



Corrigendum

Corrigendum to “Diverse RNA viruses of arthropod origin in the blood of fruit bats suggest a link between bat and arthropod viromes” [Virology 528 (2019) 64–72]

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Following e-publication of our manuscript (Bennett et al., 2019), it was brought to our attention that the hepatitis B virus (HBV) sequences reported in hammerheaded fruit bats (*Hypsignathus monstrosus*) from the Republic of Congo bear resemblance to both wild-type woodchuck hepatitis virus (WHV) and WHV post transcriptional regulatory element (WPRE) sequences incorporated into cloning vectors. To investigate this possibility, we created a 462 nt codon-based probabilistic alignment of the polymerase/X-gene overlap region of all putative bat HBVs and the most closely related WHV variant (GenBank accession number J04514), as well as the WPRE element of the most closely related cloning vector (GenBank accession number AB902850) using the PRANK algorithm (Löytynoja, 2014) implemented in Translator X (Abascal et al., 2010). Within this region, all sequences (bats, WHV and WPRE) were identical. Therefore, the putative bat HBVs are indistinguishable from both wild-type WHV and the WPRE within this region. Following this analysis we mapped raw sequencing reads to common vectors and found other reads related to pcDNA™ 3.4-TOPO® TA plasmids (Life Technologies, Carlsbad, CA, USA). Although neither laboratory involved in the

processing of these samples has used cloning vectors containing WPRE, we cannot rule out the possibility that the sequences are present as the result of contamination of reagents. The characterization of putative HBV sequences in bats should therefore be considered inconclusive pending further investigation.

References

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