

**Neonatal pain and *COMT* Val158Met genotype in relation to serotonin transporter
(*SLC6A4*) promoter methylation in very preterm children at school age**

by

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Abstract

Children born very preterm are exposed to repeated neonatal procedures that induce pain and stress during hospitalization in the neonatal intensive care unit (NICU). The COMT Val158Met genotype is involved with pain sensitivity, and early life stress is implicated in altered expression of methylation of the serotonin transporter. We examined: (1) whether methylation of the serotonin transporter gene (SLC6A4) promoter differs between very preterm children and full-term controls at school age, (2) relationships with child behavior problems, and (3) whether the extent of neonatal pain exposure interacts with the COMT Val158Met genotype to predict SLC6A4 methylation at 7 years in the very preterm children. We examined the associations between the COMT genotypes, neonatal pain exposure (adjusted for neonatal clinical confounders), SLC6A4 methylation and behavior problems. Very preterm children had significantly higher methylation at 7/10 CpG sites in the SLC6A4 promoter compared to full-term controls at 7 years. Neonatal pain (adjusted for clinical confounders) was significantly associated with total child behaviour problems on the Child Behavior Checklist (CBCL) questionnaire (adjusted for concurrent stressors and 5HTTLPR genotype, $p = 0.035$). CBCL Total Problems was significantly associated with greater SLC6A4 methylation in very preterm children ($p = 0.01$). Neonatal pain (adjusted for clinical confounders) and COMT Met/Met genotype were associated with SLC6A4 promoter methylation in very preterm children ($p = 0.001$). These findings provide evidence that both genetic predisposition and early environment need to be considered in understanding susceptibility for developing behavioral problems in this vulnerable population.

Preface

A version of the thesis has been published. **Chau CMY**, Ranger M, Sulistyoningrun D, Devlin AM, Oberlander TF, Grunau RE (2014) Neonatal pain and COMT Val158Met genotype in relation to serotonin transporter (SLC6A4) promoter methylation in very preterm children at school age. *Frontiers Behavioral Neurosci.* Dec 2; 8: 409. doi: 10.3389/fnbeh.2014.00409. eCollection 2014. The research presented in this thesis is from work conducted in BC Children's & Women's Hospitals and the Child & Family Research Institute, led by principal investigator Dr. Ruth E. Grunau. I carried out data collection, conducted the genotyping, performed the statistical analysis, and wrote the first draft of the manuscript.

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Dedication

This thesis is dedicated to my family and especially my wife Winnie and my daughter Kathryn, for their caring and their unreserved love, and all the support during my study.

I would also like to dedicate this thesis to the friendship and memory of Harry Wong (1971 – 2010), my best friend who struggled with depression for many years. I hope my research can further the understanding of the mechanism of mood disorders.

1 Introduction

Infants born very preterm (24-32 weeks gestational age [GA]) spend weeks to months in the neonatal intensive care unit (NICU) during a delicate and critical phase of very rapid brain development, and programming of stress systems (Grunau et al., 2007). In the NICU, these infants require numerous invasive medical procedures to diagnose, treat and monitor life-threatening conditions. This environment contrasts greatly from the calm and protective maternal intrauterine environment, thus exposing these fragile neonates to repeated highly stressful and potentially painful experiences that are developmentally unexpected. Since stress and pain cannot be distinguished in immature neonates, we have used the term “pain/stress”. Despite major improvement in the care of very preterm infants, rates of neurodevelopmental problems in children born very preterm do not appear to have improved, affecting about 50% of survivors (Aarnoudse-Moens, Weisglas-Kuperus, van Goudoever, & Oosterlaan, 2009; Gray, Indurkha, & McCormick, 2004). There are concerns regarding long-term consequences of pain/stress in very preterm neonates. Recent work from our group found that procedural pain/stress exposure (controlling for clinical factors related to prematurity, such as gestational age, postnatal infection, cumulative morphine dose, days of mechanical ventilation, illness severity on day 1, and number of surgeries) was associated with altered grey and white matter maturation (Brummelte et al., 2012; Ranger et al., 2013; Vinall et al., 2013), corticospinal tract development (Zwicker, Yoon et al., 2013; Zwicker, Grunau et al., 2013), poorer motor (Zwicker et al., 2013), cognitive (Doesburg et al., 2013; Grunau et al., 2009), and behavioral functioning (Ranger, Synnes, Vinall, & Grunau, 2014; Vinall,

Miller, Synnes, & Grunau, 2013) in very preterm children. Moreover, greater cumulative exposure to neonatal pain/stress has been associated with altered developmental trajectory of stress hormone (cortisol) expression (i.e. programming of the hypothalamic-pituitary-adrenal axis [HPA]) long after NICU discharge (Grunau et al., 2007; Grunau et al., 2013; Miller, Chen, & Parker, 2011). However, given similar exposure to neonatal pain/stress, not all children born very preterm will have neurodevelopmental problems. Therefore, genetic predisposition and interactions with the environment may play an important role in understanding the variation in neurodevelopmental outcomes in children born very preterm.

Gene-environment interactions during a critical neonatal period of rapid brain development play an important role in cognition and behavior formation, and may contribute to the individual differences of biobehavioral and cognitive outcomes in very preterm children. Early life adversity and stress exposure are associated with alterations in DNA methylation and changes in gene expression (Bagot et al., 2012; McGowan et al., 2009; Meaney, 2010). DNA methylation is a critical epigenetic mechanism regulating gene expression and has been suggested as a possible molecular mechanism explaining the diversity in behavioral outcomes that follow exposure to early life stressful events (Caspi et al., 2003; McGowan et al., 2009; Rutter, Moffitt, & Caspi, 2006). Given the repeated exposure to neonatal pain/stress in very preterm children, DNA methylation offers a promising direction that may enable us to better understand how exposure to adverse/stressful early life events may lead to enduring changes in neuronal function (Karsten & Baram, 2013). Furthermore, associations between neonatal clinical factors and the functional polymorphisms in genes involved in brain signal transmission and

neurogenesis may allow us to understand the mechanisms underlying gene-environment interactions and the potential impact on cognitive and behavioral development.

We have taken a hypothesis-based targeted gene approach. It is well established that behavioral problems such as attention deficit problems, internalizing (depressive/anxiety symptoms), and to some extent externalizing (aggressive, hyperactivity symptoms) behaviors are prevalent in children born very preterm (Aarnoudse-Moens et al., 2009; Bhutta, Cleves, Casey, Craddock, & Anand, 2002; Gray et al., 2004). Serotonin and dopamine are two key stress and mood regulatory neurotransmitters and related regulatory genes have been identified. Serotonin (5-hydroxytryptamine, 5HT) is a neurotransmitter widely distributed in the central nervous system. Its synthesis starts early in gestation and plays a key role in early brain development and later emotion, attention, cognition, and learning during childhood (Lesch, 2007; Lucki, 1998; Weikum et al., 2013). Central to the regulation of intrasynaptic serotonin concentrations is the presynaptic membrane-bound serotonin transporter protein (5HTT, encoded by *SLC6A4*). Variants in the serotonin transporter promoter region (*5HTTLPR*), are associated with altered gene expression and 5HTT concentrations, and therefore have a critical role in determining intrasynaptic serotonin signaling (Hanley & Oberlander, 2012). The short (S) allele of *5HTTLPR* results in approximately 50% reduction in serotonin reuptake compared to the long (L) allele (Heils et al., 1996). S allele carriers may have greater vulnerability for emotional disorders (Homberg & Lesch, 2011), particularly in the context of early life stress (Caspi et al., 2003) [recent reviews (Kuzelova, Ptacek, & Macek, 2010; Serretti, Kato, De Ronchi, & Kinoshita, 2007)]. Manipulations of 5HT signaling, either via pharmacologic 5HTT

blockade or *SLC6A4* knock-out in mouse models, that increase serotonin concentrations during developmentally sensitive periods and are associated with lasting behavioral, neurophysiological, and neuroanatomical changes in animal models (Homberg, Schubert, & Gaspar, 2010; Olivier, Blom, Arentsen, & Homberg, 2011; Simpson et al., 2011) and increased risk for anxiety/depression symptoms in humans (Oberlander et al., 2010; Weikum et al., 2013). Recently, methylation of the *SLC6A4* promoter was shown to be associated with early childhood adversity in adults with major depression (Kang et al., 2013). Therefore, examining the impact of early life stress on changes in the methylation of the *SLC6A4* promoter in very preterm children may increase our understanding of how early changes in serotonin signaling might be associated with altered neurodevelopmental outcomes previously reported in this population.

The catechol-*O*-transferase (*COMT*) gene encodes for a key enzyme in the metabolism of dopamine (DA), norepinephrine (NE), and epinephrine (EPI) (Lotta et al., 1995). The Met/Met genotype of the *COMT* Val158Met variant is associated with more than a three to four fold decrease in COMT enzyme activity and DA catabolism, which leads to an increase in DA availability and reduced myelination (Chen et al., 2004; Lotta et al., 1995). This is especially significant in the prefrontal cortex (PFC) where COMT activity is the primary determinant of synaptic DA concentrations (Garris & Wightman, 1994; Karoum, Chrapusta, & Egan, 1994). *COMT* variants have been associated with cognitive functions (Blasi et al., 2005; Dumontheil et al., 2011); and mood disorders (Aberg, Fandino-Losada, Sjöholm, Forsell, & Lavebratt, 2011; Enoch, Xu, Ferro, Harris, & Goldman, 2003; Olsson et al., 2007). For example, individuals with the Met allele are at increased risk for anxiety (Enoch et al., 2003; Olsson et al., 2007).

Moreover, Zubieta and colleagues reported effects of the *COMT* Val158Met genotype on μ -opioid system activation in young adults, where individuals with the Met/Met genotype had greater pain sensitivity and negative emotions to pain compared to individuals with the Met/Val and Val/Val genotypes (Zubieta et al., 2003). Further, the Val allele has been associated with increased risk of schizophrenia in both European and Asian populations (Fan et al., 2005), and decreased cognitive stability (Bialecka et al., 2008). *COMT* and *5HTT* have important functional roles in regulating neurotransmission with mood and behavior brain-related pathways, and given that both have functional genetic variants, researchers have begun to investigate their potential interaction in various pathologies (Olsson et al., 2007; Radua et al., 2013),

Since both dopaminergic and serotonergic systems play a critical role in mood regulation, there has been a considerable amount of interest in their potential interactions. In rodents, exposure of the striatum and nucleus accumbens to serotonin increased dopamine release (review by (Sasaki-Adams & Kelley, 2001). Dopamine and serotonin systems also showed a significant degree of convergence and plasticity in the rat medial prefrontal cortex (Benes, Taylor, & Cunningham, 2000).

To unveil gene-environment interactions that may contribute to susceptibility and resilience to early adverse environmental effects, and the associations with later behavioral outcomes, the aim of this thesis is to examine the relationships between *SLC6A4* methylation and neonatal pain/stress exposure, and whether these are moderated by the gene polymorphisms of *SLC6A4* and *COMT*. We hypothesized that methylation at school age would be altered in those born very preterm due to the pain/stress neonatal environment. We further explored whether child behavior problems, concurrent child

stress level, and parental factors were associated with differences in methylation. To investigate the effects of neonatal pain/stress on child behavior problems and *SLC6A4* methylation, in the very preterm group only, we examined whether neonatal procedural pain/stress exposure (adjusted for clinical confounders) and/or concurrent stressors are associated with child behavioral problems at age 7 years. Finally, in very preterm group only, we examined the effect of neonatal procedural pain/stress exposure (adjusted for clinical confounders) and *COMT* Val158Met genotype on *SLC6A4* methylation at 7 years. Given that *COMT* Val158Met genotype has been reported to be associated with pain sensitivity, we hypothesized that the extent of early pain/stress exposure would interact with the *COMT* Val158Met genotype to affect *SLC6A4* methylation.

2 Methods

2.1 Participants

Participants were part of a larger longitudinal study of long-term effects of neonatal pain/stress on brain, stress and neurodevelopment of children born very preterm (24-32 weeks gestation) [e.g. (Grunau et al., 2007; Grunau et al., 2009)], who were admitted to the level III NICU at Children's & Women's Health Centre of British Columbia between 2000 and 2004. A total of 111 school age children, 61 born very preterm and 50 born full-terms were included in the current study (56 boys/55 girls; mean age 7.78 y [± 0.65] range 6.3 - 10.8 years). Parents completed questionnaires while children were undergoing psychometric testing.

All of the children had an IQ score above 70 on the Wechsler Intelligence Scale for Children – 4th Ed. (Wechsler, 2003). None had major cognitive, sensory, motor impairments, or was diagnosed with autism. We included in our sample three very preterm children with intraventricular hemorrhage (IVH) grade 1 or 2, and two grade 3 or 4, on neonatal ultrasound. This study was approved by the Clinical Research Ethics Board of the University of British Columbia and the Research Ethics Board of the B.C. Children's & Women's Hospitals, and conforms to the conventions set out in the Declaration of Helsinki. Written informed consent was obtained from parents and assent from children.

2.2 Neonatal Data

Medical and nursing chart review of children born very preterm was carried out by an experienced neonatal research nurse. The data collection included but was not limited to, GA, birth weight, illness severity on day 1 (Score for Neonatal Acute Physiology [SNAP]- II (Richardson, Corcoran, Escobar, & Lee, 2001), days of mechanical ventilation, presence of culture proven infection, number of surgeries, and cumulative dose of morphine (Table 2). We quantified neonatal pain/stress as the number of skin-breaking procedures (e.g., heel lance, peripheral intravenous or central line insertion, chest-tube insertion, and nasogastric tube insertion) during the stay in the NICU, as previously reported [e.g. (Brummelte et al., 2012; Grunau et al., 2009)]. Each attempt at a procedure was counted as one skin-break; all nursing staff in our NICU have been trained to precisely record each attempt. Cumulative morphine exposure was calculated as the average daily dose (i.e. intravenous dose plus intravenous-equivalent oral dose) adjusted for daily body weight, multiplied by the number of days morphine was administered.

2.3 Assessments

Children completed the Wechsler Intelligence Scale for Children – Fourth Edition (WISC-IV) (Wechsler, 2003). A parent (110 mothers, 1 father) completed the following questionnaires:

- Child Behavior Checklist (CBCL) for children ages 6 to 18 years (Achenbach & Rescorla, 2000), the most widely used questionnaire for identifying problem behaviors in children. Ratings are on a 3-point Likert scale [ranging from 0 (not true) to 2 (very true or often true)] on 113 items regarding child behavior in the past 6 months. The checklist is

comprised of eight syndrome scales (Anxious/Depressed, Withdrawn/Depressed, Social Problems, Somatic Complaints, Thought Problems, Attention Problems, Aggressive Behavior, and Rule-Breaking Behavior) and two higher order-factors of Internalizing and Externalizing Problems. Raw scores were converted to age-standardized scores (T scores with mean = 50 and SD = 10) based on the normative samples of children for age range separately by sex (Achenbach & Rescorla, 2000). The Total Problem T-score was used as an indicator of overall emotional and behavioural problems of the child, and yields an alpha coefficient of 0.97 (Achenbach & Rescorla, 2000).

- Beck Depression Inventory – 2nd Edition (BDI-II) (Beck, Ward, Mendelson, Mock, & Erbaugh, 1961) a 21-item self-report multiple-choice questionnaire widely used to assess the presence and severity of symptoms of depression, was used to evaluate parent depression. The scale yields a single score that ranges from 0 to 63, with higher scores indicating higher level of depression; reliability alpha coefficient 0.92 (Gatewood-Colwell, Kaczmarek, & Ames, 1989).

- State-Trait Anxiety Inventory (Spielberger, C.D., Gorsuch, R.L., Lushene, R., Vagg, P.R., Jacobs, G.A., 1983) comprised of two separate 20-statement self-report scales: the State-Anxiety scale to evaluate how respondents feel “right now, at this moment” and the Trait-Anxiety scale how respondents generally feel. Only the Trait Anxiety Scale was used in the present study as an indicator of parent general anxiety symptoms. Scores range from 20 to 80; reliability alpha coefficient 0.86 (Spielberger, C.D., Gorsuch, R.L., Lushene, R., Vagg, P.R., Jacobs, G.A., 1983).

2.4 Hair Cortisol

Cortisol was assayed from hair as an integrated measure of stress level (HPA activity) in the previous two months. Hair samples were collected from the vertex posterior of the head, as this area has been shown to have the lowest coefficient of variation in hair cortisol concentrations (Sauve, Koren, Walsh, Tokmakejian, & Van Uum, 2007). A cluster of hair strands (~2-3mm diameter) was cut at the base of the hair shaft from five small spots. The hair samples were secured on a cardboard card with tape, labeled, and stored in individual sealed plastic bags at room temperature until analysis. The most proximal 2 cm from the scalp of each hair sample was utilized for the assay. Ten to 15 mg from each hair sample was placed in scintillation vials. To remove external contaminants, hair samples were washed twice by immersion in 3 mL of isopropanol and incubated at room temperature in a centrifuge at 100 RPM for 3 minutes. After decanting the isopropanol, samples were allowed to dry for at least 12 hours. After drying, 1 mL of methanol was added to each scintillation vial. Hair was then finely minced with surgical scissors. The vials were sealed with paraffin film and incubated for 16 hours at 50°C in a centrifuge at 100 RPM. Following methanol extraction each cortisol-containing methanol solution was transferred into 5 mL test tubes and evaporated on a test tube hot plate under a steady stream of nitrogen gas. The residue was then reconstituted with 250 µL of phosphate buffered saline. These reconstituted samples were analyzed using the salivary enzyme linked immunoassay kit (Alpco Diagnostics, Salem, NH, USA). The intra-assay and inter-day coefficients of variation were 8.9% and 5.1%, respectively. The kit reported a sensitivity of 1.0 ng/mL.

2.5 Genotyping

Genomic DNA was extracted from saliva using Oragene OG-500 and prepIT-L2P collection kit (DNA Genotek/OraSure Technologies Inc., Bethlehem, Pennsylvania). The *COMT* Val158Met (rs4680) variant was genotyped using TaqMan SNP Genotyping Assay reagents and an Applied Biosystems 7300 Real Time PCR System (Applied Biosystems, Carlsbad, California). Call rate was 100%. The Hardy-Weinberg equilibrium of allelic distribution of the cohort was examined and compared to the population distribution by chi-square test.

The L and S alleles of the *5HTTLPR* serotonin transporter variant (rs25531) was genotyped by polymerase chain reaction (PCR) with the following primers stpr5, 5'-GGCGTTGCCGCTCTGAATGC and stpr3, 5'-GAGGGACTGAGCTGGACAACCAC to generate a 484-bp (S short allele) or a 528-bp (L long allele) product, distinguished by agarose gel electrophoresis.

2.6 Epigenetic Analysis

Using the DNA from saliva, the methylation status of a CpG-rich region in the *SLC6A4* promoter was quantified by bisulfite Pyrosequencing (Dupont, Tost, Jammes, & Gut, 2004) as previously described (Devlin, Brain, Austin, & Oberlander, 2010). This region of the *SLC6A4* promoter has been reported to be differentially methylated and associated with changes in *SLC6A4* mRNA expression (Devlin et al., 2010; R. Philibert et al., 2007; R. A. Philibert et al., 2008). Briefly, we have analyzed a region of the *SLC6A4* promoter between -479 and -350, relative to the transcriptional start site, which contains 10 CpG sites and is adjacent to exon 1a (Devlin et al., 2010). Genomic DNA was bisulfite-treated

using the EZ DNA Methylation Gold Kit (Zymo Research) following the manufacturer's instructions and stored at -20°C until further analyzed. A 130 bp fragment of the *SLC6A4* promoter was amplified by PCR from bisulfite-treated DNA using HotStar Taq DNA Polymerase (Qiagen) and the following primers for *SLC6A4*: PMHSERTF, 5'-GTATTGTTAGGTTTTAGGAAGAAA GAGAGA-3' and PMHSERTR, 5'-AAAATCCTAACTTTCCTACTCT TTA ACTT-3' (IDT Inc, Coralville, IA), with the reverse primer containing a biotin at the 5' end. PCR products were purified and sequenced using a PyroMark MD System (Biotage, Foxboro, MA) following the manufacturer's suggested protocol and the following sequencing primer PMHSERTS, 5'-AAACTACACAAAAAACAAT-3' (IDT). The percent methylation at each CpG site was quantified using the Pyro Q-CpG software, version 1.0.9 (Biotage).

2.7 Statistical Analysis

T-tests were used to compare child characteristics between very preterm and full-term groups. The number of skin-breaking procedures was log-transformed and shown to be normally distributed by the Komogorov-Smirnov Normality Test. Percent Methylation of the 10 *SLC6A4* CpG sites were arcsine transformed to address the issue of heteroscedasticity (Laird, 2010; Lin, Du, Huber, & Kibbe, 2008). Principle component analysis (PCA) was used to reduce the data in contrast to using the mean methylation of selected CpG sites because of significant variances. This has been used by others to examine *SLC6A4* promoter methylation; the first PCA factor has the largest possible variance and was extracted to represent the overall methylation (Beach, Brody, Todorov, Gunter, & Philibert, 2010). To examine the relationship between *COMT* Val158Met

genotypes and cumulative neonatal pain/stress (adjusted for clinical confounders), generalized linear modeling (GLM) was used. GLM provides an extension of general linear models and relaxes the requirement of equality or constancy of variances that is required in traditional linear models. Statistical analyses were performed using the Statistical Package for Social Sciences (SPSS) version 22 (IBM, Somers, NY); p -values < 0.05 were considered statistically significant.

3 Results

3.1 Participant Characteristics

Child and parent characteristics of 111 school age children (61 born very preterm; 50 born full-term) are summarized in Table 1a. Parents of very preterm children had significantly higher self-reported depression on the Beck Depression Inventory, compared to parents of full-term children ($p = 0.02$). Children born very preterm (in this sample that excluded children with low IQ and sensory-motor impairments) showed a trend towards higher total behavior problems on the Child Behavior Check List (CBCL) completed by parents, compared to full-terms ($p = 0.06$). Neonatal characteristics of the very preterm children are shown in Table 1b. Genotype frequencies of *COMT* Val158Met (Val/Val, Val/Met, and Met/Met) and the *5HTTLPR* variant (L/L, L/S or S/S) are shown in Table 1c. Due to the low frequencies of the S allele for *5HTTLPR*, subjects with homozygous S alleles (S/S) and the L/S genotype were grouped together in all analyses. There were no significant differences in genotype frequency between very preterm and full-term children, and the distribution of *5HTTLPR* and *COMT* Val158Met genotypes had no significant discrepancy from the Hardy-Weinberg equilibrium ($p = 0.21$ and $p = 0.36$ respectively).

Table 1a. Child and parent characteristics

	Very Preterm (<i>N</i> =61) mean (SD)	Full-term (<i>N</i> =50) mean (SD)	<i>p</i>-value
Child age (years)	7.7 (0.3)	7.9 (0.9)	0.090
Child hair cortisol (ng/ml)	2.33 (0.35)	2.38 (0.33)	0.468
Child CBCL Total Problems T score	51.3 (10.4)	47.5 (10.0)	0.055
Child CBCL Internalizing Behavior T score	51.3 (10.3)	50.3 (10.7)	0.616
Child CBCL Externalizing Behavior T score	48.7 (9.6)	47.9 (10.3)	0.694
Parent BDI-II	6.9 (8.0)	4.0 (4.6)	0.020
Parent STAI Trait anxiety	35.4 (9.7)	34.2 (8.3)	0.471

SD, standard deviation; CBCL, Child Behavior Check List; BDI-II, Beck Depression Inventory 2nd edition; STAI, State Trait Anxiety Inventory.

Table 1b. Neonatal characteristics of children born very preterm

<i>N</i> = 61	Mean (SD)	Range
Male (number, %)	36 (59)	
Gestational age at birth (weeks)	28.2 (2.1)	25.0 – 32.9
Birth weight (g)	1134 (390)	520 – 2265
Skin-breaks	142 (89)	30 – 446
Cumulative morphine dose (mg)	2.27 (4.8)	0 – 22.9
Days of mechanical ventilation	16 (17)	1 – 58
Illness severity day I (SNAP-II)	15.7 (11.6)	0 – 45
Number of surgeries	0.5 (0.8)	0 – 3
Postnatal infection (number, %)	27 (44)	

SD, standard deviation; SNAP-II, score for neonatal acute physiology (severity of illness index)
Skin-breaks (i.e. neonatal pain/stress) is equal to the number of skin-breaking procedures from birth to term equivalent age or hospital discharge; cumulative morphine dose is equal to daily morphine exposure adjusted for daily weight; postnatal infection is counted as the presence of a culture proven infection.

Table 1c. Allelic distribution of *COMT* and *SERT* genotypes

	Genotype	Preterm	Full-term	Chi-square <i>p</i> -value ¹	Hardy-Weinberg Equilibrium <i>p</i> -value ²
<i>SERT</i> 5HTTLPR	LL	19	10	0.17	0.21
	LS +SS	41	40		
<i>COMT</i> rs4680 (C_25746809_50)	GG Val/Val	20	13	0.78	0.36
	AG Val/Met	30	26		
	AA Met/Met	10	9		

¹ *p*-values from Pearson Chi-Square tests between preterm and full-term children.

² *p*-values from Hardy-Weinberg Equilibrium between allelic distributions

L, Long allelic variant of *SLC6A4* promotor; S, Short allelic; *SERT*, serotonin promoter gene; *COMT*, Catechol-*O*-methyltransferase

3.2 *SLC6A4* methylation in very preterm and full-term children

A region of the *SLC6A4* promoter between -479 and -350, relative to the transcriptional start site, which contains 10 CpG sites and is adjacent to exon 1a was analyzed (Devlin et al., 2010). The region of *SLC6A4* analyzed was within the same CG-rich region shown to be differentially methylated and associated with changes in *SLC6A4* mRNA expression (R. Philibert et al., 2007; R. A. Philibert et al., 2008), and was shown to be associated with depressed mood (Devlin et al., 2010; R. A. Philibert et al., 2008). T-tests with Bonferroni correction for multiple comparisons were used to compare the transformed methylation in the 10 *SLC6A4* CpG sites (CpG 1 – 10) between the very preterm and full-term groups. Seven out of the 10 *SLC6A4* CpG sites had significantly higher methylation (CpG 1, 3, 4, 5, 8, 9, 10) and CpG 2 had lower methylation in very preterm children compared to full-term children (Table 2a). CpG 1, 2, 3, 4, 5 remained significant after correction for multiple comparisons. Overall, at age 7 years, children born very preterm had higher *SLC6A4* methylation compared to children born full-term. A graphical representation of the results was shown in figure 1.

Table 2. *SLC6A4* percent methylation in preterm and full-term children

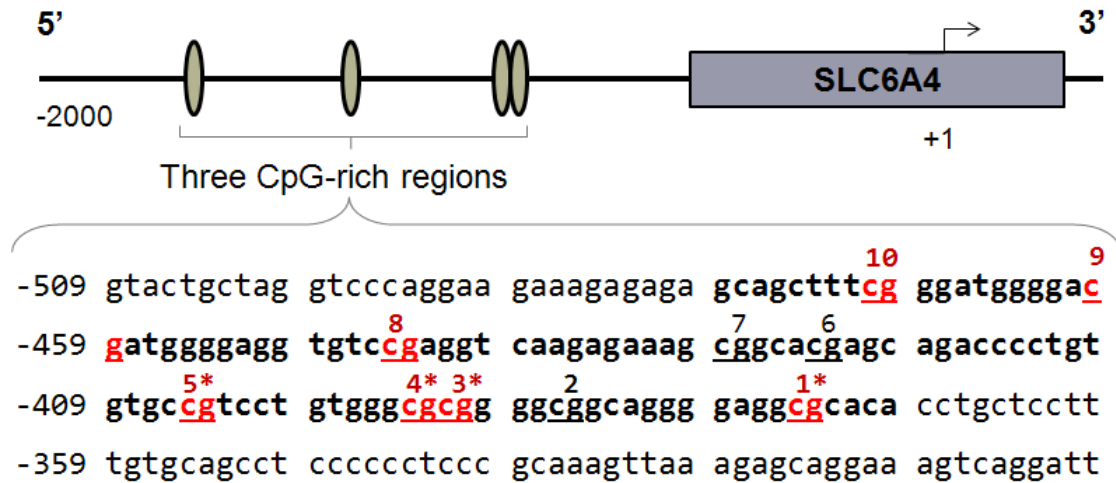
<i>SLC6A4</i> CpG sites	Preterm (<i>N</i> =61) mean (SD*)	Full-term (<i>N</i> =50) mean (SD)	<i>p</i> -value**
CpG 1	3.79 (0.92)	3.15 (0.72)	< 0.0001 †
CpG 2	1.60 (0.66)	2.00 (0.44)	< 0.0001 †
CpG 3	4.96 (1.06)	4.17 (0.74)	< 0.0001 †
CpG 4	1.79 (0.60)	1.32 (0.52)	0.001 †
CpG 5	4.06 (0.87)	2.69 (0.69)	< 0.0001 †
CpG 6	1.49 (0.60)	1.62 (0.43)	0.142
CpG 7	2.87 (0.75)	2.93 (0.70)	0.777
CpG 8	3.48 (0.88)	3.09 (0.65)	0.009
CpG 9	3.52 (0.81)	3.11 (0.73)	0.008
CpG 10	6.08 (1.43)	5.42 (1.23)	0.017

*SD, standard deviation of % methylation.

** *p*-values of t-tests of the arcsine transformed *SLC6A4* methylation ($\sin^{-1}((\% \text{ methylation} / 100)^{1/2})$) between the preterm and full-term groups.

† significant after controlled for multiple comparisons by Bonferroni correction.

Figure 1. Different methylation pattern in *SLC6A4* promoter region between children born very preterm and full-term.



Underlined: 10 CpG sites in the *SLC6A4* promoter region

* $p < .05$ after Bonferroni correction

3.3 Principle component analysis of *SLC6A4* methylation

Principle component analysis (PCA) was used for data reduction. Three principle components had an eigenvalue > 1 , and together they accounted for 57% of the total variance in *SLC6A4* methylation. Principle Component 1 (PC1) (eigenvalue = 3.2) explained 32% of variance, while PC2 (eigenvalue = 1.4) and PC3 (eigenvalue = 1.1) explained 15% and 10 % respectively. Loadings of the CpG sites on the three components are shown in Table 3. Given that PC1 was the most prominent factor in the PCA, we limited our analyses to this component representing the most significant aspect of methylation in *SLC6A4* CpG 1 – 10 in the present study.

Table 3. PCA component loadings of 10 CpG sites

<i>SLC6A4</i> CpG sites	Component 1	Component 2	Component 3
CpG 1	0.653	-0.120	0.018
CpG 2	-0.107	0.746	0.247
CpG 3	0.591	-0.029	0.404
CpG 4	0.541	-0.466	0.217
CpG 5	0.763	-0.408	0.031
CpG 6	0.031	0.225	0.801
CpG 7	0.527	0.453	-0.185
CpG 8	0.624	0.142	-0.018
CpG 9	0.748	0.269	-0.174
CpG 10	0.546	0.372	-0.278

PCA, principal component analysis

Component 1 (eigenvalue = 3.2) explained 32% of variance

Component 2 (eigenvalue = 1.4) explained 14% of variance

Component 3 (eigenvalue = 1.1) explained 11% of variance

3.4 *SLC6A4* methylation and child behavior problems

To investigate factors contributing to the altered *SLC6A4* methylation in very preterm children, GZLM analyses were then performed separately in very preterm and full-term children to determine the relationship with *SLC6A4* methylation. The CBCL Total Problem T score, concurrent parental depressive symptoms (BDI II) and trait anxiety (STAI), hair cortisol concentration as an index of cumulative stress level and perceived stress of the child, and *5HTTLPR* genotype (LL, LS and SS) were entered simultaneously as covariates to determine the effect on *SLC6A4* methylation (component 1 in PCA). *5HTTLPR* genotype was included as a covariate because it may contribute to *SLC6A4* methylation differences (Beach, Dogan, Brody, & Philibert, 2013). In very preterm children only (but not full-terms), higher CBCL total behavior problems score was significantly related to greater *SLC6A4* methylation ($r^2 = 0.13$; $p = 0.01$) after adjusting for the other concurrent factors. Results of the GZLM for the very preterm children were summarized in table 4a and results for full-term children were summarized in 4b. Only the model of very preterm children had a significant omnibus test ($p = 0.035$). As *COMT* Val158Met genotype may be associated with emotion and behavior regulation in children (Albaugh et al., 2010; Sheikh et al., 2013), it was included in a separate model; *COMT* genotype had no significant relationship with methylation ($p = 0.518$). Also, alternative models were built separately to examine whether CBCL externalizing and internalizing T scores were associated with *SLC6A4* methylation. Before adjusting for multiple comparisons externalizing ($p = 0.035$) and internalizing ($p = 0.077$) were marginally

significant, however neither was significant after adjusting for multiple comparisons of externalizing and internalizing scores.

Table 4a. Generalized linear modeling analysis to predict *SLC6A4* methylation in very preterm children

Parameter	B ^a	Std. Error	95% Confidence Interval		p-value
			Lower	Upper	
CBCL Total Problems T-score	0.042	0.0161	0.010	0.074	0.010
Child Hair Cortisol Level	0.024	0.4018	-0.764	0.811	0.953
Parent BDI-II	-0.037	0.0293	-0.094	0.020	0.207
Parent STAI Trait Anxiety Score	0.023	0.0216	-0.020	0.065	0.295
Child <i>5HTTLPR</i> LL	0.577	0.3048	-0.020	1.175	0.058

Omnibus test: $p = \mathbf{0.035}$

GZLM results showing CBCL Total Problem T-score (adjusted for concurrent stressors, hair cortisol, and *5HTTLPR* genotype) associated with *SLC6A4* methylation in children born very preterm

Model: *SLC6A4* methylation = CBCL Total Problem T-score + Child hair cortisol + BDI-II + STAI anxiety + *5HTTLPR* genotypes

^a Unstandardized regression coefficient

CBCL, Child Behavior Check List; BDI-II, Beck Depression Inventory 2nd edition; STAI, State Trait Anxiety Inventory; L, Long allelic variant of *SLC6A4* promoter; S, Short allelic.

Table 4b. Generalized linear modeling analysis to predict *SLC6A4* methylation in full-term children

Parameter	B ^a	Std. Error	95% Confidence Interval		p-value
			Lower	Upper	
CBCL Total Problems T-score	0.040	0.0190	0.003	0.077	0.036
Child Hair Cortisol Level	0.316	0.4928	-0.649	1.282	0.521
Parent BDI-II	0.027	0.0444	-0.060	0.113	0.550
Parent STAI Trait Anxiety Score	-0.023	0.0272	-0.076	0.031	0.406
Child <i>5HTTLPR</i> LL	0.377	0.3951	-0.398	1.151	0.340

Omnibus test: $p = .314$

GZLM results showing CBCL Total Problems T-score (adjusted for concurrent stressors, hair cortisol, and *5HTTLPR* genotype) associated with *SLC6A4* methylation in children born very preterm

Model: *SLC6A4* methylation = CBCL Total Problems T-score + Child hair cortisol + BDI-II + STAI anxiety + *5HTTLPR* genotypes

^a Unstandardized regression coefficient

CBCL, Child Behavior Check List; BDI-II, Beck Depression Inventory 2nd edition; STAI, State Trait Anxiety Inventory; L, Long allelic variant of *SLC6A4* promotor; S, Short allelic.

3.5 Neonatal pain/stress and child behavior problems

To further advance our understanding of neonatal pain/stress in relation to child behavior problems at 7 years, GZLM was used to investigate the association between number of skin-breaks and CBCL Total Problem T score. Predictors were neonatal pain/stress (cumulative skin breaking procedures from birth to term equivalent age) adjusted for clinical confounders related to prematurity (GA at birth, number of days on mechanical ventilation, illness severity on day 1 [SNAP-II], number of surgeries, presence of culture proven infection, cumulative dose of morphine), and concurrent parental depressive symptoms (BDI II) and trait anxiety (STAI), and child stress level (hair cortisol) as covariates. Greater neonatal pain/stress (after adjustment for all covariates) was associated with higher total child behavior problem score on the Child Behavior Checklist (CBCL) ($p = 0.035$, $r^2 = 0.39$). *5HTTLPR* variants were then added in a subsequent model and were not significant ($p = 0.866$). GZLM results are summarized in Table 5.

Table 5. Generalized linear modelling analysis of CBCL Total Problems T scores predicted by neonatal pain/stress

Parameter	B ^a	Std. Error	95% Confidence Interval		p-value
			Lower	Upper	
Skin-breaks	17.99	8.54	1.25	34.73	0.035
Neonatal infection	3.80	2.89	-1.86	9.47	0.188
Cumulative morphine dose	8.88	6.41	-3.68	21.44	0.166
Days of ventilation	-0.04	0.16	-0.35	0.27	0.779
SNAP-II day 1	0.14	0.12	-0.11	0.38	0.279
Number of surgery	-2.24	1.93	-6.03	1.55	0.246
Gestational age (GA)	2.93	.88	1.21	4.65	0.001
Child Hair Cortisol Level	2.18	3.36	-4.40	8.76	0.516
Parent BDI-II	0.56	0.25	0.07	1.06	0.025
Parent STAI Trait Anxiety Score	-0.01	0.18	-0.37	0.35	0.959

GZLM results showing CBCL Total Problems T scores was predicted by neonatal pain/stress
Model: CBCL Total Problems T scores = skin-breaks + Infection + morphine exposure + days of ventilation + SNAP-II + surgery + GA + Child hair cortisol + BDI-II + STAI anxiety
^a Unstandardized regression coefficient

SNAP-II, score for neonatal acute physiology (severity of illness index)
 Skin-breaks (i.e. neonatal pain/stress) is equal to the number of skin-breaking procedures from birth to term equivalent age or hospital discharge; cumulative morphine dose is equal to daily morphine exposure adjusted for daily weight; postnatal infection is counted as the presence of a culture proven infection.

3.6 Effect of Neonatal pain/stress and COMT Val158Met genotypes on SLC6A4 methylation in very preterm children

To test our hypothesis that neonatal pain/stress would interact with *COMT* Val158Met genotype to affect *SLC6A4* methylation (PC1), a GZLM model was built in the very preterm group only, with neonatal pain/stress (cumulative skin breaking procedures from birth to term equivalent age) and *COMT* Val158Met genotypes (Val/Val, Val/Met, Met/Met), and clinical confounders related to prematurity (GA, number of days on mechanical ventilation, SNAP-II day 1, number of surgeries, presence of culture proven infection, cumulative dose of morphine) as covariates. All variables and interactions were entered simultaneously in the model. GZLM results are summarized in Table 6a and b. There was no significant effect in the model with main effects only (Table 6a). However, there was a significant interaction between *COMT* Val158Met genotype and neonatal pain/stress after adjusting for clinical confounders (Table 6b). Greater number of skin breaking procedures (independent of these covariates) was significantly associated with lower overall *SLC6A4* methylation (PC1 of PCA) in children with *COMT* Met/Met genotype ($r^2 = .46$, $p = 0.001$). This interaction is illustrated in Figure 2. Concurrent parental depressive symptoms (BDI-II) and trait anxiety (STAI), hair cortisol level, and *5HTTLPR* variants were included in a further model and none of them yielded significant results ($p = 0.330$, 0.062 , 0.142 , and 0.388 respectively). All results were summarized in Figure 3.

Table 6a. Generalized linear modelling analysis of *SLC6A4* methylation predicted by *COMT* genotype and neonatal pain/stress with main effects only

Parameter	B ^a	Std. Error	95% Confidence Interval		p-value
			Lower	Upper	
COMT Val/Val	0.528	0.4740	-0.401	1.457	0.266
COMT Val/Met	0.089	0.4165	-0.727	0.905	0.831
COMT Met/Met	0 ^b	-	-	-	-
Skin-breaks	0.129	1.0373	-1.904	2.163	0.901
Neonatal infection	0.542	0.3617	-.170	1.247	0.136
Cumulative morphine dose	-0.051	.8077	-1.634	1.532	0.950
Days of ventilation	0.012	0.0177	-0.023	0.046	0.511
SNAP-II day 1	0.010	0.0148	-0.019	0.039	0.512
Number of surgery	-0.196	0.2478	-0.682	0.289	0.429
Gestational age (GA)	0.168	0.1131	-0.053	0.390	0.137

GZLM results showing *SLC6A4* methylation was predicted by *COMT* genotype and neonatal pain/stress
Model: *SLC6A4* Methylation = *COMT* genotype + Infection + skin-breaks + morphine exposure + days of ventilation + SNAP-II + surgery + GA

^a Unstandardized regression coefficient

SNAP-II, score for neonatal acute physiology (severity of illness index)^b Set to zero because this parameter was redundant as the reference group

Skin-breaks (i.e. neonatal pain/stress) is equal to the number of skin-breaking procedures from birth to term equivalent age or hospital discharge; cumulative morphine dose is equal to daily morphine exposure adjusted for daily weight; postnatal infection is counted as the presence of a culture proven infection.

Table 6b. Generalized linear modelling analysis of *SLC6A4* methylation predicted by *COMT* genotype and neonatal pain/stress

Parameter	B ^a	Std. Error	95% Confidence Interval		p-value
			Lower	Upper	
COMT Val/Val X Skin-breaks	-0.401	1.3908	-3.127	2.325	0.773
COMT Val/Met X Skin-breaks	1.550	0.9558	-0.324	3.423	0.105
COMT Met/Met X Skin-breaks	-5.634	1.6642	-8.896	-2.373	0.001
COMT Val/Val	-10.012	4.0286	-17.908	-2.116	0.013
COMT Val/Met	-14.469	3.4845	-21.298	-7.639	0.000
COMT Met/Met	0 ^b	-	-	-	-
Skin-breaks	0 ^b	-	-	-	-
Neonatal infection	0.542	0.3137	-0.073	1.157	0.084
Cumulative morphine dose	-0.237	0.7364	-1.681	1.206	0.747
Days of ventilation	0.006	0.0153	-0.024	0.036	0.710
SNAP-II day 1	0.016	0.0132	-0.010	0.042	0.216
Number of surgery	-0.007	0.2234	-0.445	0.431	0.976
Gestational age (GA)	0.150	0.1057	-0.057	0.357	0.155

GZLM results showing *SLC6A4* methylation was predicted by *COMT* genotype and neonatal pain/stress

Model: *SLC6A4* Methylation = (*COMT* genotype x skin-breaks) + Infection + *COMT* genotype + skin-breaks + morphine exposure + days of ventilation + SNAP-II + surgery + GA

^a Unstandardized regression coefficient

SNAP-II, score for neonatal acute physiology (severity of illness index)

^b Set to zero because this parameter was redundant as the reference group

Skin-breaks (i.e. neonatal pain/stress) is equal to the number of skin-breaking procedures from birth to term equivalent age or hospital discharge; cumulative morphine dose is equal to daily morphine exposure adjusted for daily weight; postnatal infection is counted as the presence of a culture proven infection.

Figure 2. Greater neonatal pain/stress was associated with lower *SLC6A4* promoter methylation in very preterm children with *COMT* Met/Met genotype.

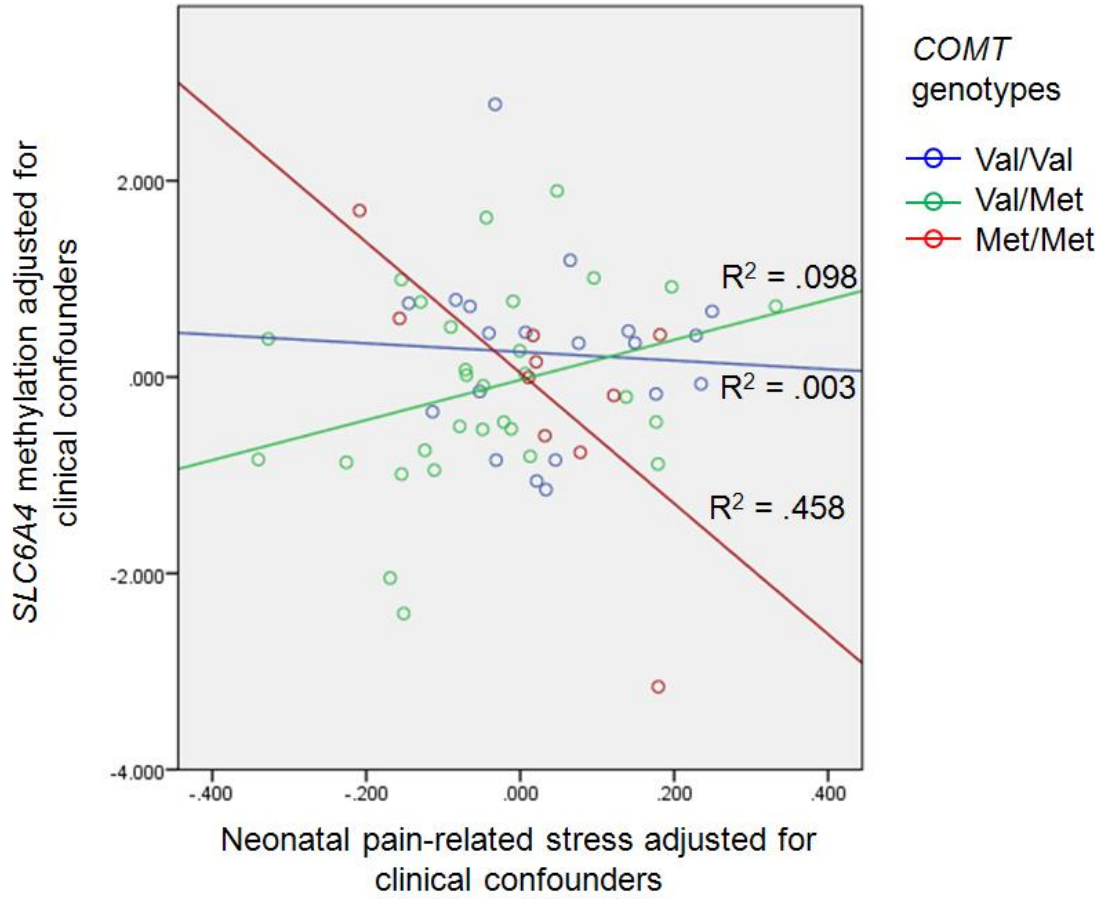
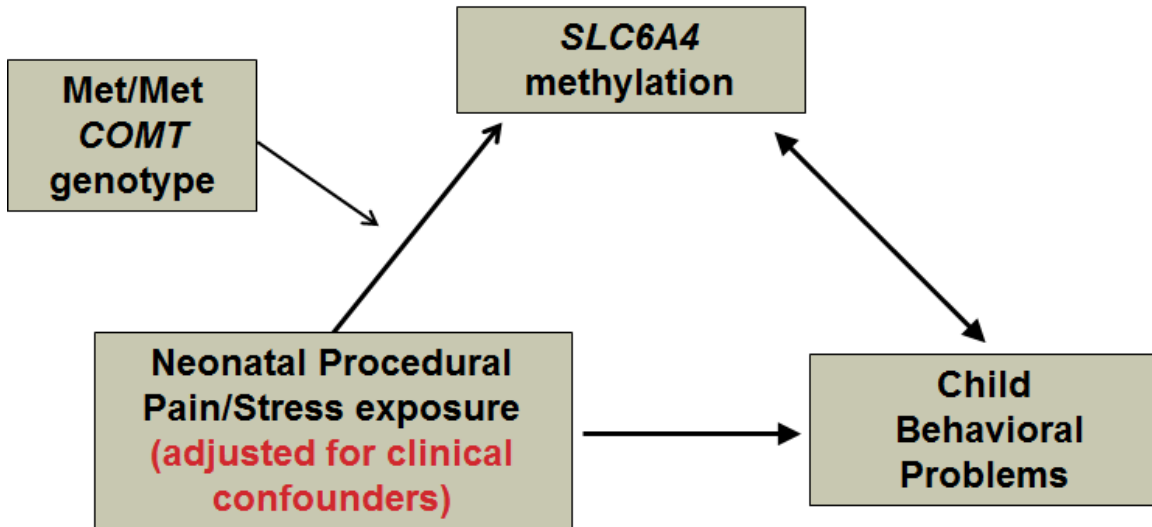


Figure 3. Summary of results



In summary:

- Preterm children had higher SLC6A4 methylation, which was associated with greater concurrent behavioral problems
- Greater neonatal procedural pain/stress (adjusted for clinical confounders) was associated with greater behavioral problems
- Neonatal procedural pain/stress exposure is associated with altered methylation of the SLC6A4 promoter in children born very preterm, but only among individuals with the COMT 158 Met/Met genotype

4 Discussion

In this study, we demonstrated that children born very preterm have higher *SLC6A4* promoter methylation compared to full-term children. Furthermore, we found that the pain/stress of repeated invasive procedures that very preterm infants are exposed to while in the NICU during the first weeks to months of life was related to this altered *SLC6A4* methylation; however, this was only seen in those children with the *COMT* 158 Met/Met genotype. Importantly, the association between early pain/stress and *SLC6A4* methylation at age 7 years was independent of other neonatal clinical factors and concurrent environmental stressors. Finally, we found that in very preterm (but not full-term) children, higher methylation at age 7 years was associated with child behavior problems, after adjusting for concurrent parent stressors, child cumulative cortisol levels, and the child *5HTTLPR* genotype. The CBCL Total Problem T score was used as an index of overall emotional and behavioral problems of the child (Achenbach & Rescorla, 2000), which has been reported to be associated with both concurrent and life time exposure to environmental stress (Compas, Howell, Phares, Williams, & Giunta, 1989). We found that the children's *SLC6A4* methylation was related to the total behavior problems, but not to specific domains of internalizing or externalizing problems, after adjusting for multiple comparisons. Importantly, the fact that the CBCL total problems scores were related to the overall *SLC6A4* methylation only in very preterm children suggests an epigenetic pathway of altered behavior unique to these children exposed to early life pain/stress. We then identified that among the neonatal factors to which only the preterm infants are exposed, greater procedural pain/stress exposure was associated with higher child behavior problems after controlling for concurrent stressors and *5HTTLPR*

genotype. In the same cohort of very preterm children, we have previously reported that greater neonatal procedural pain/stress exposure was associated with higher internalizing behaviors at 18 months and at school age (Ranger et al., 2014; Vinall et al., 2013), after accounting for similar clinical factors related to prematurity. In the present study the main goal was to explore the relationship between neonatal pain/stress (adjusted for clinical confounders) and *SLC6A4* methylation within the very preterm group in an attempt to further advance our understanding of possible mechanisms that could explain the relationship between prematurity and child behavioral problems.

In the present study, our findings are consistent with prior research on long-term effects of altered 5HT signaling. Manipulations of 5HT signaling, either via pharmacologic 5HTT blockade or *SLC6A4* knock-out in mouse models, have shown that increase serotonin concentrations during developmentally sensitive periods are associated with lasting behavioral, neurophysiological, and neuroanatomical changes in animal models (Homberg et al., 2010; Olivier et al., 2011; Simpson et al., 2011) and increased risk for anxiety/depression symptoms in humans (Oberlander et al., 2010; Weikum et al., 2013). Previous studies have shown effects of early life adversity on overall higher methylation in *SLC6A4* promoter in adults who were adopted in infancy (Beach et al., 2010; Oberlander et al., 2010; Weikum et al., 2013) and in patients with major depression and bipolar disorder (Sugawara et al., 2011; Zhao, Goldberg, Bremner, & Vaccarino, 2013). After our original publication, a recent study confirmed our finding that infants born very preterm who had high exposure to pain had increased *SLC6A4* promoter methylation from birth to discharge (Provenzi et al., 2015).

Since both dopaminergic and serotonergic systems play a critical role in mood and behavior regulation, there has been a considerable amount of interest in their potential interactions. For example, drugs enhancing dopaminergic function such as bupropion are also effective antidepressants (Sugawara et al., 2011; Zhao et al., 2013). In rodents, exposure of the striatum and nucleus accumbens to serotonin increased dopamine release [review by (Sasaki-Adams & Kelley, 2001)]. Dopamine and serotonin systems have also shown a significant degree of convergence and plasticity in the rat medial prefrontal cortex (Benes et al., 2000).

In children born very preterm we found that greater neonatal pain/stress (adjusted for clinical confounders) was significantly associated with lower *SLC6A4* promoter methylation, however this was only seen in those children with the *COMT* 158 Met/Met genotype. Previous studies in healthy adults have reported that homozygosity for the *COMT* 158 Met-allele was associated with greater pain sensitivity compared to individuals with the Met/Val and Val/Val genotypes (Zubieta et al., 2003). Therefore, it is possible that the *COMT* 158 Met/Met genotype may be more susceptible (or vulnerable) to neonatal pain/stress. The lower *SLC6A4* methylation in children with the Met/Met genotype may reflect a stress-sensitive genetic variation by which the already heightened response to early life pain/stress of these children was biologically reduced. Accordingly, it appears that *COMT* 158, a key dopamine-regulatory allele, may contribute to vulnerability or resilience to early life procedural pain/stress during a period of physiological immaturity. However in the current study, it is not possible to determine the functional effects of *SLC6A4* methylation and whether increases or decreases in *SLC6A4* methylation have positive or negative implications during childhood. Given that

the *COMT* Val158Met genotype (Met/Met) differentially interacted with early exposure to neonatal pain/stress to affect subsequent methylation of *SLC6A4*, we speculate that lower *SLC6A4* methylation in very preterm children with the *COMT* 158 Met/Met genotype suggests a possible resiliency or protective mechanism for children who are exposed to early pain/stress (Armbruster et al., 2012). One possible explanation is the increased cognitive stability linked to *COMT* 158 Met-allele as reported previously in infants (Markant, Cicchetti, Hetzel, & Thomas, 2014), children, (Diamond, Briand, Fossella, & Gehlbach, 2004) and adults (Barnett, Jones, Robbins, & Muller, 2007). According to the tonic/phasic dopamine theory, the Met allele may enhance tonic dopamine while Val enhances phasic dopamine. Phasic dopamine may be important for updating working memory traces, via D₂ receptors, while tonic dopamine may enhance stability of traces, via D₁ receptors (Cohen, Braver, & Brown, 2002). The sustained D₁ activation (tonic dopamine) helps prevent “uncontrolled, spontaneous activation of task-irrelevant representation” (Durstewitz, Seamans, & Sejnowski, 2000; Durstewitz & Seamans, 2002), and may function as a buffer for stressful early environment (Bilder, Volavka, Lachman, & Grace, 2004).

The present study investigated the methylation status of the *SLC6A4* promoter from saliva samples, since serotonergic neurons cannot be examined (Durstewitz & Seamans, 2002). Previous studies have found relationships between blood DNA methylation and mood disorders such as depression (Devlin et al., 2010; Ghadirivasfi et al., 2011; Nohesara et al., 2011; R. Philibert et al., 2007). Genome-wide methylation analysis revealed the DNA methylation levels between blood and postmortem brain tissues to be highly correlated ($r = 0.90$) (Horvath et al., 2012). Another genome-wide

DNA methylation study has shown that DNA from white blood cells and saliva have 97% of genes with similar methylation patterns, and saliva samples consistently had lower methylation levels than blood samples (Thompson et al., 2013). Also, methylation of *MB-COMT* from DNA in postmortem brain tissues and saliva were found to be closely related (Nohesara et al., 2011). Therefore, the use of saliva methylation status is justified. In this study, the overall methylation differences between full-term and very preterm children were small but the relative percentage differences between the groups were in the same range as found by others in different populations (e.g. Devlin et al., 2010; Kang et al., 2013).

Our findings suggest that the highly stressful environment of repeated exposure to procedural pain/stress that very preterm infants undergo during their stay in the NICU contributes to higher *SLC6A4* methylation and greater behavioral problems at school-age in children born very preterm, compared to full-term. Importantly, the need for diagnostic or therapeutic procedures is determined by the infant's immaturity and illness severity; therefore, we adjusted statistically for multiple clinical factors including gestational age at birth, illness severity, infections, duration of mechanical ventilation, surgeries, and dosage of morphine across the NICU stay. Future studies are needed to evaluate whether specific strategies to manage neonatal pain may ameliorate long-term epigenetic changes in very preterm infants.

5 Conclusion

This study suggests that early repeated procedural pain/stress exposure is associated with altered methylation of the *SLC6A4* promoter in children born very preterm, but only among individuals with the *COMT* 158 Met/Met genotype. We found a complex relationship between epigenetic modifications, *COMT* Val158Met genotype and early exposure to highly stressful environmental events that induce pain in children born during a critically sensitive developmental period. These findings may indicate that preterm infants with the *COMT* Val158Met genotype experience pain/stress differently and as a result the long term biological impact of early pain/stress differs, and thereby could have implications for subsequent serotonin signaling. These findings begin to address mechanisms underlying pathways leading to behavioral problems or resilience in this vulnerable population.

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