

CORRECTION

Correction: Hepatitis B Virus (HBV) Variants in Untreated and Tenofovir Treated Chronic Hepatitis B (CHB) Patients During Pregnancy and Post-Partum Follow-up

Boris Virine, Carla Osiowy, Shan Gao, Tong Wang, Eliana Castillo, Steven R. Martin, Samuel S. Lee, Kimberley Simmonds, Guido van Marle, Carla S. Coffin

[Fig 1](#), “Neighbor-joining phylogenetic reconstruction of the HBV pre-S/S (A, N = 20), Pre-C/C (B, N = 11) and full genome (C, N = 3) using the bootstrap method,” and [Fig 2](#), “Comparison of distance amongst HBV quasispecies in patients during pregnancy and post-partum in pre-S/S (A, N = 5) and pre-C/C (B, N = 5) region. Measurement of distance within patient samples is shown and compared to measurement of distance within patient samples categorized by genotype. A comparison of relative evolutionary distances of patient samples collected at different time points is shown,” do not appear in full. Please view the full [Fig 1](#) and [Fig 2](#) here.



 OPEN ACCESS

Citation: Virine B, Osiowy C, Gao S, Wang T, Castillo E, Martin SR, et al. (2015) Correction: Hepatitis B Virus (HBV) Variants in Untreated and Tenofovir Treated Chronic Hepatitis B (CHB) Patients During Pregnancy and Post-Partum Follow-up. PLoS ONE 10(12): e0145898. doi:10.1371/journal.pone.0145898

Published: December 21, 2015

Copyright: © 2015 Virine et al. This is an open access article distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

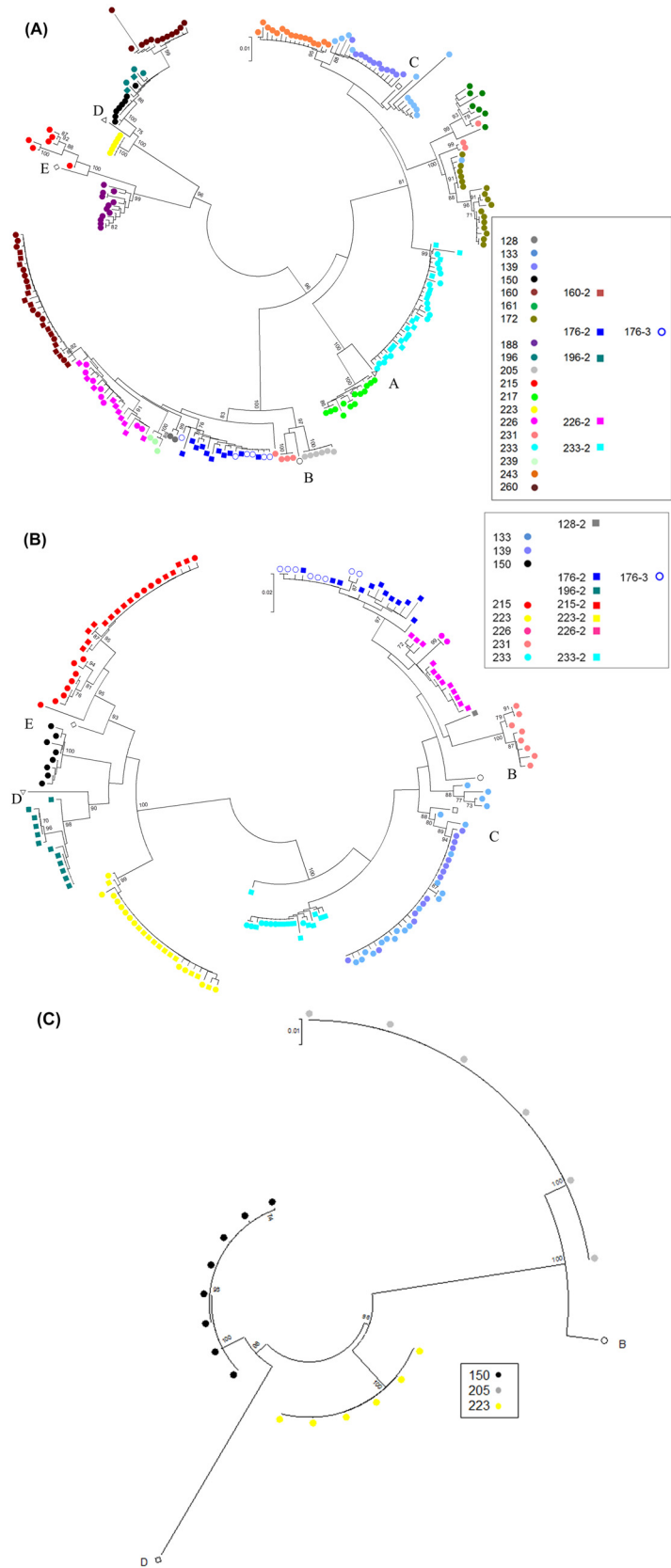


Fig 1. Neighbor-joining phylogenetic reconstruction of the HBV pre-S/S (A, N = 20), Pre-C/C (B, N = 11) and full genome (C, N = 3) using the bootstrap method. Clustering is prominent between individual cases, indicating a greater degree of variation between individuals, than amongst each of their viral quasispecies. Bootstrap values greater than 70 were considered significant. Case #146 was excluded from analysis as only the pre-S1 region was sequenced.

doi:10.1371/journal.pone.0145898.g001

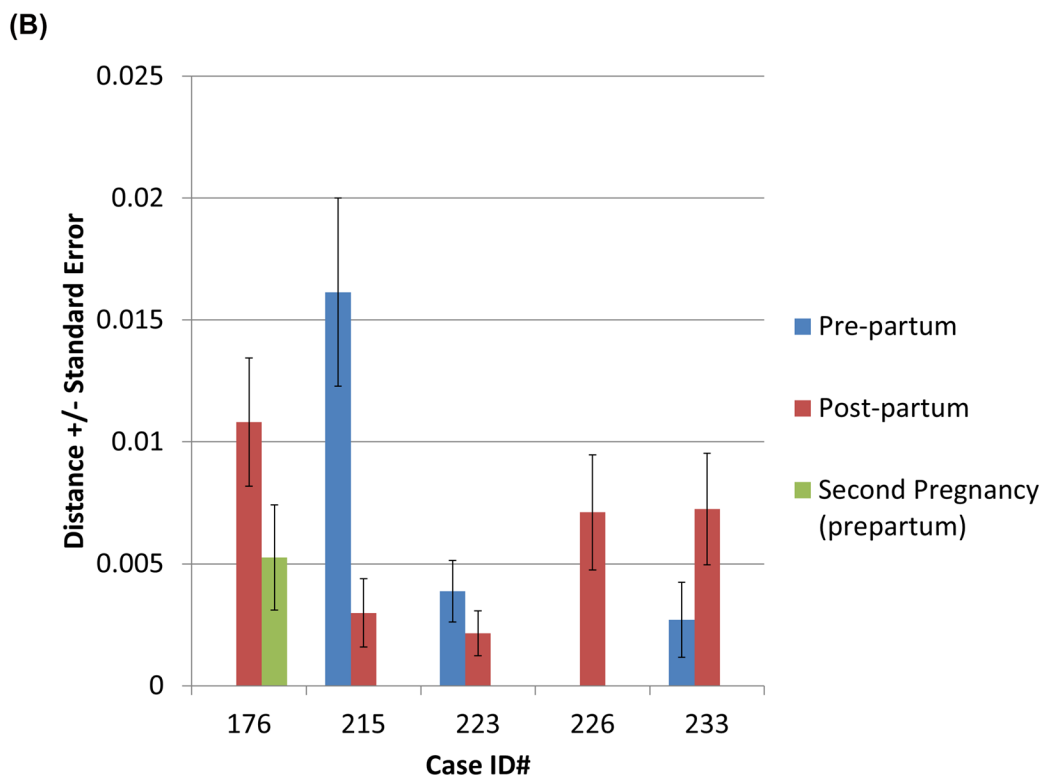
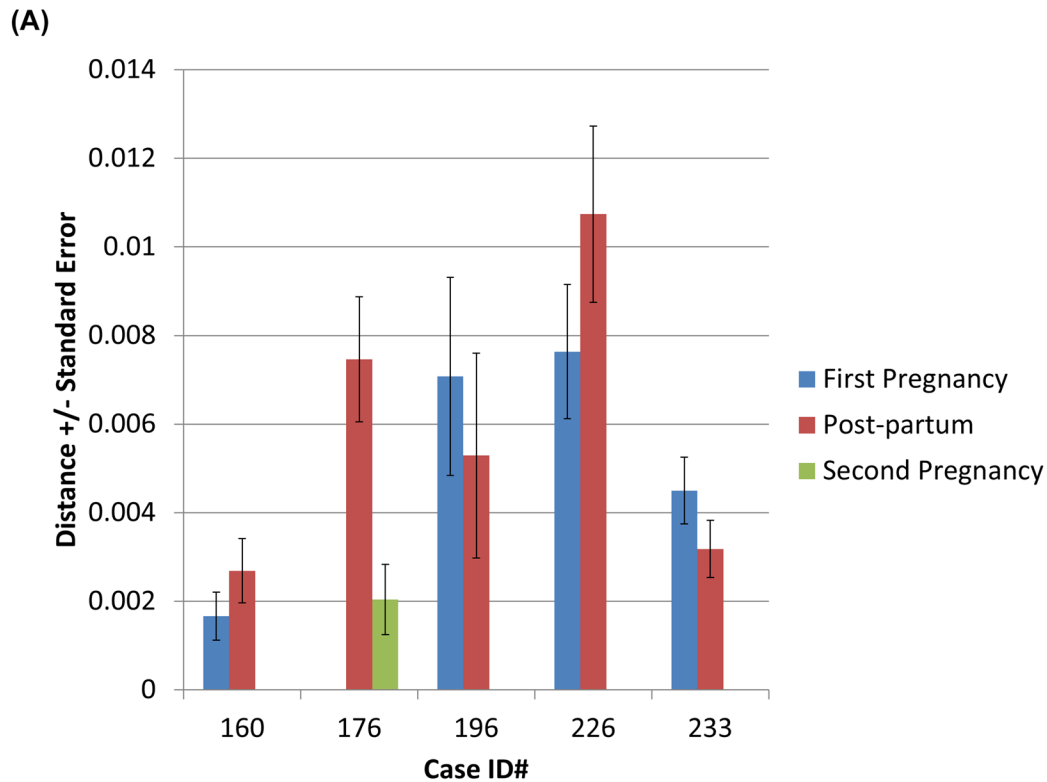


Fig 2. Comparison of distance amongst HBV quasispecies in patients during pregnancy and post-partum in pre-S/S (A, N = 5) and pre-C/C (B, N = 5) region. Measurement of distance within patient samples is shown and compared to measurement of distance within patient samples categorized by

genotype. A comparison of relative evolutionary distances of patient samples collected at different time points is shown. Measurement of HBV distance within each individual sample is shown and compared to measurement of distance within individuals categorized by genotype. A comparison of relative evolutionary distances of HBV in each sample collected at different time points is shown.

doi:10.1371/journal.pone.0145898.g002

Reference

1. Virine B, Osiowy C, Gao S, Wang T, Castillo E, Martin SR, et al. (2015) Hepatitis B Virus (HBV) Variants in Untreated and Tenofovir Treated Chronic Hepatitis B (CHB) Patients during Pregnancy and Post-Partum Follow-Up. PLoS ONE 10(10): e0140070. doi:[10.1371/journal.pone.0140070](https://doi.org/10.1371/journal.pone.0140070) PMID: [26474400](https://pubmed.ncbi.nlm.nih.gov/26474400/)