_004172.4: c.556T>A), A329T (NM\_004172.4: c.985G>A), V393I (NM\_004172.4: c.1177G>A), and R499Q (alias R454Q, XM\_024446182.1: c.1361G>A) (De Vries et al., 2009; Choi et al., 2017a,b; Iwama et al., 2018) increased protein expression but decreased glutamate uptake and anion channel function in *hEAAT1*. One mutation (M128R: NM\_004172.4: c.383T>G) led to complete loss of transport and channel function, accompanied by decreased protein expression. Only one of the tested mutations, threonine to alanine substitution

at position 318 in *hEAAT1* (T318A: RefSeq NM\_004172.4: c.952A>G), increased anion conductance and L-glutamate uptake through increased membrane insertion by factors of 2.4 and 1.6, respectively (Chivukula et al., 2020) (Figure 4). To understand how these subtle changes in function result in cerebellar incoordination, additional disease models need to be generated and analyzed.

*SLCIA3* variants are not only associated with episodic ataxia 6. We reported a *SLCIA3* mutation in a young man with migraine with aura including hemiplegia (T387P); this mutation prevents glutamate transport by impairing  $\text{K}^+$  binding



(Kovermann et al., 2017). A sequence variant predicting E219D in EAAT1 (RefSeq: NM\_004172.4: c.657G>C) was recently associated with Tourette syndrome and hemiplegic migraine (Adamczyk et al., 2011); the variant shown to increase the surface expression of EAAT1 (Adamczyk et al., 2011). However, the E219D variant is also found in healthy individuals (gnomAD v2.1.1)—both heterozygous and homozygous—(Karczewski et al., 2020); therefore, this variant alone is unlikely to be responsible for Tourette syndrome. Gene duplication of *SLC1A3* was reported in patients with autism and attention deficit hyperactivity disorder (van Amen-Hellebrekers et al., 2016). Both *SLC1A3* duplication and the E219D variant might increase glutamate-activated anion channel currents in glial cells, and subsequent changes in anion currents or anion concentration in radial-glia-like cells might modify network formation during development, thus contributing to complex neuropsychiatric diseases. The EAAT3 variant R445W was found in a patient with symptoms of obsessive compulsive disorder who was also diagnosed with dicarboxyluria. R445 is highly conserved within vertebrate EAATs, and The R445W variant of EAAT3 has changed glutamate affinity (Bailey et al., 2011). Since this residue is critical for the anion selectivity of EAAT anion channels (Machtens et al., 2015; Cater et al., 2016), it is tempting to speculate that this variant might also affect the ion channel function of EAAT3.

## GLIAL CHLORIDE HOMEOSTASIS UNDER ISCHEMIC STRESS

Reduced intracellular [ATP] is expected to inhibit primary active  $\text{Na}^+\text{-K}^+\text{-ATPase}$  and, thus, increase intracellular  $[\text{Na}^+]$  and extracellular  $[\text{K}^+]$ . Since such alterations stimulate NKCC and KCC transport, and also enhance EAAT anion currents *via* impaired neurotransmitter uptake, energy restrictions are likely to interfere with glial chloride homeostasis. Engels et al. recently studied glial  $[\text{Cl}^-]_{\text{int}}$  under transient ischemic stress in acute brain slices by FLIM. Whereas,  $[\text{Cl}^-]_{\text{int}}$  and cell volumes stayed constant during 10 min of chemical ischemia, energy depletion during blockage of NKCC1 and KCCs significantly changed  $[\text{Cl}^-]_{\text{int}}$ . Thus, metabolic stress upregulates  $\text{Cl}^-$  inward and outward transport; increases in  $\text{Cl}^-$  flux in both directions compensate for each other and keep glial  $[\text{Cl}^-]_{\text{int}}$  constant during transient moderate ischemia (Engels et al., 2021).

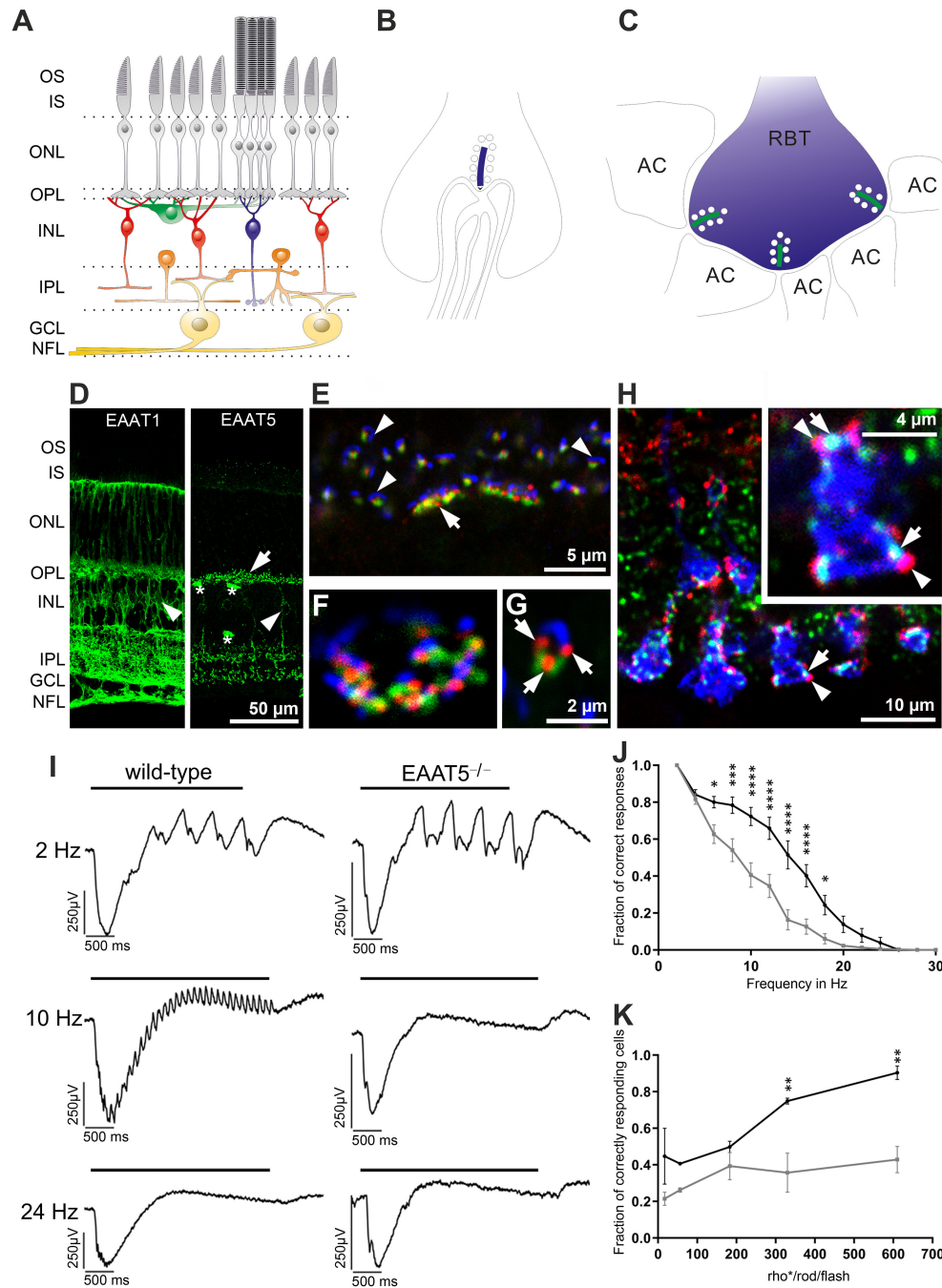
Glial  $[\text{Cl}^-]_{\text{int}}$  under both control conditions and transient energy restriction can be quantitatively described with mathematical models, in which ion transport in pre- and post-synaptic neurons and astrocytes are described with a set of differential equations (Engels et al., 2021; Kalia et al., 2021). Differences in  $[\text{Cl}^-]_{\text{int}}$  between cortical and hippocampal astrocytes under both control conditions and energy restriction could be modeled by varying NKCC and KCC densities. The role of EAAT anion channels during ischemic chloride homeostasis was tested by modifying the TBOA-sensitive leak conductance in such simulations. This did not affect the modeling results, indicating that EAAT anion channels contribute only slightly to energy restriction-induced changes in glial  $[\text{Cl}^-]_{\text{int}}$ . Taken together, these results support the notion that glial  $[\text{Cl}^-]_{\text{int}}$

is in dynamic equilibrium between chloride inward transport and outward flux/transport by cation-coupled transporters and EAAT anion channels and that changes in transport rates are compensated during the initial phases of transient ischemia.

## EAAT5 IMPROVES TEMPORAL RESOLUTION IN THE RETINA

The retina is a well-layered neuronal network (Figure 6A). Glutamate is released by photoreceptors (gray) in the outer plexiform layer (OPL) and bipolar cells (red and blue) in the inner plexiform layer (IPL). Photoreceptor synapses are complex structures with invaginations that harbor several post-synaptic processes and a pre-synaptic ribbon decorated with synaptic vesicles marking the glutamate release site at each invagination (Figure 6B, rod terminal, ribbon in blue). Each bipolar cell terminal makes several output synapses with ribbons and with two postsynaptic processes per ribbon (Figure 6C, shown for a rod bipolar terminal (RBT, blue, an interneuron relaying information from rod photoreceptors), ribbons in green, AC, amacrine cell process). EAAT1 is expressed at high levels in Müller cells (Figure 6D, left) and is assumed to mediate most of the retinal glutamate uptake (Derouiche and Rauen, 1995; Rauen et al., 1996, 1998; Lehre et al., 1997; Pow and Barnett, 1999; Izumi et al., 2002; Sarthy et al., 2005). EAAT2 is expressed in photoreceptors and bipolar cells (Rauen et al., 1996, 1998; Harada et al., 1998; Rauen and Wiessner, 2000), suggesting that it has a role in glutamate reuptake and recycling in glutamatergic cells. EAAT5 expression has been described in both synaptic layers and the somata of some bipolar, amacrine, and ganglion cells, as well as in photoreceptors, including their inner segments (Pow and Barnett, 2000; Wersinger et al., 2006). However, a recent study (Gehlen et al., 2021) found that *mEAAT5* is strongly expressed in a punctate manner (Figure 6D, right) and is closely associated with glutamate release sites (indicated by the presence of synaptic ribbons) on both rod and cone photoreceptors in the outer plexiform layer (Figures 6E–G) and rod bipolar cells in the inner plexiform layer of the mouse retina (Figure 6H). While rod bipolar cell terminals were decorated with numerous *mEAAT5*-positive puncta (Figure 6H, colors correspond to scheme in Figure 6C), the label in cone bipolar cells was less clear. Evidence for EAAT5 expression in photoreceptors and rod bipolar cells also comes from electrophysiological studies (Eliasof and Werblin, 1993; Picaud et al., 1995b; Hasegawa et al., 2006; Veruki et al., 2006; Wersinger et al., 2006; Bligard et al., 2020). The striking difference in the expression patterns of EAAT1 and EAAT5 suggests that they have different functions. Owing to its close association with the glutamate-release site, EAAT5 is perfectly located to mediate glutamate-driven negative feedback.

Recordings from isolated retinæ *in vitro* revealed that *mEAAT5* is important to achieve high temporal resolution of retinal light responses when both rods and cones are active (Gehlen et al., 2021). When recording local field potentials in response to flicker stimuli of different frequencies (Figure 6I), temporal resolution was significantly compromised in *mEAAT5*<sup>-/-</sup> compared with wild-type retina (Figure 6J). A



**FIGURE 6** | Expression and role of EAAT5 in the retina. **(A)** Schematic diagram of the retinal network (photoreceptors in gray, horizontal cells in green, cone bipolar cells in red, rod bipolar cell in blue, amacrine cells in orange, ganglion cells in yellow) with synapses formed in the outer plexiform layer (OPL) and inner plexiform layer (IPL). GCL, ganglion cell layer; INL, inner nuclear layer; IPL, inner plexiform layer; IS, inner segments; NFL, nerve fiber layer; ONL, outer nuclear layer; OPL, outer plexiform layer; OS, outer segments. **(B)** Synapse at a rod terminal with presynaptic ribbon (blue) and invaginating post-synaptic processes of bipolar and horizontal cells. **(C)** Synapses at a rod bipolar terminal (RBT) with two post-synaptic amacrine processes (AC) per ribbon (green). **(D)** Comparison of EAAT1 (left) and EAAT5 (right) expression. EAAT1 is widely expressed in retinal Müller cells (arrowhead), whose processes span the entire retina. EAAT5 is mostly found in bright puncta (arrow) in both OPL and IPL and is expressed weakly in some bipolar cell bodies (arrowhead). Asterisks mark blood vessels stained unspecifically by the secondary antibody. **(E–G)** Triple staining with antibodies against mGluR6 (green, on ON-bipolar cell dendrites), EAAT5 (red), and piccolo (blue, synaptic ribbon, glutamate-release site) in the OPL of a wild-type retina. **(E)** EAAT5 puncta are always highly associated with the glutamate-release site. Arrow: cone terminal; arrowheads: rod terminals. **(F)** Higher magnification image showing the terminal of a cone in horizontal view. **(G)** Rod terminal in side view (three EAAT5 puncta are seen at the rod terminal, arrows). **(H)** Triple staining in the IPL, showing close association of EAAT5 puncta (red, arrowheads) with the synaptic ribbons (green, arrows) on rod bipolar cell terminals (blue, colors correspond to scheme in **C**). **(I)** Recordings of local field potentials in response to flicker stimuli of different frequencies. In contrast to the wild-type retina (left), EAAT5<sup>-/-</sup> retina (right) did not resolve the 10-Hz flicker stimulus. Bar represents duration of the flicker stimulus (total stimulus duration: 3 s; individual flash

(Continued)

**FIGURE 6** | duration: 20 ms; 610 activated rhodopsin molecules ( $\rho^*$ ) per rod and flash ( $\rho^*/\text{rod}/\text{flash}$ ); mesopic conditions). **(J)** The fraction of correct responses was significantly reduced in EAAT5<sup>-/-</sup> (gray curve) compared with wild-type (black curve) retina. Stimulus parameters were the same as in **(I)**. **(K)** The impact of EAAT5 on temporal resolution in ON-ganglion cells increases with stimulus intensity [indicated as activated rhodopsin molecules ( $\rho^*$ ) per rod and flash ( $\rho^*/\text{rod}/\text{flash}$ )]; flicker stimulus: 12 Hz, total stimulus duration: 3 s; individual flash duration: 20 ms. Black: wild type; gray: EAAT5<sup>-/-</sup>. Levels of significance are: \* $p \leq 0.05$ ; \*\* $p \leq 0.01$ ; \*\*\* $p \leq 0.001$ ; \*\*\*\* $p \leq 0.0001$ . Figure is modified and reprinted from Gehlen et al. (2021), with permission.

similar pattern was observed upon comparing the light responses of individual ganglion cells in the form of action potential trains. Moreover, the effect of *mEAAT5* on temporal resolution grew stronger with increasing stimulus intensity (**Figure 6K**), consistent with the fact that the light-evoked modulation of glutamate release—and, hence, the impact of EAAT5—depends on the brightness of the stimulus. The effect of *mEAAT5* deletion is in perfect agreement with the postulated role for EAAT5 at rod bipolar cell terminals, where it was shown to act as a glutamate-gated chloride channel (Veruki et al., 2006; Wersinger et al., 2006) and may be important for gain control (Bligard et al., 2020). Upon depolarization of the rod bipolar cell, glutamate release at the output synapse would activate not only the glutamate receptors on postsynaptic cells but also presynaptic EAAT5, leading to chloride influx, hyperpolarization of the cell, and consequently, reduced bipolar cell output. This negative feedback would curtail the bipolar cell response to individual flashes during repetitive stimulation and, therefore, increase temporal resolution. However, the effect of EAAT5 on glutamate buffering and reuptake in the synaptic cleft might also help to fine-tune the action of glutamate at post-synaptic cells. The synergistic action of both mechanisms might account for the increased temporal resolution in wild-type retina.

Obviously, the role of EAAT5 in photoreceptor terminals needs to be addressed in future studies. Hasegawa et al. (2006) reported that EAAT5-mediated glutamate clearance at the photoreceptor synapse is important for shaping light responses at rod-rod bipolar cell synapses in mice. However, the photoreceptor synapse is highly complex and a number of feedback mechanisms have been described. EAAT5 knockout in photoreceptors might lead to elevated levels of glutamate in the synaptic cleft, thus triggering a variety of possible mechanisms. For example, a metabotropic glutamate receptor was reported on cone terminals, and this might become activated and could affect the rate of glutamate release (Van Hook et al., 2017). EAAT5 might also affect photoreceptor output *via* its function as chloride channel by regulating  $[\text{Cl}^-]_{\text{int}}$  at the terminal. In salamander photoreceptors, chloride dynamics in the photoreceptor terminal affect the activation properties of voltage-activated calcium channels (Thoreson et al., 2000, 2003; Thoreson and Bryson, 2004; Li et al., 2008) and, hence, synaptic transmission.

In white perch retina, a glutamate-gated chloride conductance (probably mediated by EAAT5) was also found postsynaptic to photoreceptors on dendrites of certain ON-bipolar cell types that receive a mixed input from rods and cones (Grant and Dowling, 1995). As photoreceptors are depolarized in the dark, their glutamate must hyperpolarize ON-bipolar cells. Typically, glutamate binding to mGluR6 closes TRPM1 channels in ON-bipolar cells (Koike et al., 2010; Morgans et al., 2010), leading to hyperpolarization. The ON-bipolar cells recorded by Grant and Dowling (1995) also contain a mGluR6 cascade that

relays information by rod input, while cone input activates the EAAT anion conductance. Thus, in this particular ON-bipolar cell type, hyperpolarization is achieved by two functionally distinct mechanisms.

Interestingly, EAAT5 was also reported at the ribbon synapses of vestibular hair cells (Dalet et al., 2012) but not at the calyx of Held (Palmer et al., 2003), a well-studied conventional glutamatergic synapse. Compared with conventional synapses, ribbon synapses are characterized by much higher and sustained vesicular release based on graded potentials. It is, therefore, tempting to speculate that EAAT5-mediated feedback triggered by glutamate release might be a common mechanism to regulate synaptic output at ribbon synapses.

## CONCLUSIONS

Glutamate transport seems to be inseparably linked to anion channel function. Even archaeobacterial EAAT homologs exhibit this curious dual function (Ryan and Mindell, 2007; Machtens et al., 2015), and not only EAAT glutamate transporters but also vesicular glutamate transporters can function as anion channels (Schenck et al., 2009; Eriksen et al., 2016). In recent years, considerable progress has been made in assigning cellular processes to EAAT anion channels in selected cell types. In glial cells, EAAT1 and EAAT2 anion channels have been shown to contribute to glial chloride homeostasis (Untiet et al., 2017; Engels et al., 2021) under normal conditions. In a human genetic disease, gain of function in EAAT anion currents causes severe neurological symptoms by impairing glial chloride homeostasis (Winter et al., 2012; Kovermann et al., 2020). In non-retinal neurons, the role of EAAT anion channels has not yet been addressed. We postulate that presynaptic EAAT2 transporters (Petr et al., 2015) may contribute to cytoplasmic  $[\text{Cl}^-]_{\text{int}}$  in nerve terminals. As the anion channel function of vesicular glutamate transporters likely also affects glutamate accumulation in synaptic vesicles (Martineau et al., 2017), EAAT2 anion channels might contribute to setting vesicular glutamate concentrations. Additionally, presynaptic EAAT2 might fulfill similar roles to EAAT5 in the retina and mediate negative feedback in glutamate release; however, presynaptic  $[\text{Cl}^-]_{\text{int}}$  is not currently known. The potential roles of anion channels associated with epithelial EAAT isoforms (Kanai and Hediger, 1992; Bailey et al., 2011) have not yet been investigated.

The cellular physiology and pathophysiology of EAAT anion channels are insufficiently understood, but recent progress leaves little doubt that this transport function, which was initially thought to represent transporter slippage (i.e., ion flux through accidental pore opening due to imperfect coordination of transporters during coupled transport), serves important cellular functions.



## AUTHOR CONTRIBUTIONS

PK, ME, FM, and CF wrote the manuscript. PK and FM generated the figures. All authors approved the submitted version.

## FUNDING

This work was supported by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation)

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to CF (FA 301/13-1) as part of the Research Unit FOR 2795 (Synapses under stress) and by the German Ministry of Education and Research (E-RARE network Treat-ION, BMBF 01GM1907C to CF).

## ACKNOWLEDGMENTS

The authors gratefully acknowledge the computing time granted through JARA on the supercomputer JURECA at the Forschungszentrum Jülich.

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