Global and site-specific changes in 5-methylcytosine and 5-hydroxymethylcytosine after extended post-mortem interval

Jeffrey A. Gross, McGill University
Corina Nagy, McGill University
Li Lin, Emory University
Éic Bonneil, Universite de Montreal
Marissa Maheu, McGill University
Pierre Thibault, Universite de Montreal
Naguib Mechawar, McGill University
Peng Jin, Emory University
Gustavo Turecki, McGill University

Journal Title: Frontiers in Genetics
Volume: Volume 7
Publisher: Frontiers Media | 2016-06-23, Pages 120-120
Type of Work: Article | Final Publisher PDF
Publisher DOI: 10.3389/fgene.2016.00120
Permanent URL: https://pid.emory.edu/ark:/25593/rqv5g

Final published version: http://dx.doi.org/10.3389/fgene.2016.00120

Copyright information:

© 2016 Gross, Nagy, Lin, Bonneil, Maheu, Thibault, Mechawar, Jin and Turecki.

This is an Open Access work distributed under the terms of the Creative Commons Attribution 4.0 International License (https://creativecommons.org/licenses/by/4.0/).

Accessed July 27, 2023 5:02 AM EDT
Global and Site-Specific Changes in 5-Methylcytosine and 5-Hydroxymethylcytosine after Extended Post-mortem Interval

Jeffrey A. Gross†, Corina Nagy†, Li Lin2, Éric Bonneil3, Marissa Maheu1, Pierre Thibault3, Naguib Mechawar1, Peng Jin2 and Gustavo Turecki*†

1 Department of Psychiatry, McGill Group for Suicide Studies, Douglas Mental Health University Institute, McGill University, Montreal, QC, Canada, 2 Department of Human Genetics, Emory University School of Medicine, Atlanta, GA, USA, 3 Institute for Research in Immunology and Cancer, Université de Montréal, Montreal, QC, Canada

There has been a growing interest in the study of epigenetic mechanisms to elucidate the molecular bases of human brain-related diseases and disorders. Frequently, researchers utilize post-mortem tissue with the assumption that post-mortem tissue decay has little or no effect on epigenetic marks. Although previous studies show no effect of post-mortem interval on certain epigenetic marks, no such research has been performed on cytosine modifications. In this study, we use DNA from the brains of adult Sprague Dawley rats subjected to post-mortem intervals at room temperature, ranging from 0 to 96 h, to assess the stability of cytosine modifications, namely 5-methylcytosine and 5-hydroxymethylcytosine. Our results indicate that neither global nor site-specific levels of 5-methylcytosine and 5-hydroxymethylcytosine are affected by the post-mortem intervals we studied. As such, the use of post-mortem tissue to study cytosine modifications in the context of neurological or neuropsychiatric disorders is appropriate.

Keywords: epigenetics, post-mortem interval, 5-methylcytosine, 5-hydroxymethylcytosine, stability

INTRODUCTION

There has been growing interest in the investigation of epigenetic changes associated with disease states. Among pathological conditions of the brain, post-translational histone modifications, non-coding RNAs, and cytosine modifications have all been associated with developmental disorders, neurological diseases, psychiatric illnesses, and cancers, among others.

In particular, 5-methylcytosine (5mC) has been the most widely studied epigenetic modification. Research has shown 5mC to be central to the establishment of tissue-specific gene expression, cell differentiation, genomic imprinting, and X-inactivation. Recently, however, interesting research provided evidence showing that 5mC can be oxidized to 5-hydroxymethylcytosine (5hmC) in a reaction catalyzed by the ten–eleven translocation (TET) enzymes (Kriaucionis and Heintz, 2009; Tahiliani et al., 2009; Ito et al., 2010). This finding led to the discovery of additional oxidative products, namely 5-formylcytosine (5fC) and 5-carboxylcytosine (5caC). Together, these oxidative products of 5mC have led to the proposal of active DNA demethylation, where methylation is removed from a cytosine base by successive oxidations and base excision repair. Although clues are rapidly emerging, questions still remain on the dynamics of the cytosine
demethylation pathway and the functions of these intermediate molecules. Nevertheless, growing evidence points to the involvement of 5mC and its oxidative products in human diseases and disorders.

To determine the function of cytosine modifications in human brain diseases, such as those related to neuropsychiatric, neurodevelopmental, and neurodegenerative phenotypes, many researchers must rely on post-mortem brain tissue to conduct their studies. Typically, post-mortem studies report post-mortem interval (PMI), which represents the amount of time between a subject's death and collection and processing of the brain. It has previously been shown that DNA is stable across extended PMIs (Hynd et al., 2003), while the same is true for microRNAs (miRNAs) and some histone modifications (Huang et al., 2006; Stan et al., 2006; Nagy et al., 2015). It has also been hypothesized that the skull protects the brain from oxidative damage during extended PMIs (Hynd et al., 2003), which is of interest given that 5hmC, 5fC, and 5caC are oxidative products of 5mC. Although initial reports confirm that lengthy PMIs may not alter epigenetic landscapes, their effects on DNA demethylation products have yet to be determined. In this report, we provide evidence that these cytosine modifications are stable during post-mortem intervals and can reflect the actual status of 5mC and 5hmC at the time of death in post-mortem tissue.

MATERIALS AND METHODS

Experimental Design
Sprague Dawley rats (Charles River Laboratories International, Wilmington, MA, USA) were selected as a model to test the effects of PMI. Young adult rats (60-days old, n = 16) were caged independently and allowed to habituate to the environment for one week. The animals were then sacrificed by gas asphyxiation and left in open air for various PMIs. In order to mimic natural biological circumstances, the rats were subjected, at room temperature, to PMIs ranging from 0 to 96 h, and a fixed time of 24 h at 4°C to simulate the time a human donor typically spends in the morgue before tissue collection. Eight different PMI time points (n = 2 per PMI) were investigated: Control (immediate dissection and flash freezing in isopentane cooled to −50°C), 0, 6, 12, 24, 48, 72, and 96h (Figure 1). All but the control animals, which were processed immediately after death with no PMI, were kept at 4°C for 24h before processing. After processing, all samples were stored at −80°C. This study was approved by the Douglas Hospital Research Centre's Animal Research Committee (#04/15).

DNA Extraction for LC–MS, ELISA, and 5hmC Capture
DNA was extracted from rat brain using a phenol:chloroform:isoamyl extraction protocol. Briefly, 40 mg of frozen tissue was homogenized in lysis buffer and incubated overnight with proteinase K. DNA was treated with RNAse A prior to phenol:chloroform:isoamyl extraction. NanoDrop 2000 spectrophotometer and Quant-IT PicoGreen (Thermo Scientific, Waltham, MA, USA, Cat. #: P7589) were used to assess the DNA purity and concentration.

Liquid Chromatography–Mass Spectrometry (LC–MS)
One microgram of genomic DNA per sample was incubated with 5 units of the DNA Degradase Plus (Zymo Research, Irvine, CA,
USA, Cat.# E2021) enzyme overnight at 37°C. Samples were loaded and separated on a homemade reversed-phase column (150 μm i.d. × 150 mm), with a gradient going from 0 to 10% B in 18 min and a 600 nl/min flow rate on an Easy nLC (Thermo Scientific, Waltham, MA, USA) connected to a Fusion Orbitrap (Thermo Scientific, Waltham, MA, USA). MS analysis consists of a PRM acquisition method for C, mC, and hmC, consisting, respectively, of a SIM scan at m/z at 228.1, 242.1, and 256.1, followed by tandem mass spectra for each transition at a normalized collision energy (NCE) of 30%. Ion chromatograms

| Target | Forward primer | Reverse primer | Length (bp) |
|--------|----------------|----------------|-------------|
| Ifg2–1 | TTGTGGGCTCCATTGAGTTT | ACGGCGTCCGTCTCATTAT | 118 |
| Ifg2–2 | AAACCCTCCTGTGTGAGAGAT | ACAACCTATCCGCAAGAGT | 135 |
| Ifg2–3 | ACTCTTGGGAGATCGCTTGT | AAGCACCACACGACTTCC | 104 |
| Ifg2–4 | GGAAGTCGATGTTGGTGCTT | CAAAATGAAAGGTGCTCAACAA | 114 |
| h19–1 | GGCGAGTGAAGGTGCTGCTT | GCCTCGCTCCTCTAACCCTTTT | 124 |
| h19–2 | TGGCTGCACCTGACCTTCACT | CCGAGACGGTCTCCTTGT | 119 |
| h19–3 | TGGCTGCACCTGACCTTCACT | CCGAGACGGTCTCCTTGT | 119 |

FIGURE 2 | Global levels of 5mC and 5hmC show no differences across increasing PMI. (A,B) Global levels of 5mC (A) and 5hmC (B) were measured by LC/MS (H = 10.36; p = 0.1690 and H = 11.88; p = 0.1044, respectively). (C,D) LC/MS results for 5mC (C) and 5hmC (D) were validated using ELISA-based quantification (H = 10.28; p = 0.1733 and H = 7.103; p = 0.4182, respectively). Dunn’s multiple comparisons tested individual PMIs against the CTRL. n = 2 per PMI. Significance set at p < 0.05.
were extracted for fragment ions \( m/z \) 112.0505, 126.0661, and 142.0611.

**ELISA-Based Global 5mC and 5hmC Quantification**

One hundred nanograms of DNA per sample were denatured, as per manufacturer's guidelines, and added to Zymo Research ELISA kits (Zymo Research, Irvine, CA, USA, Cat. # D5325 and D5425 for 5mC, and 5hmC, respectively). Primary and secondary antibodies were added following manufacturer's guidelines. Plates were allowed to develop at room temperature and absorbance was read at 405nm for both kits.

**DNA Extraction for EpiTYPER**

DNA was extracted from 40 mg of frozen rat brain tissue using the Qiagen DNeasy Blood & Tissue kit (Qiagen Inc., Toronto, ON, Canada, Cat. # 69506). NanoDrop 2000 spectrophotometer (Thermo Scientific, Waltham, MA, USA) was used to assess the purity and concentration of the DNA. DNA was bisulfite converted using EpiTect Bisulfite Kit (Qiagen Inc., Toronto, ON, Canada, Cat. # 59104). Briefly, DNA was treated with sodium bisulfite, cycling between 95 and 60°C for 5 h. These conditions result in deamination of the cytosine into a uracil, except in the presence of a modified cytosine. The combination of 5mC and 5hmC was assessed using the EpiTYPER service platform from the McGill University Genome Quebec Innovation Centre. The Centre designed the primers for \( h19 \) and \( Igf2 \), which are maternally and paternally imprinted regions, respectively, using EpiDesigner. Regional coordinates for \( h19 \) and \( Igf2 \) were chr1: 222,641,272–222,641,531 and chr1: 202,911,352–202,911,723, respectively.

**5hmC Capture**

5hmC from rat brain DNA was captured using selective chemical labeling, as previously described (Song et al., 2011). Final concentrations of captured DNA were measured using Qubit Fluorometric Quantitation (Life Technologies, Carlsbad, CA, USA). Site-specific levels of 5hmC were assessed by quantitative real-time polymerase chain reaction (qRT-PCR) on Applied Biosystems' 7900HT Fast Real-Time PCR System (Applied Biosystems, Carlsbad, CA, USA). SYBR green primers were tiled across the same \( h19 \) and \( Igf2 \) loci as the EpiTYPER analyses. Primer sequences are listed in Table 1. The 9600 emulation thermal cycle protocol was: 50°C for 2 min, 95°C for 10 min, and 40 repetitions of 95°C for 15 s and 60°C for 1 min. The data were extracted by relative quantification using Applied Biosystems’ SDS 2.4 and RQ Manager 1.2.1 software. Data were normalized using input DNA, which represents non-captured sheared DNA.

**Statistical Analyses**

All statistical tests were performed using GraphPad Prism 6. The specifics of each test are outlined in the results section. Statistical significance was set at \( p < 0.05 \). Error bars represent Mean ± S.E.M.

**RESULTS**

DNA cytosine methylation is considered a highly stable nucleotide modification that remains unchanged over time (Barrachina and Ferrer, 2009), largely due to the strong covalent bond between the methyl group and the 5’ carbon of cytosine. Indeed DNA methylation was previously shown to withstand various changes in pH with no differences observed even in extremes (Ernst et al., 2008). Since this covalent bond is maintained during cytosine oxidation, the stability of the demethylation intermediates should also remain stable across increasing PMI. To evaluate this hypothesis, the primary cytosine modifications, 5mC and 5hmC, were tested both globally and at specific loci for 8 different PMIs.

**Global Levels of 5mC and 5hmC**

We first explored global levels of each cytosine modification by LC–MS. Two subjects per time point were run in duplicate. Kruskal–Wallis ANOVA followed by Dunn's multiple comparison tests showed no effect of PMI on global 5mC (\( H = 10.36; p = 0.1690 \)) or 5hmC (\( H = 11.88; p = 0.1044 \)) levels (Figures 2A,B). As an alternative method to detect global levels, we used absorbance-based ELISA kits with antibodies specific to 5mC and 5hmC. Kruskal–Wallis ANOVA followed by Dunn's multiple comparison tests confirmed that increasing PMI does not alter global 5mC (\( H = 10.28; p = 0.1733 \)) or 5hmC (\( H = 7.103; p = 0.4182 \)) levels (Figures 2C,D).

**Site-Specific Levels of 5mC and 5hmC**

We also wanted to know whether 5mC and 5hmC show loci-specific stability. To do so, we investigated two genes, \( h19 \) and \( Igf2 \), both of which are known to undergo parental imprinting in humans and rats. Bisulfite conversion followed by EpiTYPER was used to assess the combination of 5mC and 5hmC, while levels of 5mC were assessed using 5mC capture followed by qRT-PCR. Two-way ANOVA showed no significant interaction between CpG cytosine modification and PMI for the \( h19 \) (\( F_{(14,42)} = 0.3603; p = 0.9987 \)) (Figure 3A) or \( Igf2 \) (\( F_{(42,49)} = 0.6150; p = 0.9453 \)) (Figure 3B) loci, while Dunnett’s multiple comparison test showed no difference in CpG cytosine modification between the control and increasing PMIs. Similarly, two-way ANOVA also showed no significant interaction between locus-specific 5mC and PMI for \( h19 \) (\( F_{(14,42)} = 0.07283; p > 0.9999 \)) (Figure 4A) or \( Igf2 \) (\( F_{(21,32)} = 0.1145; p > 0.9999 \)) (Figure 4B), while Dunnett’s multiple comparison test showed no difference in 5hmC levels between the control and increasing PMIs.

**DISCUSSION**

The use of post-mortem tissue is an invaluable resource to investigate biological processes in the brain. However, using tissue collected postmortem may present certain limitations. Of great interest is how the PMI may affect the quality of tissue and our ability to generate reliable data. As cytosine modifications are a focus of much of the research in the field
FIGURE 3 | Site-specific levels of cytosine modifications across the h19 and Igf2 loci remain stable with increasing PMI. EpiTYPER was used to analyze the percent of methylation + hydroxymethylation at the h19 (A) and Igf2 (B) loci \( F_{(35,42)} = 0.3603; p = 0.9987 \) and \( F_{(42,49)} = 0.6150; p = 0.9453 \), respectively. Dunnett’s multiple comparisons tested %5mC + 5hmC of individual PMIs against the CTRL for each CpG, \( n = 2 \) per PMI. Significance set at \( p < 0.05 \).

doing epigenetics, it is of paramount importance to understand whether PMI alters the DNA demethylation pathway. In this study, we show that global and loci-specific levels of cytosine modifications remain largely unchanged across increasing PMIs. This data lends weight to the notion that cytosine modifications are stable and can be accurately assessed in postmortem research.

Our findings are reassuring considering the longevity of DNA integrity after death. Interestingly, it was recently determined that the half-life of DNA is 521 years (Allentoft et al., 2012). Although this study referred to a specific mitochondrial DNA sequence from fossils, research suggests a distinct stability of DNA, especially from the brain (Bar et al., 1988). These findings are pertinent when considering the potential for oxidative damage occurring during death. Since oxidation of 5mC results in downstream modifications to cytosine, it may be presumed that these modifications are susceptible to degradation following death. Our results counter this presumption and show an impressive stability of the tested cytosine modifications. Our findings are more in line with the proposal that cortical DNA is particularly stable, as it is protected by the skull from environmental contamination (Bar et al., 1988; Hynd et al., 2003).

This study is not without several methodological limitations. To best mimic human conditions, Sprague Dawley rats were selected as a model for PMI as their genetic backgrounds are similar to humans. Although it would have been ideal to also take into account the effects of agonal conditions, such as long hospital stays, comas, or hypoxic states, subjecting the rats to these antemortem conditions would not be ethical.
In addition, when studying brain tissue exposed to long post-mortem intervals, distinguishing brain anatomy is quite challenging. In this study, we used similar sections from the frontal region of each brain, although the exact region cannot be reported. Furthermore, although bisulfite conversion does not distinguish between 5mC and 5hmC (Huang et al., 2010) for site-specific methylation analysis, we saw no differences in 5hmC through the accompanying 5hmC capture. As such, 5hmC is unlikely to represent a significant variation in the EpiTYPER analyses, thereby making them generalizable to 5mC as well. Another potential limitation was our inability to quantify 5fC or 5caC, however, given the very low abundance of these demethylation intermediates across tissue types (Ito et al., 2011), this should not come as a surprise. In fact, previous studies utilized thymine DNA glycosylase (TDG) knockdowns or knockouts to increase the levels of 5fC and 5caC (Shen et al., 2013; Song et al., 2013; Wu et al., 2014; Neri et al., 2015). Nevertheless, given the inherent stability of DNA, along with the stability of 5mC and 5hmC, we hypothesize that 5fC and 5caC would not be affected by increasing PMI. To confirm this hypothesis, further studies could first create a TDG knockout animal, then continue with the PMI protocol described in this manuscript.

Taken together, the results presented here may enhance confidence in future research studying cytosine modifications in post-mortem samples. Undoubtedly, the continuing debate regarding the function of these modifications as DNA demethylation intermediates (He et al., 2011; Shen et al., 2013) or as a transcriptional regulators (Mellen et al., 2012; Lister et al., 2013; Wen et al., 2014; Gross et al., 2015) will require more in-depth analyses using post-mortem tissue. Furthermore, the stability of these modifications across PMIs allows researchers...
to continue elucidating the function of cytosine modifications in brain-related diseases and disorders.

AUTHOR CONTRIBUTIONS

JG, CN, and GT designed the study; JG and CN performed all the analyses; CN, MM, and NM performed the animal work; JG, EB, and PT performed the LC–MS; JG and CN performed the ELISAs; JG and CN performed EpiTYPER; JG, LL, and PJ performed 5hmC capture; All authors wrote and approved the manuscript.

REFERENCES

Allentoft, M. E., Collins, M., Harker, D., Haile, J., Oskam, C. L., Hale, M. L., et al. (2012). The half-life of DNA in bone: measuring decay kinetics in 158 dated fossils. Proc. Biol. Sci. 279, 4724–4733. doi: 10.1098/rspb.2012.1745

Bar, W., Kratzer, A., Machler, M., and Schmid, W. (1988). Postmortem stability of DNA. Forensic Sci. Int. 39, 59–70. doi: 10.1016/0338-0490(88)90118-1

Barrachina, M., and Ferrer, I. (2009). DNA methylation of Alzheimer disease and tauopathy-related genes in postmortem brain. J. Neuropathol. Exp. Neurol. 68, 880–891. doi: 10.1097/NEN.0b013e3181fae46

Ernst, C., McGowan, P. O., Deleva, V., Meaney, M. J., Szyf, M., and Turecki, G. (2008). The effects of pH on DNA methylation state: in vitro and post-mortem brain studies. J. Neurosci. Methods 174, 123–125. doi: 10.1016/j.jneumeth.2008.06.027

Gross, J. A., Pacis, A., Chen, G. G., Barreiro, L. B., Ernst, C., and Turecki, G. (2015). Characterizing 5-hydroxymethylcytosine in human prefrontal cortex at single base resolution. BMC Genomics 16:672. doi: 10.1186/s12864-015-1875-8

He, Y. F., Li, B. Z., Li, Z., Liu, P., Wang, Y., Tang, Q., et al. (2011). Tet-mediated conversion of 5-methylcytosine to 5-formylcytosine and 5-carboxylcytosine. Cell Res. 21, 1123, 1–11. doi: 10.1038/nature09303

Ito, S., D’Alessio, A. C., Taranova, O. V., Hong, K., Sowers, L. C., and Zhang, Y. (2010). Role of Tet proteins in 5mC to 5hmC conversion, ES-cell self-renewal and inner cell mass specification. Nature 466, 1129–1133. doi: 10.1038/nature09303

Ito, S., Shen, L., Dai, Q., Wu, S. C., Collins, L. B., Sweenberg, J. A., et al. (2011). Tet proteins can convert 5-methylcytosine to 5-formylcytosine and 5-carboxylcytosine. Science 333, 1300–1303. doi: 10.1126/science.1210597

Kriaucionis, S., and Heintz, N. (2009). The nuclear DNA base 5-hydroxymethylcytosine. Nat. Biotechnol. 27, 68–70. doi: 10.1038/nbt.1732

Liang, J. S. (2009). Chromatin immunoprecipitation in postmortem brain. J. Neuropathol. Exp. Neurol. 68, 1046–1052. doi: 10.1097/NEN.0b013e3181a49f0a

Mellen, M., Ayata, P., Dewell, S., Kriaucionis, S., and Heintz, N. (2012). MeCP2 binds to 5hmC enriched within active genes and accessible chromatin in the nervous system. Cell 151, 1417–1430. doi: 10.1016/j.cell.2012.11.022

Nagy, C., Maheu, M., Lopez, J. P., Vaillancourt, C., Czuceanu, C., Gross, J. A., et al. (2015). Effects of postmortem interval on biomolecule integrity in the brain. J. Neuropathol. Exp. Neurol. 74, 459–469. doi: 10.1097/NEN.000000000000190

Neri, F., Incarnato, D., Krepelova, A., Rapelli, S., Anselmi, F., Parlatò, C., et al. (2015). Single-base resolution analysis of 5-formyl- and 5-carboxylcytosines reveals promoter DNA methylation dynamics. Cell Rep. doi: 10.1016/j.celrep.2015.01.008 [Epub ahead of print].

Shen, L., Wu, H., Diep, D., Yamaguchi, S., D’Alessio, A. C., Fung, H. L., et al. (2013). Genome-wide analysis reveals TET- and TDG-dependent 5-methylcytosine oxidation dynamics. Cell 153, 692–706. doi: 10.1016/j.cell.2013.04.002

Song, C. X., Szulwach, K. E., Dai, Q., Fu, Y., Mao, S. Q., Lin, L., et al. (2013). Genome-wide profiling of 5-formylcytosine reveals its roles in epigenetic priming. Cell 153, 678–691. doi: 10.1016/j.cell.2013.04.001

Song, C. X., Szulwach, K. E., Fu, Y., Dai, Q., Yi, C., Li, X., et al. (2011). Selective chemical labeling reveals the genome-wide distribution of 5-hydroxymethylcytosine. Nat. Biotechnol. 29, 68–72. doi: 10.1038/nbt.1732

Stan, A. D., Ghose, S., Gao, X. M., Roberts, R. C., Lewis-Amezua, K., Hatanpaa, K. J., et al. (2006). Human postmortem tissue: what quality markers matter? Brain Res. 1123, 1–11. doi: 10.1016/j.brainres.2006.09.025

Tahiliani, M., Koh, K. P., Shen, Y., Pastor, W. A., Bandukwala, H., Brudno, Y., et al. (2009). Conversion of 5-methylcytosine to 5-hydroxymethylcytosine in mammalian DNA by MLL partner TET1. Science 324, 930–935. doi: 10.1126/science.1170116

Wen, L., Li, X., Yan, L., Tan, Y., Li, R., Zhao, Y., et al. (2014). Whole-genome analysis of 5-hydroxymethylcytosine and 5-methylcytosine at base resolution in the human brain. Genome Biol. 15, R49. doi: 10.1186/gb-2014-15-3-r49

Wu, H., Wu, X., Shen, L., and Zhang, Y. (2014). Single-base resolution analysis of active DNA demethylation using methylase-assisted bisulfite sequencing. Nat. Biotechnol. 32, 1231–1240. doi: 10.1038/nbt.3073

ACKNOWLEDGMENTS

This work was supported by grants to GT from the Canadian Institutes of Health Research MOP93775, MOP11260, MOP119429, and MOP119430; from the National Institutes of Health 1R01DA033684-01; and by the Fonds de Recherche du Québec – Santé through a Chercheur National salary award and through the Quebec Network on Suicide, Mood Disorders, and Related Disorders. JG is supported by a CIHR Frederick Banting and Charles Best Doctoral fellowship and CN is supported by the Fonds de Recherche du Québec – Santé Doctoral award.

Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Copyright © 2016 Gross, Nagy, Lin, Bonneil, Maheu, Thibault, Mechawar, Jin and Turecki. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) or licensor are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.