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Reminder: Invitation to review a manuscript for BMC Genetics - GTIC-D-15-00246

1 message

BMC Genetics Editorial Office <em@editorialmanager.com> Sun, Oct 11, 2015 at 10:31 PM
Reply-To: BMC Genetics Editorial Office <bmcgenet@biomedcentral.com>
To: Shicheng Guo <scguo@ucsd.edu>

GTIC-D-15-00246
DNA methylation in peripheral tissue of schizophrenia and bipolar disorder: a systematic review
Nina Teroganova, BMedSci (Hons), PhD candidate; Leah Girshkin, BSc, MBMSc, PhD (candidate); Catherine M Suter, BAppSc, BSc (Hons), PhD; Melissa J Green, BA, MLitt, PhD
BMC Genetics

Dear Dr. Guo,

Recently I contacted you to ask if you could review the above manuscript that was submitted to BMC Genetics.

As we have not yet heard from you but are aiming for a fast peer review process, I would be grateful if you could let me know whether or not you are able to review this manuscript by accessing the system using the following link and choosing either accept or decline.

http://GTIC.edmgr.com/

If you have forgotten your username or password please use the "Send Username/Password" link to get your login information. For security reasons, your password will be reset.

The title, authors and abstract of the manuscript are at the end of this email.

I look forward to hearing from you within the next few days.

Please note that this is an automatic email, so if you have recently contacted us regarding your review then please ignore this reminder.

Best wishes,

Editorial Office
BMC Genetics
http://www.biomedcentral.com/bmcgenet

Abstract: Background: Increasing evidence suggests the involvement of epigenetic processes in the development of schizophrenia (SZ) and bipolar disorder (BD), and recent reviews have focused on findings in post-mortem brain tissue. A systematic review was conducted to synthesise and evaluate the quality of available evidence for epigenetic modifications (specifically DNA methylation) in peripheral blood and saliva samples of SZ and BD patients in comparison to healthy controls.
Methods: Original research articles using humans were identified using electronic databases. There were 33 included studies for which data were extracted and graded in duplicate on 22 items of the Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) statement, to assess methodological precision and quality of reporting.
Results: There were 15 genome-wide and 18 exclusive candidate gene loci investigations for DNA methylation studies. A number of common genes were identified as differentially methylated in SZ/BD, which were related to reelin, brain-derived neurotrophic factor, dopamine (including the catechol-O-methyltransferase gene), serotonin and glutamate, despite inconsistent findings of hyper-, hypo-, or lack of methylation at these and other loci. The

mean STROBE score of 59% suggested moderate quality of available evidence; however, wide methodological variability contributed to a lack of consistency in the way methylation levels were quantified, such that meta-analysis of the results was not possible.
Conclusions: Moderate quality of available evidence shows some convergence of differential methylation at some common genetic loci in SZ and BD, despite wide variation in methodology and reporting across studies. Improvement in the clarity of reporting clinical and other potential confounds would be useful in future studies of epigenetic processes in the context of exposure to environmental and other risk factors.