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Genetic dys-regulation of astrocytic glutamate transporter EAAT2 and its implications in neurological disorders and manganese toxicity

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Abstract

Astrocytic glutamate transporters, the excitatory amino acid transporter (EAAT) 2 and EAAT1 [glutamate transporter 1 (GLT-1) and glutamate aspartate transporter (GLAST) in rodents, respectively], are the main transporters for maintaining optimal glutamate levels in the synaptic clefts by taking up more than 90% of glutamate from extracellular space thus preventing excitotoxic neuronal death. Reduced expression and function of these transporters, especially EAAT2, has been reported in numerous neurological disorders, including amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease, schizophrenia and epilepsy. The mechanism of down-regulation of EAAT2 in these diseases has yet to be fully established. Genetic as well as transcriptional dys-regulation of these transporters by various modes, such as single nucleotide polymorphisms (SNPs) and epigenetics, resulting in impairment of their functions, might play an important role in the etiology of neurological diseases. Consequently, there has been an extensive effort to identify molecular targets for enhancement of EAAT2 expression as a potential therapeutic approach. Several pharmacological agents increase expression of EAAT2 via NF- κ B and CREB at the transcriptional level. However, the negative regulatory mechanisms of EAAT2 have yet to be identified. Recent studies, including those from our laboratory, suggest that the transcriptional factor yin yang 1 (YY1) plays a critical role in the repressive effects of various neurotoxins, such as manganese (Mn), on EAAT2 expression. In this review, we will focus on transcriptional epigenetics, and translational regulation of EAAT2.

Keywords

manganese; EAAT2; GLT-1; single nucleotide polymorphisms; RNA splicing; transcription; epigenetic; NF- κ B; YY1; HDACs

1. Introduction

Astrocytes are critically involved in neuronal function and survival, as they produce neurotrophic factors, such as brain-derived neurotrophic factor (BDNF) and glia-derived

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neurotrophic factor (GDNF), as well as express two main glutamate transporters responsible for the removal of excessive glutamate from the synaptic clefts [1, 2]. Glutamate is the major excitatory neurotransmitter in the central nervous system (CNS), playing a major role in memory and cognitive function [3], and glutamate transporters as such prevent the overstimulation of post-synaptic glutamate receptors that lead to excitotoxic neuronal injury [4, 5]. Among the five subtypes of glutamate transporters identified, glutamate aspartate transporter (GLAST) and glutamate transporter-1 (GLT-1) [excitatory amino acid transporter (EAAT) 1 and 2 in humans, respectively], are predominantly expressed in astrocytes. They are responsible for the uptake of excess glutamate from the extracellular space [6-8], supported by the fact that knockdown of either GLT-1 or GLAST in mice increases extracellular glutamate levels, leading to excitotoxicity related neurodegeneration and progressive paralysis [9]. In the adult brain, that EAAT2 accounts for >90% of the extracellular glutamate clearance [10-12], since the genetic deletion of both alleles of GLT-1 in mice led to the development of lethal seizures [13]. On the other hand, EAAT1 plays a major role during development [14]. Notably, reduction of EAAT2 expression and function is associated with numerous neurological disorders including amyotrophic lateral sclerosis (ALS), Alzheimer's disease (AD), Parkinson's disease (PD), schizophrenia and epilepsy [2, 15]. For example, EAAT2 protein expression is decreased in ALS [12] and AD patients [16], and cultured astrocytes from AD patients also show reduction of both EAAT1 and EAAT2 protein levels along with attenuated glutamate uptake [17]. Accordingly, potential drugs that target to enhance the expression and function of these transporters may serve as efficient therapeutics modalities to combat these diseases [2, 11].

Dysregulation of EAAT1 and EAAT2 expression and function occurs at multiple levels from abnormal genetic coding to altered posttranslational modifications. Genetic dysregulation of EAAT2, such as single nucleotide polymorphisms (SNPs) and aberrant mRNA splicing of EAAT2 are known to impair EAAT2 expression and function, and are linked to several neurological diseases [18, 19]. Several pharmacological agents, such as ceftriaxone [20], estrogen [21], tamoxifen [21, 22] and riluzole [23] increase EAAT1 and EAAT2 expression at the transcription level via activation of nuclear factor κ B (NF- κ B) [22, 24]. Negative regulatory mechanisms of EAAT1 and EAAT2 at the transcription level have been linked to the transcription factor yin yang 1 (YY1) [25] and YY2 [26]. Manganese (Mn) and tumor necrosis factor- α (TNF- α) decreased EAAT2 via activation of YY1 [27]. Herein, we discuss the genetic and transcriptional modulatory mechanisms of EAAT2 linked to neurological disorders.

2. Genetic regulation of EAAT2 associated with neurological disorders

2.1. EAAT2 regulation by RNA splicing

Altered EAAT2 splice variants have been found in ALS as well as in other diseases, such as AD, and this abnormal splicing of EAAT2 mRNA contributes to the loss of EAAT2 protein in these diseases [28, 29]. An AD mouse model expresses altered EAAT2 splice variants in response to hypoxia [30]. Treatment with 3-nitropropionic acid (a chemical hypoxic agent) prior to deposition of amyloid altered the expression of the 5'-splice forms of mouse EAAT2/5UT3, EAAT2/5UT4, and EAAT2/5UT5 in the frontal cortex, hippocampus and

cerebellum of the APP23 transgenic mouse model [30]. This indicates that hypoxia facilitates alternative splicing of EAAT2 in an AD model, providing a possible molecular mechanism linking higher vascular risk to early pathophysiology of AD. The splicing variants of EAAT2 mRNA containing a long 5'-UTR are associated with increased EAAT2 protein expression at the translational level in response to extracellular factors such as corticosterone and retinol [31]. Alternative splicing also occurs in the C-terminal of EAAT2, resulting in three different variants, referred to as GLT-1a, GLT-1b and GLT-1c [32]. GLT-1a is a normal form, containing 11 exons, while GLT-1b and GLT-1c terminate at exon 10 by generating a new C-terminus sequence. EAAT2 RNA splicing events regulated by 5'-regulatory sequences are impaired in astrocytic tumors [33] as human glioma cells U251 express aberrant EAAT2 mRNA, resulting in reduction of EAAT2 protein levels [33]. These observations indicate that the alternate RNA splicing variations of EAAT2 are linked to several neurological diseases, including ALS, AD and glioma.

2.2. EAAT2 regulation by single nucleotide polymorphisms (SNPs)

The EAAT2 promoter contains consensus sites for several transcription factors (TFs) and thus, SNPs in these regions could alter TF bindings to the EAAT2 promoter, resulting in dysregulation of EAAT2 expression and function. Nucleotide change from A to C in -181 position of the EAAT2 promoter transform the consensus sequences of activator protein-2 (AP-2) (a positive TF) to GC-binding factor-2 (GCF-2) (a negative TF), resulting in decreased EAAT2 expression and glutamate uptake [18]. Increased plasma glutamate levels associated with this SNP might trigger strokes. Moreover, the same A to C SNPs on -181 position of the EAAT2 promoter decreases EAAT2 expression and increases plasma glutamate levels during relapse in multiple sclerosis (MS) patients [34]. Another study conducted in a healthy Japanese population revealed that the -181 A to C SNPs in the EAAT2 promoter affects the personality trait of reward dependence [35]. Recently, this SNP variant rs4354668 (-181 A to C) in EAAT2 gene has gained more attention regarding its role in various neurological disorders. For example, EAAT2 -181 A to C variant that causes lower EAAT2 expression and leads to higher prefrontal cortex glutamate levels is associated with impaired prefrontal cognitive performance during schizophrenia [36]. Moreover, this EAAT2 SNP variant has been reported to be responsible for increased recurrence of episodes in bipolar disorder and lower gray matter volumes with poorer working memory performance in schizophrenic patients [37, 38]. The SNPs in EAAT2 gene are linked to higher susceptibility to schizophrenia in the Japanese population [39]. Another study reported the EAAT2 SNP variant rs1885343 in which the GG genotype decreases EAAT2 protein expression compared to AA or AG genotypes in the nucleus accumbens [40].

On the other hand, polymorphism in coding regions of EAAT2, resulting from replacement of the amino acid glycine with arginine (EAAT2 G603A variant), confer vulnerability to risk-taking behavior in alcoholics and is also associated with alcoholic cirrhosis [41, 42]. DNA demethylation on selective DNA demethylation on selective

3. Transcriptional regulation of EAAT2

The EAAT2 promoter contains cis-elements for several transcription factors, such as NF- κ B, Sp1, N-myc, NFAT and YY1 [44]. Several pharmacological agents, such as epidermal

growth factor (EGF), transforming growth factor- α (TGF- α), dibutyryl-AMP increase EAAT2 promoter activity, mRNA and protein levels, whereas tumor necrosis factor- α (TNF- α) decrease EAAT2 expression in primary human fetal astrocytes [44].

3.1. Positive transcriptional regulation of EAAT2

Several studies have shown that the NF- κ B pathway is critical for positive transcription of EAAT2. EGF, ceftriaxone and estrogenic compounds including 17 β -estradiol as well as tamoxifen and raloxifene (selective estrogen receptor modulators [SERMs]) activate the NF- κ B pathway to enhance EAAT2 expression at the transcriptional level [22, 24, 44, 45]. The EAAT2 promoter contains at least three NF- κ B binding motifs at -583, -272 and -251 in the promoter sequences and mutations in any of these sites significantly decrease EAAT2 promoter activity [22, 46]. EGF enhances expression of EAAT2 mRNA and protein levels via activation of NF- κ B binding to -583 site of the EAAT2 promoter [46]. EGF increases phosphorylation of MEK1/2 rather than activating the conventional I κ B pathway in order to activate NF- κ B and subsequent increase of EAAT2 mRNA levels. Ceftriaxone, a β -lactam antibiotic, enhances EAAT2 expression and function in the brain, exerting neuroprotective effects in an ALS mouse model [20]. NF- κ B binding site at -272 of the EAAT2 promoter is critical for the ceftriaxone-induced increase in EAAT2 promoter activity [24]. Ceftriaxone activates the conventional NF- κ B pathway with degradation of I κ B α and nuclear translocation of p65 isoform of NF- κ B [24]. Moreover, neurons enhance EAAT2 expression in astrocytes when they are co-cultured [47, 48]. Although factors released from neurons that are responsible for increasing astrocytic EAAT2 expression are not well understood, NF- κ B appears to be critically involved in neuronal activation of EAAT2 [49]. NF- κ B binding sites at -583 or -251 of the EAAT2 promoter are important for neuronal activation of EAAT2 promoter activity and both NF- κ B isoforms, p65 and p50, interact with these sites to enhance EAAT2 promoter activity [49]. In addition, the activation of kappa B-motif binding phospho-protein (KBPP) is involved in neuronal activation of EAAT2 promoter activity [50]. Reduced KBPP expression is correlated with transcriptional dysfunction of EAAT2, decreasing EAAT2 mRNA and protein levels. We have reported that 17 β -estradiol via GPR30 [51] and tamoxifen as well as raloxifene, can all exert neuroprotection [52-56] and enhance EAAT2 expression by activation of the NF- κ B pathway [22, 27]. These observations suggest that NF- κ B serves as a critical transcription factor mediating the effects of positive modulators of EAAT2. Nonetheless, the disturbed positive NF- κ B regulation of EAAT2 associated with lower EAAT2 expression under neuropathologic condition remains to be established.

Other transcription factors, such as cAMP response element binding protein (CREB) might also positively regulate EAAT2 promoter activity. We have reported that CREB plays a critical role in tamoxifen-induced up-regulation of EAAT2 in *in vitro* culture of rat primary astrocytes [22]. Mutation of CREB binding site at -308 of the EAAT2 promoter significantly decreases EAAT2 promoter activity. Tamoxifen activates both NF- κ B and CREB to increase EAAT2 promoter activity, establishing that both factors are critical in tamoxifen-induced enhancement of EAAT2 expression [22].

PI3K/Akt is also positively modulating transcriptional regulation of EAAT2 [44, 57]. Overexpression of Akt increases EAAT2 mRNA levels and mediates EGF-enhanced EAAT2 expression [57]. The protein kinase A (PKA) also mediates dbcAMP- and tamoxifen-enhanced EAAT2 promoter activity [22, 44].

3.2. Negative transcriptional regulation of EAAT2

Most of the studies on the mechanisms of EAAT2 regulation have been directed at positive regulation. Few have addressed negative regulatory mechanisms of EAAT2 expression. One such study reported that a negative regulatory mechanism of EAAT2 is mediated by TNF- α where the latter decreases EAAT2 mRNA expression by co-activation of both NF- κ B and N-myc concurrently [46].

The transcription factor yin yang 1 (YY1) is a critical negative regulator of astrocytic glutamate transporters. YY1 is a multifunctional transcription factor, acting as a transcriptional initiator, activator or repressor, depending on its interaction with available cellular co-factors [58]. YY1 is a critical transcription factor in regulating a variety of biological processes such as cell proliferation and differentiation, DNA repair, and apoptosis [59], regulating multiple genes involved in cell cycle transitions, many of which are oncogenes and tumor-suppressor genes [58]. YY1 also plays an important role in the brain, as it is involved in neural development, neuronal function, developmental myelination, yet it may also contribute to neurological diseases [60]. For example, YY1 might be involved in the pathogenesis of AD by beta-site precursor protein-cleaving enzyme 1 (BACE1) promoter in neurons and astrocytes [61]. BACE1 cleaves amyloid precursor protein (APP) to produce β -amyloid, which deposits in the AD brain and is one of the major hallmarks of AD. YY1 has also been reported to play a role in the regulation of genes that are involved in heritable neurodegenerative disease Charcot-Marie-Tooth disease and in a severe neurodevelopmental disorder called Rett syndrome [62, 63]. In addition, a role for YY1 in the negative regulation of EAAT2 has been implicated given its ability to serve as a co-repressor of astrocyte elevated gene-1 (AEG-1) to repress EAAT2 at the transcriptional level, resulting in reduced glutamate uptake in astrocytes [26]. We have also reported that YY1 is a critical repressor of the EAAT2 promoter, as overexpression of YY1 decreases, whereas knockdown of YY1 or mutation of YY1 binding site in the EAAT2 promoter increases EAAT2 promoter activity [27].

4. Epigenetic deregulation in neurological disorders

Epigenetic modifications such as methylation or acetylation of histones and methylation of DNA are altered in several genes including GLT-1 (EAAT2) associated with neurodegeneration [64]. Epigenetic DNA methylation involve DNA methyltransferases (DNMT), an enzyme transferring a methyl group from S-adenosyl-l-methionine to the carbon 5 position of cytosine resulting in gene silencing [65]. Methylation of the SNCA gene, coding for alpha-synuclein, which is involved in formation of Lewy body in PD, is known to take place, leading to a decrease of gene expression in PD patients [66]. DNA methylation modification is also found in postmortem frontal cortex tissue derived from bipolar disorder (BD) and AD patients, showing hypomethylation of cyclooxygenase-2 (COX-2) and hypermethylation of the BDNF promoter regions in these patients [67].

DNMT mRNA expression is altered in suicide brains, and this change is associated with increased methylation of a gamma-aminobutyric acid (GABA) A type receptor (GABA_A) alpha1 subunit gene whose mRNA expression is reduced in the cortex [68]. Human subjects who experience childhood abuse show increased methylation of a stress responder the glucocorticoid receptor (GR) promoter along with reduced expression of GR mRNA levels in the hippocampus [69]. Chronic social stress induces histone modifications in the BDNF promoter along with reduced BDNF mRNA levels [70]. These observations suggest that alteration in epigenetic regulation mechanisms are closely associated with altered gene expression in neurological disorders.

4.1 Epigenetic dysregulation of EAAT2

Histone modification by acetylation also plays a major role in the epigenetic regulation of EAAT2 expression. Histone acetylation modification is characterized by the addition and removal of acetyl moiety from acetyl-coenzyme A to the ε-amino group of lysine residue; this reaction is carried out by two enzymes, histone acetyltransferases (HATs) and histone deacetylases (HDACs) [71]. Histone deacetylases (HDACs) inhibitors, such as TSA and valproic acid (VPA) increase EAAT2 mRNA and protein levels, indicating the role of acetylation in regulating EAAT2 expression [64, 72, 73]. In addition, CREB-binding protein (CBP), a HAT, has been reported to contribute as a co-repressor of YY1 in the negative regulation of EAAT2 [26].

DNA demethylation on selective CpG sites of the GLT-1 (EAAT2) promoter is highly correlated to increased GLT-1 mRNA levels in mouse brain astrocytes in response to neuronal stimulation [74]. However, low level of methylation was found on CpG sites of EAAT2 promoter from postmortem motor cortex of human ALS patients. Nonetheless, the limitations of using human postmortem tissues could compromise the methylation analysis of EAAT2 promoter for several reasons; (1) detection of the methylation changes in bulk tissue may not represent the loss of EAAT2/GLT1 in the limited area in patient with ALS or transgenic rodent models of ALS, (2) quantification of EAAT2 mRNA may not be accurate due to the repeated freeze-thaw cycle for tissue sample storage which might lead to unstable RNA, and (3) a small sample size for control and patients with ALS. The same authors suggested that a large-scale whole genome DNA methylation analysis of the pathological tissues of larger number of patients with ALS and controls is warranted to reveal the possible epigenetic changes involved in ALS astrocytes in the future [74].

Moreover, DNA methylation analysis in human glioma cell lines and human brain tissue has shown that increased methylation in the EAAT2 promoter is associated with reduced EAAT2 expression [75]. The inhibition of DNMT restores EAAT2 transcription, suggesting a role for methylation in reduction of EAAT2 transcription [75]. Region-specific expression of EAAT2 appears to be associated with the methylation status of the EAAT2 promoter, since higher methylation is detected in the cerebellum compared to the cortex, and is inversely correlated with the region-specific EAAT2 expression [76]. Dexamethasone increases EAAT2 expression in the cortex, but its effect in the cerebellum is minimal due to hypermethylation of EAAT2 in that region [77]. Moreover, neuronal regulation of EAAT2

expression in neuronal-astrocyte co-cultures induces hypomethylation of CpG sites on the EAAT2 promoter, resulting in increased EAAT2 mRNA levels [62].

5. Post translational deregulation of EAAT2

Palmitoylation is one of the posttranslational modifications of proteins in which palmitate is attached to cysteine residues via a thioester linkage by palmitoyl acyl transferases (PATs) (reviewed in [78]). Palmitoylation at cysteine38 (C38) is required for normal EAAT2 (GLT-1) function [79], thus inhibition of palmitoylation severely impairs glutamate uptake. Palmitoylation of EAAT2 (GLT-1) has been shown to be reduced in the YAC128 HD mouse model along with decrease of glutamate uptake, suggesting the role of palmitoylation in EAAT2 (GLT-1) function [79].

Sumoylation is also playing a role in EAAT2 posttranslational modulation. Sumoylated EAAT2 localizes to intracellular compartments, while non-sumoylated EAAT2 resides on the plasma membrane, consistent with the results that desumoylation increases EAAT2-mediated glutamate uptake in primary astrocytes [80]. Moreover, caspase-3 cleaved EAAT2 generates sumoylated proteolytic fragment (CTE), followed by intracellular accumulation of sumoylated CTE in organelles, such as the nucleus and endosome in spinal cord astrocytes of ALS mice [80, 81]. Prolonged nuclear accumulation of CTE induces neuronal toxicity by axonal growth impairment in primary motor neurons, suggesting that sumoylated proteolytic fragment of the astroglial glutamate transporter EAAT2 could participate to the pathogenesis of ALS [81]. Based on these recent findings, sumoylation has been considered as an important pathway in ALS [82].

Ubiquitination of the C-terminal tail of EAAT2 (GLT-1) has also been reported. Ubiquitination mediates internalization and degradation of EAAT2 (GLT-1) via PKC, resulting in decrease of glutamate uptake in C6 glioma cells or primary cortical cultures, suggesting that this ubiquitin-mediated PKC-dependent degradation of EAAT2 might possibly increase under pathological conditions [83]. Activation of PKC increases the ubiquitination of EAAT2 (GLT-1) both *in vitro* and *in vivo* experimental conditions, leading to accumulation of ubiquitinated EAAT2 (GLT-1) in the intracellular compartment [84]. Accordingly, inhibition of the ubiquitin-activating enzyme E1 promotes the retention of GLT-1 at the plasma membrane. The translocation of EAAT2 (GLT-1) from the recycling endosomes to the plasma membrane is blocked by inhibition of the deubiquitinating enzyme (DUB) ubiquitin C-terminal hydrolase-L1, suggesting the existence of specific ubiquitination/deubiquitination cycles in regulating optimal concentrations of GLT-1 at the cell surface [85].

6. Mn-induced transcriptional reduction of EAAT2

Manganese (Mn) is well known to decrease expression of EAAT1 as well as EAAT2 with consequential reduction of glutamate uptake [45, 53, 86, 87]. However, the mechanisms of Mn-induced reduction of EAAT1 and 2 at the transcriptional level remain to be established. We have reported that YY1 might be the critical transcription factor in mediating Mn's effect on reduced EAAT2 expression and function [27].

6.1. Role of YY1 in Mn-induced repression of EAAT2

Although Mn is an essential trace element in the body, serving as a cofactor for enzymes such as MnSOD and glutamine synthetase, its chronic excessive accumulation in the brain from environmental or occupational sources leads to a neurological disorder called manganism that shares similar pathological features with PD [88, 89]. Moreover, Mn neurotoxicity is also known to contribute to the development of multiple neurodegenerative disorders including AD, PD, ALS and Huntington disease (HD) [90]. Despite of its significant impact on multiple neurodegenerative diseases, the mechanisms of Mn-induced neurotoxicity are not completely understood. Several mechanisms, including oxidative stress and mitochondrial impairment have been reported [91-93]. Mn-induced excitotoxic neuronal injury is also considered to be a critical mechanism involved in Mn neurotoxicity. MK801, an *N*-methyl-D-aspartate (NMDA) antagonist blocks excitotoxic lesions in the striatum of Mn-injected rats [94]. Moreover, Mn decreases the expression and function of both astrocytic glutamate transporters, EAAT1 and EAAT2 [45, 53, 86, 87], representing a critical mechanism for Mn-induced neurotoxicity. Since there is no direct binding sites for Mn at the DNA levels identified, it is likely that Mn-induced oxidative stress [95] and inflammation [96] might mediate its repressive actions on glutamate transporters. We have found that YY1 mediates Mn-induced inhibitory effects on EAAT2. Mn increases YY1 promoter activity, mRNA and protein levels [27]. Mn enhances YY1 binding to its consensus sites in the EAAT2 promoter and accordingly, mutation of YY1 binding sites attenuate the Mn-induced decrease in EAAT2 promoter activity, indicating that YY1 is a critical transcriptional mediator in Mn-induced repression of EAAT2 [27].

6.2. Mechanism of Mn-induced repression of EAAT2 via YY1

Mn likely activates YY1 via proinflammatory mediators, as it potentiates the release of several inflammatory molecules including prostaglandins, cytokines, such as TNF- α , interleukin (IL)-6, IL-1 β , as well as nitric oxide from activated glial cells [96-99]. TNF- α and IL-1 β are negative regulators of EAAT2 and they decrease EAAT2 mRNA and protein levels in astrocytes [44, 46, 100-102]. Findings from our studies indicate that Mn increases production of TNF- α which, in turn, increases YY1 promoter activity, mRNA and protein levels in astrocytes [27], suggesting that TNF- α mediates Mn effects on reduction of EAAT2 expression via YY1.

NF- κ B is involved also in Mn-induced repression of EAAT2 via YY1. Although NF- κ B is a major positive regulator of EAAT2, resembling other inflammatory cytokines, such as TNF- α , Mn activates the NF- κ B pathway [103], it represses EAAT2. We have shown that Mn activates YY1 via activation of NF- κ B, and moreover, Mn-induced activation of the YY1 pathways is dominant over its activation of NF- κ B, overriding the positive effects of NF- κ B on EAAT2 [27].

7. Conclusion

The reduced expression and function of astrocytic glutamate transporter EAAT1 and EAAT2 has been associated with numerous neurodegenerative diseases. Accordingly, understanding the precise molecular mechanisms involved in the transcriptional and

translational dys-regulation of EAAT2, as well as other altered genetic regulatory mechanisms, such as SNPs and epigenetics is critical for the development of efficacious drugs for treatment of the neurological disorders associated with impairment of EAAT2 expression (Fig. 1). At the transcriptional level, the NF- κ B and CREB pathways play critical roles in enhancing EAAT2 expression, mediating the effects of positive modulators of EAAT2. In addition, delineating the negative regulatory mechanisms of EAAT2 will be highly beneficial, because targeting this pathway can rescue and reverse the reduced expression and function and potentially delay the progression of neurodegenerative diseases. The YY1 pathway contributes to negative regulation of EAAT2, mediating TNF- α - and Mn-induced inhibitory effects on EAAT2 expression and function. Taken together, understanding positive and negative regulatory mechanisms of EAAT2 expression will offer novel therapeutic approaches to treat neurological disorders associated with excitotoxic neuronal injury.

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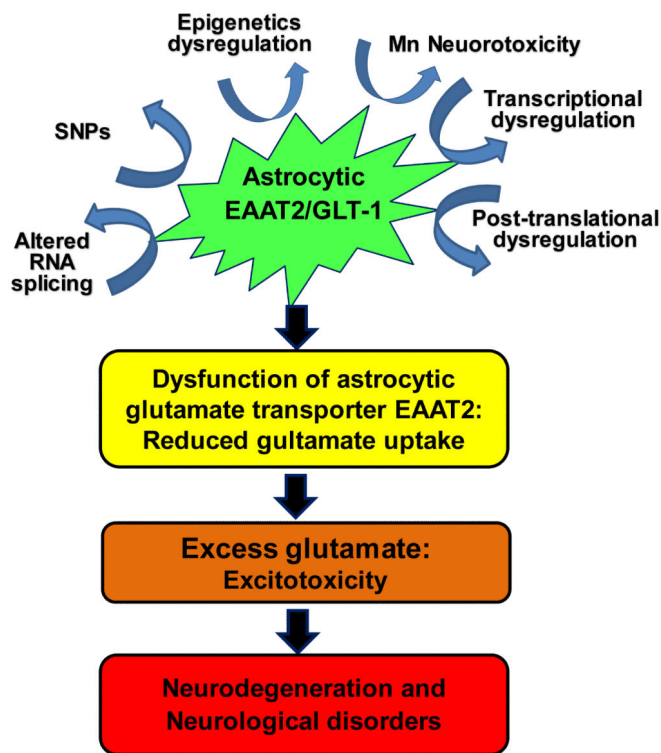


Fig. 1. Proposed mechanisms of dysregulated EAAT2 expression and function that lead to excitotoxic neurodegeneration at multiple gene regulation levels

At genetic level, altered RNA splicing and SNPs play, while at transcriptional level, YY1 and NF- κ B as a repressor and an activator of EAAT2, respectively. Moreover, YY1 mediates the inhibitory modulation of EAAT2 induced by TNF- α as well as Mn as a part of its neurotoxicity mechanism. Epigenetic modifiers such as HDACs and post-translational modulators such as ubiquitin also play roles in the modulation of EAAT2 expression and function. The dysregulation of any of aforementioned mechanisms might lead to a decrease of EAAT2 expression and function resulting in triggering the excitotoxic neuropathological changes in many neurological disorders.