CORRECTION



Open Access

Correction: A whole genome association study of mother-to-child transmission of HIV in Malawi

Bonnie R Joubert^{1*}, Ethan M Lange^{2,3,4}, Nora Franceschini¹, Victor Mwapasa⁵, Kari E North^{1,4}, Steven R Meshnick¹, the NIAID Center for HIV/AIDS Vaccine Immunology

Abstract

A correction to: Bonnie R Joubert, Ethan M Lange, Nora Franceschini, Victor Mwapasa, Kari E North, Steven R Meshnick and the NIAID Center for HIV/AIDS Vaccine Immunology. **A whole genome association study of mother-tochild transmission of HIV in Malawi**. *Genome Medicine* 2010, **2**:17.

We wish to report some corrections to our study [1], none of which alters the interpretation of the data or the conclusions drawn. After publication of this work we noted that the sample size required further clarification.

Results

A total of 246 infants (114 cases, 132 controls; 116 males, 121 females, 9 with imputed gender) passed laboratory quality control. Statistical quality control removed 15 individuals for low genotyping, resulting in a total of 231 individuals (103 cases, 128 controls; 114 males, 117 females). Of the 655,352 SNPs tested, 68,297 failed statistical quality control due to HWE P < 0.001 in the controls (N = 431), low genotyping rate (N = 21,589), or for MAF < 0.01 (N = 53,477), where some overlap of SNPs across exclusion criteria existed. Results were presented for 587,055 SNPs.

Additional data files

Additional data files 1 and 2 containing the corrected data are available online with this article.

Additional material

Additional file 1: A Word document giving effect estimates for top SNPs of interest, by mode of transmission. The data provided represent the genome-wide association analysis by mode of HIV transmission.

Additional file 2: A Word document giving effect estimates for SNPs near or within genes associated with HIV/AIDS. The data provided represent the genome-wide association analysis for specific

* Correspondence: bjoubert@unc.edu

¹Department of Epidemiology, Gillings School of Global Public Health, University of North Carolina, Chapel Hill, NC 27599, USA

Full list of author information is available at the end of the article

BioMed Central

regions that have previously demonstrated association with HIV/AIDS, described in the Introduction section.

Author details

¹Department of Epidemiology, Gillings School of Global Public Health, University of North Carolina, Chapel Hill, NC 27599, USA. ²Department of Genetics, School of Medicine, University of North Carolina, Chapel Hill, NC 27599, USA. ³Department of Biostatistics, Gillings School of Global Public Health, University of North Carolina, Chapel Hill, NC 27599, USA. ⁴Carolina Center for Genome Sciences, University of North Carolina, Chapel Hill, NC 27599, USA. ⁵College of Medicine, University of Malawi, Blantyre, Malawi.

Received: 1 October 2010 Accepted: 11 October 2010 Published: 11 October 2010

Reference

 Joubert Bonnie R, Lange Ethan M, Franceschini Nora, Mwapasa Victor, North Kari E, Meshnick Steven R, the NIAID Center for HIV/AIDS Vaccine Immunology: A whole genome association study of mother-to-child transmission of HIV in Malawi. Genome Medicine 2010, 2:17.

doi:10.1186/gm197

Cite this article as: Joubert *et al.*: **Correction:** A whole genome association study of mother-to-child transmission of HIV in Malawi. *Genome Medicine* 2010 **2**:76.

© 2010 Joubert et al.; licensee BioMed Central Ltd. This is an open access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/2.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.