



# White Matter Microstructure in Bipolar Disorder Is Influenced by the Interaction between a Glutamate Transporter EAAT1 Gene Variant and Early Stress

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## Abstract

Glutamate is the principal excitatory neurotransmitter in the central nervous system. In mature brains, it is critically involved in neuroplasticity and, at high levels, neurotoxicity. The concentrations of glutamate in the extracellular space are maintained at low physiological levels by molecular glutamate transporters (excitatory amino acid transporters-EAATs). Adverse childhood experiences (ACEs) are highly reported in bipolar disorder (BD) and interact with the glutamatergic system in the brain. The aim of the study is to investigate the effect of a glutamate transporter polymorphism *EAAT2*-181A > C (rs4354668) and exposure to ACE on white matter microstructure in patients with BD. We assessed 175 bipolar subjects using diffusion tensor imaging, Risky Families Questionnaire, and *EAAT2* rs4354668 variants. We observed an interaction between ACE and rs4354668: carriers of the G allele showed lower axial diffusivity compared to T/T homozygotes when exposed to high stress and higher axial diffusivity than T/T when exposed to low stress. Since the mutant G allele has been associated with a reduced transcriptional activity and expression of the transporter protein, and early stress is associated with a reduced expression of the *EAAT2*, we could hypothesize that after exposure to high levels of ACE G/G homozygotes are more vulnerable to stress reporting the highest damage as a consequence of an excess of free glutamate.

**Keywords** Adverse childhood experiences · Glial glutamate transporter · EAAT2 · SLC1A2 · Bipolar disorder · TBSS

## Introduction

Glutamate is the principal excitatory neurotransmitter in the central nervous system, and glutamatergic neurons are highly represented in the cerebral cortex and limbic regions of the brain. In brain development, glutamate affects neuronal migration, differentiation, and survival, whereas in mature

brains, it is critically involved in neuroplasticity and when it is present at high levels, neurotoxicity. Accumulation of excess extracellular glutamate and subsequent overstimulation of glutamatergic receptors and recruitment of extrasynaptic receptors increases the production of reactive and excitotoxic oxygen/nitrogen species, which induce oxidative stress leading to neuronal death [1]. Recent studies also suggest that this same mechanism can lead to toxic injury of oligodendrocytes forming white matter's myelin sheaths and consequently to axon demyelination [2–4]. Indeed, oligodendrocytes have been shown to express AMPA and kainate receptors [5] in their soma and NMDA receptors in their processes [6–8].

Changes in white matter (WM) integrity are considered biomarkers of bipolar disorder (BD) [9]. Post-mortem studies showed a reduction in the numerical density of oligodendroglial cells in BD [10–13], and in vivo studies consistently documented changes in WM microstructure that have been associated with the genetic risk for BD [14, 15], impulsivity and suicide [16], cognitive performances [17, 18], response to treatment [19], and environmental stressors [20].

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Also, alterations in the glutamatergic system have been suggested to contribute to the pathophysiology of depression [21]. Indeed, elevated levels of glutamate have been reported in pediatric [22] and adult patients affected by BD [23, 24] [25, 26]. Furthermore, inhibition of glutamate release and reduction in glutamate levels in depressed BD patients parallel antidepressant response [27–29].

The inactivation of glutamate is handled by a series of molecular glutamate transporters (excitatory amino acid transporters-EAATs) which are membrane-bound pumps that closely resemble ion channels. These transporters regulate the concentration of glutamate in the extracellular space, maintaining it at low physiological levels in order to promote biological function without promoting toxicity [30]. Among the five human excitatory amino acid transporters that have been cloned, *EAAT2* is responsible for up to 95% of extracellular glutamate clearance [31] and is expressed primarily on astrocytes [32], but it is also expressed by axons [33]. Increased astrocytic *EAAT2* expression appears to afford greater neuroprotection under excitotoxic conditions [34, 35]. Impaired glutamate uptake by dysfunction or reduced expression of *EAAT2* can lead to phenomena of excitotoxicity that have been implicated in the pathogenesis of various neurodegenerative diseases, including Alzheimer's disease, Huntington's disease, amyotrophic lateral sclerosis [1], and also schizophrenia [36–39]. Also, post-mortem studies observed a reduced expression of the membrane transporter *EAAT2* in major depression [40].

The gene encoding *EAAT2* in humans is *SLC1A2* [solute carrier family 1 (glial high-affinity glutamate transporter), member 2], located on chromosome 11p13–12 [41]. A T-to-G (DNA forward strand) functional polymorphism (rs4354668) at –181 bp from the transcription start site of the *EAAT2* gene, which is commonly known as –181A > C, was described by Mallolas and colleagues [42]. This mutation results in less transporter expression with the G allele inducing a 30% reduction in promoter activity compared with the T allele. Post-mortem studies showed lower mRNA expression levels of *EAAT2* in the PFC [43] and locus coeruleus [44] of patients with major depressive disorder, as well as lower *EAAT2* immunoreactivity in the orbitofrontal cortex of depressed individuals compared with controls [45]. Furthermore, in multiple sclerosis, patients with the mutant allele showed an increase of 53.9% in glutamate levels during relapse as compared to those with the wild type [46].

Among the possible factors leading to a long-lasting altered glutamate homeostasis in the brain, a prominent role of stress has been suggested. A review of this topic suggests that chronic stress may affect both glutamate release and clearance [47]. Accordingly, under stress, when elevated levels of glutamate are present, effects of altered function of glutamate transporters are likely to be most pronounced. Also, stress exerts a detrimental effect on WM microstructure in several fiber

tracts contributing to the functional integrity of the brain in BD [48]. These effects of ACE likely associate with other detrimental influences on WM integrity observed in BD: increased genetic liability to familial BD has been associated with reduced WM integrity in patients and their unaffected relatives [14], and genetic factors affecting the severity of BD also influence WM integrity [49]. Gene\*environment interactions, including ACE, could then play a major role in the observed relationship between BD and altered DTI measures of WM integrity. Following this line of reasoning, we investigated the effect of a polymorphism in the promoter region of *EAAT2* gene on WM integrity in bipolar patients exposed to different levels of ACE.

## Methods

### Patients and Data Collection

We studied 175 Caucasian subjects (110 females, 65 males) consecutively referred to our university hospital for BD type I (DSM-V—Diagnostic and Statistical Manual of Mental Disorders, 5th Edition [50]-criteria; SCID—Structured Clinical Interview for DSM-V clinical version). Exclusion criteria were other diagnoses on Axis I, mental retardation, history of epilepsy, and major medical and neurological disorders. Sixty patients (34%) took lithium in the previous 6 months. About 50% of patients were taking antidepressant drugs (SSRI 25%; SNRI 16%; tricyclics 8%), and 24% were taking antipsychotics.

Severity of ACE was rated on the Risky Families Questionnaire (RFQ) [51] after MRI scanning. The RFQ has been adapted from an instrument originally developed to assess the relation of family stress to mental and physical health outcomes in adulthood [52]. The instrument is aimed at rating the degree of harsh parenting with overt family conflict and deficient nurturing experienced by the children in their familial environment. Previous research validated this questionnaire against clinical interviewers; the dual assessment (questionnaire and interview) demonstrated high agreement and reliability [53]. This approach has been proven successful in detecting the structural and functional brain correlates of ACE in adult life [51, 54]. In agreement with previous studies [54–56], the participants were then divided into two subgroups, using median values as a discriminant between high and low scores of the RFQ.

All data were collected on the same day. The work described has been carried out in accordance with The Code of Ethics of the World Medical Association (Declaration of Helsinki). After complete description of the study to the subjects, a written informed consent was obtained. The local ethical committee approved all the research activities.

## Genotyping

DNA was extracted from whole blood by a manual extraction, using the “Illustra blood genomic Prep Midi Flow kit” (GE Healthcare, Milan, Italy). To identify the polymorphism *EEAT2*—181A > C T/G (DNA forward strand), a standard polymerase chain reaction (PCR) was carried with the following primers: 5'-GCC ACC TGT GCT TTG CTG-3' and 5'-TGA TGT CAG CTC TCG ACG AA-3'. The PCR was carried out in a 10- $\mu$ l volume containing 150 ng genomic DNA, 1  $\mu$ l of 1 $\times$  Hot Master Taq Buffer with Mg<sup>++</sup> (Eppendorf), 0.1  $\mu$ l of each primer [50 uM], 1  $\mu$ l of deaza-dNTPs [10 mM], 0.5  $\mu$ l of dimethyl sulfoxide (DMSO) solution (Sigma-Aldrich, Milan, Italy), and 0.1  $\mu$ l of Hot Master Taq [5 U/ $\mu$ l] (Eppendorf). After an initial step of 5 min at 94 °C, 35 cycles of amplification (35 s at 94 °C, 35 s at 58 °C, 45 s at 70 °C) and a final extension step of 10 min at 70 °C were performed. An aliquot of PCR product was digested using *Msp* I (20 U/ $\mu$ l) (New England Biolabs, England, UK) and incubated at 37 °C for 8 h; fragments were separated in agarose gels. Depending on the presence of two or three restriction *Msp* I sites, either three fragments (allele T) or four fragments (allele G) were produced.

## Brain Imaging Procedures and Data Analysis

Diffusion tensor imaging was performed on a 3.0 Tesla scanner (Gyrosan Intera, Philips, Netherlands) using SE Echo-planar imaging (EPI) and the following parameters: TR/TE = 8753.89/58 ms, FoV (mm) 231.43 (ap), 126.50 (fh), 240.00 (rl); acquisition matrix 2.14  $\times$  2.71  $\times$  2.31; 55 contiguous, 2.3-mm thick axial slices reconstructed with in-plane pixel size 1.88  $\times$  1.87 mm; SENSE acceleration factor = 2; 1 b0 and 35 non-collinear directions of the diffusion gradients; b value = 900 s/mm<sup>2</sup>. Fat saturation was performed to avoid chemical shift artifacts. On the same occasion and using the same magnet 22 Turbo Spin Echo (TSE), T2 axial slices (TR = 3000 ms; TE = 85 ms; flip angle = 90°; turbo factor 15; 5 mm thick, axial slices with a 512  $\times$  512 matrix and a 230  $\times$  230-mm<sup>2</sup> field of view), and T2w FLAIR (TR = 11,000 ms; TE = 120 ms; flip angle = 90°; turbo factor 21; 5 mm thick, axial slices with a 400  $\times$  400 matrix and a 230  $\times$  230-mm<sup>2</sup> field of view) were acquired to rule out brain lesions.

Image analyses and tensor calculations were done using the “Oxford Center for Functional Magnetic Resonance Imaging of the Brain Software Library” (FSL 5.0; [www.fmrib.ox.ac.uk/fsl/index.html](http://www.fmrib.ox.ac.uk/fsl/index.html)) [57, 58]. For a detailed description, see Supplementary data.

Voxelwise DTI analyses were performed using nonparametric permutation-based testing [59], corrected for FWE multiple comparisons, as implemented in Randomize in FSL with general linear models (GLM). Threshold-free cluster

enhancement (TFCE) [60] was used to avoid defining arbitrary cluster-forming thresholds and smoothing levels. Voxelwise levels of significance, corrected for multiple comparisons, were then calculated with a standard permutation testing (10,000 permutations for each contrast) by building up the null distribution of the maximum TFCE scores. Corrected  $p < 0.05$  in a minimum cluster size of  $k = 100$  was considered significant.

First, an ANOVA was performed to test the interaction between ACE and rs4354668 on DTI measures of WM microstructure [Fractional anisotropy (FA), axial (AD), radial (RD), and mean diffusivity (MD)]. Post hoc *T* tests were then used to investigate the direction of the effect separately in the high ACE and low ACE groups in those WM tracts that emerged from the ANOVA. We accounted for the effects of nuisance covariates which could influence WM structure: age [61], sex [62], age at onset of the illness [63], and lithium treatment [49].

## Results

Allelic frequencies were similar to those observed for the general population ( $T = 58\%$ ;  $G = 42\%$ ) [42]. The distribution of *EAAT2* genotypes ( $T/T n = 56$ ,  $T/G n = 91$ ,  $G/G n = 28$ ) was in Hardy–Weinberg equilibrium ( $\chi^2 = 0.79$ ,  $p = 0.37$ ). Clinical and demographic data are shown in Tables 1 and 2. No difference between high ACE and low ACE (Table 1) or between genotypic groups (Table 2) reached significance when investigating clinical variables.

The ANOVA showed an interaction between the glutamate transporter polymorphism and ACE on AD in WM tracts encompassing inferior and superior longitudinal fasciculus and the inferior fronto-occipital fasciculus (Fig. 1 and Supplementary Table 1). Post hoc *T* tests (Fig. 2) showed that, in the high ACE subgroup, subjects with at least one G allele had lower AD compared to T/T subjects ( $GG < TT p < 0.001$ ;  $GT < TT p = 0.002$ ). In the low ACE subgroup, we observed the opposite pattern with subjects with at least a G allele

**Table 1** Clinical and demographic characteristics of the sample divided according to adverse childhood experiences

	Adverse childhood experiences		<i>p</i>
	High <i>n</i> = 91 Mean $\pm$ SD	Low <i>n</i> = 84 Mean $\pm$ SD	
Age (years)	46.14 $\pm$ 11.11	46.69 $\pm$ 11.15	0.74
Education (years)	11.68 $\pm$ 4.29	11.26 $\pm$ 3.78	0.49
Onset (year)	30.33 $\pm$ 10.14	31.08 $\pm$ 10.73	0.63
Duration of illness (years)	15.81 $\pm$ 10.34	15.62 $\pm$ 10.76	0.90
Number of episodes	8.93 $\pm$ 9.04	7.91 $\pm$ 8.89	0.45

**Table 2** Clinical and demographic characteristics of the sample as a whole and divided according to *SLA1A2 -181A > C* genotype

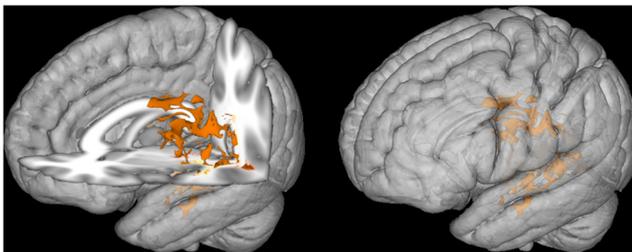
	Total sample	GG ( <i>n</i> = 28)	EAAT2 GT ( <i>n</i> = 91)	TT ( <i>n</i> = 56)	<i>p</i>
	Mean ± SD	Mean ± SD	Mean ± SD	Mean ± SD	
Age (years)	46.40 ± 11.10	44.64 ± 7.86	46.19 ± 11.29	47.62 ± 12.16	0.49
Education (years)	11.48 ± 4.05	12.5 ± 4.12	11.41 ± 3.94	11.09 ± .18	0.31
Onset (year)	30.69 ± 10.41	30.53 ± 6.67	30.28 ± 10.27	31.43 ± 12.13	0.81
Duration of illness (years)	15.72 ± 10.52	14.14 ± 9.07	15.91 ± 10.68	16.19 ± 11.01	0.68
Number of episodes	8.45 ± 8.96	9.61 ± 9.59	7.92 ± 8.74	8.74 ± 9.09	0.66
ACE	27.03 ± 9.05	28.32 ± 8.91	25.86 ± 8.95	28.30 ± 9.19	0.20

showing higher AD compared to T/T subjects (GG > TT  $p = 0.007$ ; GT > TT  $p < 0.001$ ). No direct association between EAAT2 genotypes and AD was observed.

## Discussion

This is the first study to investigate the effect of a polymorphism in the promoter region of the SLC1A2 gene on WM microstructure in BD patients exposed to different levels of ACE. Here, we show that rs4354668 exerts a significant effect on WM integrity and that this effect is moderated by ACE. When exposed to low levels of ACE, carriers of the G allele reported significantly higher AD than T/T homozygotes whereas they showed lower AD when exposed to high ACE. The opposite pattern was observed in T/T homozygotes. This finding is in agreement with a previous study from our group reporting higher gray matter volume in carriers of the G allele exposed to low ACE compared to T/T homozygotes [55] and confirms the crucial role of glutamate for the integrity of brain structure.

Here, we showed that the interaction between ACE and rs4354668 influences AD. AD represents the diffusion of water parallel to the axonal fibers, reflecting the greater freedom of water to diffuse along the principal fiber axis rather than to travel across the surrounding myelin sheaths. Both myelin and axonal microstructure, including microtubules and neurofilaments [64], contribute to this anisotropy. Higher



**Fig. 1** 3D reconstruction of white matter tracts where we observed a significant interaction between EAAT2-181A > C genotype and ACE on axial diffusivity. Voxel of significant effect surviving a significant threshold of  $p < 0.05$  corrected for multiple comparison is shown on a 3D T1-weighted image

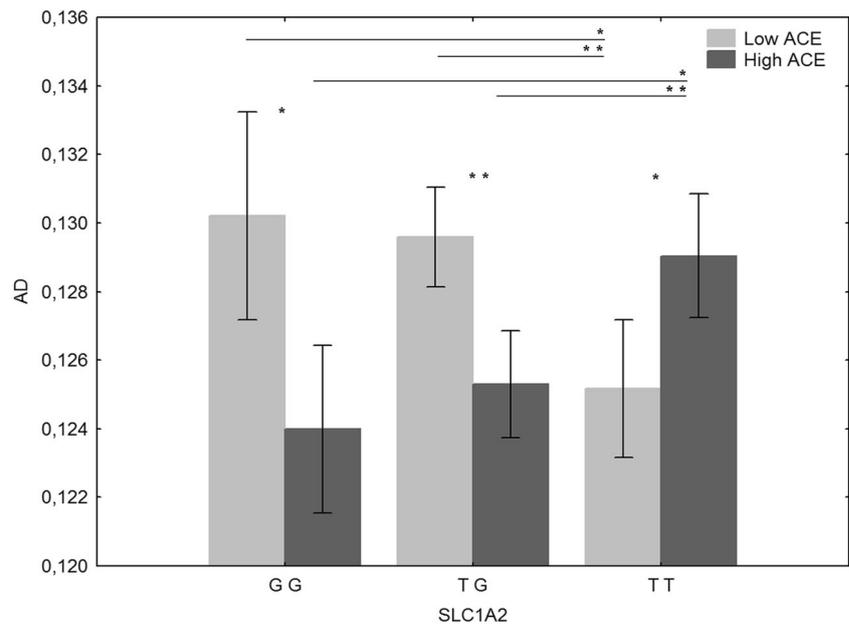
AD is associated with better functional connectivity among brain regions, and with network-related aspects of human brain function also including emotions [65], reasoning, and cognitive flexibility [66]. The WM tracts involved include fibers belonging to the neocortical association pairs and connecting the frontal lobes to more posterior regions of the brain. WM integrity of these tracts was consistently reported to be reduced in BD [14, 67–70].

In humans, ACEs have been shown to exert a detrimental effect on WM microstructure in BD [48], while animal models suggest a stress-induced increase in glutamate levels in the synaptic cleft [71]. Normally, higher levels of glutamate induce increased expression of glutamate transporters [72]. However, in animal models, helpless animals expressed significantly lower levels of EAAT2 in the hippocampus and cortex compared to littermates that did not exhibit helpless behavior [73]. Also, a reduced expression of the membrane transporters SLC1A2 was reported in major depression while a trend has been observed in bipolar subjects [40]. EAAT2 expression was also found to be reduced in oligodendrocytes following enhanced exposure to tumor necrosis factor (TNF) [74] and oxidative stress [75]. Elevated biomarkers of cell-mediated immune activation and inflammation, in the absence of active somatic immune diseases, have been consistently reported in BD [76] irrespective of mood state [77], and the inflammation-related cytokines TNF- $\alpha$ , IL-8, IFN- $\gamma$ , and IL-10 have been associated to reduced WM microstructure in BD [78] in the same tracts observed here.

All WM macroglial cells, including oligodendrocytes, express the EAAT2. This transporter contributes to maintaining basal levels of extracellular glutamate in the range of 1 to 2 mM and preventing over-activation of glutamate receptors under physiological conditions. Should the uptake of glutamate be inefficient, this could lead to an over-activation of AMPA and kainate receptors and causes oligodendrocyte death and myelin destruction [79]. Indeed, the direct inhibition of glutamate uptake in axonal tracts leads to oligodendroglial loss, massive demyelination, and severe axonal damage [80].

Following this line of reasoning, we could hypothesize that, in subjects exposed to high ACE, more efficient transporters are needed to face the reduced expression of glutamate

**Fig. 2** Post hoc *T* tests showing direction of the effects of EAAT2-181A > C genotype and ACE on axial diffusivity. \**p* < 0.005; \*\**p* < 0.001



transporters. This could explain why subjects with the less efficient G allele showed lower AD compared to T/T subjects. Similarly, we could hypothesize that after exposure to higher levels of ACE, carriers of the G allele are more vulnerable to stress and report the highest damage to brain volume as a consequence of an excess of free glutamate [1]. This is also in line with a reduced response to clozapine in G allele subjects [81]. Interestingly, G allele carriers showed also higher reward dependence [81], making them more vulnerable to high ACE. This effect could not be specific to ACE but extend to other kinds of insults such as stroke, which caused the highest damage in G/G [42]. However, the higher dependency of AD on the environment in rs4354668\*G carriers does not justify a deficit-oriented connotation of the rs4354668 variants, because the environment shapes the outcome of these fundamentally neutral common genetic factors: when facing low adversities, carriers of the rs4354668\*G allele have a higher AD in respect to T/T homozygotes. A similar effect has been described for the serotonin promoter polymorphism 5-HTTLPR, which impacts stress sensitivity, emotion regulation, and social cognition [82]: while 5-HTTLPR\*s carriers have a worse outcome of depression when exposed to ACE, with both emotional instability [83], and levels of neurotrophins [84] being proportional to the breadth of exposure to adverse events, the same \*s carriers show better outcomes when ACE levels are low [85]. It can then be surmised that common genetic variants could reveal opposite biological and behavioral effects in patients with psychiatric conditions depending on their interaction with the environment [86].

Several studies have highlighted the importance of ACE in psychiatric disorders. The present study, in agreement with the current literature, confirms that the exposure to ACE may influence the biological effect of the genetic pool. Recent

studies also suggest that early interventions may counteract the detrimental effects of ACE [87, 88]; therefore, considering the early family environment could be important for the development of personalized treatments. Indeed, patients exposed to ACE may benefit from treatments acting on brain structure like lithium salts which act on oligodendrocytes [89] and influence the lipid composition of myelin by inducing BDNF [90–92]. Accordingly, treatment with lithium salts was associated with higher AD in BD and was shown to counteract the effect of stress [49].

The major limitation of the study is the lack of information regarding previous psychopharmacological treatments, received by the patients. Recent studies showed that highly complex medication regimens are often required during naturalistic outpatient treatment of BD depression [93]. Further prospective studies will consider drug treatments and other factors (e.g., other genes, drugs, exposure to emotional and physical stressors) to assess the potential role of *SLA1A2* – 181A > C in bipolar illness. Other limitations also include issues such as generalizability, possible undetected past comorbidities, population stratification, lack of complete coverage of gene variability, and absence of placebo control. Moreover, genome-wide association studies and gene–gene and other gene–environment interactions were not taken into account.

In conclusion, we demonstrated an association between glutamate transporter polymorphism and early stress in influencing WM integrity in BD. Carriers of the rs4354668\*G allele, which is associated with less transporter expression and a 30% reduction in promoter activity compared with the T allele, showed lower AD than T/T homozygote when exposed to higher ACE, while the opposite effect was observed in the low ACE group. A reduced efficiency in

the uptake of glutamate in subjects with a reduced number of transporters could cause a higher vulnerability to neurotoxic processes. Further studies, however, are needed to better understand the possible role of genetic polymorphisms regulating glutamate transporter activity in the maintenance of WM integrity and the moderator role of ACE.

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## Compliance with Ethical Standards

The work described has been carried out in accordance with The Code of Ethics of the World Medical Association (Declaration of Helsinki). After complete description of the study to the subjects, a written informed consent was obtained. The local ethical committee approved all the research activities.

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