November 20th 2023

Miguel Romero comments on *Nature* Letter "The complete genome of an individual by massively parallel DNA sequencing".
Nature **volume 452**, pages 872–876 (2008) https://doi.org/10.1038/nature06884

NOTE: February 20th 2025. Both comments have been removed by *Nature*

Miguel Romero 9 years ago
Dr. Watson's genome appears to contain a 135 bp sequence belonging to the retrovirus HIV-1. This was revealed by BLASTN testing a 143 bp DNA Contig48983 whole genome shotgun sequence not present in the Human Reference Genome but present in Dr. Watson(1) against the HXB2 reference genome (Accession Numbers ABKV01048903.1 and K03455.1 respectively). BLASTN returned an alignment bearing a 126/135 (93%) identity, query cover 94%, no gaps and an expect value of 5X10-55. This sequence is nucleotides 7464-7498 in the HIV-1 env gp120/160 protein coding region and has only an infinitesimal probability of being a chance finding (2). The sequence is similar in length to another HIV-1 env product, the 142 bp DNA amplified by HIV-1 primers SK68/SK69 in breast, ovarian, prostate and other cancers (3) (Accession Number AF048844.1).

Could Dr. Watson's DNA have been contaminated by HIV-1 before or during sequencing? (4). If not does this raise the possibility that factor(s) common to aging and cancer may result in modifications in what amounts to tiny portions of human DNA?

References

1.www.ncbi.nlm.nih.gov/nuc...
2. www.hiv.lanl.gov/content/se...
3.Rakowicz-Szulczynska EM, Jackson B, Snyder W. Prostate, breast and gynecological cancer markers RAK with homology to HIV-1. Cancer Lett. Feb 27 1998;124:213-223.
4.Romero Fernandez-Bravo M. Contamination of genomic databases by HIV-1 and its possible consequences. A study in Bioinformatics.
2014. http://openaccess.uoc.edu/w...

Miguel Romero 8 years ago
https://doi.org/10.1038/nature-67241

My comment posted in November 2014 reported the presence of a 135 bp nucleotide sequence in the genome of Dr. James Watson that aligns with the 7464-7598 region of the HIV-1 *env* (gp120/160) gene. Subsequent BLASTN testing reveals additional high identity sequences between Dr. Watson's genome and the HIV-1 LTRs and p17 and p51 (reverse transcriptase) genes. On the one hand these extra data lend further weight to the possibility of contamination. However on the other hand, they may also signal cause for caution now that the CDC has altered its recommendations for HIV diagnosis. HIV immunoassays are no longer to be confirmed by Western blot analysis "and nonreactive or indeterminate on the antibody differentiation assay proceed to HIV-1 nucleic acid testing for resolution".

If contamination of DNA by HIV-1 sequences is as widespread as other data suggest, then the same may be anticipated in HIV nucleic acid testing facilities.

References

1. https://doi.org/10.1038/nature06884
2. https://goo.gl/kBmPzP
3. Branson BM, Owen SM, Wesolowski LG, Bennett B, Werner BG, Wroblewski KE, Pentella MA: Laboratory testing for the diagnosis of HIV infection: updated recommendations, Centers for Disease Control and Prevention and Association of Public Health Laboratories 2014. http://stacks.cdc.gov/view/...
4. It's time to dump the Western blot. NEJM Watch 2012. http://blogs.jwatch.org/hiv...
5. Romero Fernandez-Bravo M 2014. Contamination of genomic databases by HIV-1 and its possible consequences. A study in Bioinformatics. http://openaccess.uoc.edu/w...