**RESULTS**

*Selection Analyses*

Selection pressures were compared across species and proteins at the gene level using FUBAR (Figure 1). To enable comparison, a ratio of β to α for each dataset was computed at the gene level. A value closer to “0” suggests stronger purifying selection, while a value closer to “1” suggests stronger diversifying selection. Sometimes, higher β/α values could also imply relaxations of functional constraints, rather than more pressure to diversify.

Between species, it was observed that RVA had much stronger diversifying selection on genes for NSP4 and VP7 than other species. Likewise, RVB had much stronger diversifying selection on the gene for NSP3 than other species. On average, RVA had higher diversifying selection than RVB and RVC across both NSP genes and VP genes.

Across proteins, the average diversifying selection estimate for NSP genes was much higher than that of VP genes. Within NSP genes, the gene for NSP2 had the weakest diversifying selection while the gene for NSP4 had the highest average diversifying selection estimate. The gene for VP6 had the weakest diversifying selection across VP genes while the gene for VP7 had the highest average diversifying selection estimate.

Combining site-by-site results from MEME and FUBAR, eight codons across the three species were identified to be under both pervasive and episodic diversifying selection (Table 1). There was no common gene or codon among species that experienced both forms of diversifying selection.

*Molecular Clocks*

The evolutionary rates over time for each dataset was estimated in BEAST using sampling dates in addition to MSAs (Figure 2).

The mutation rates of the gene for VP7 were similar across all three species. However, interesting observations were made when taking other genes into account.

Between the three species, RVB had the highest average mutation rate. This could be attributed to high mutation rates in its genes for NSP1, NSP4, NSP5, VP2 and VP3.

Between proteins, the average mutation rate of NSP genes was higher than that of VP genes, but on the same order of magnitude. Across NSP genes, genes for NSP1 and NSP4 had the highest average mutations rates while the gene for NSP2 had the lowest average mutation rate. For the VP genes, the gene for VP3 had the highest average mutation rate, while genes for VP1 and VP6 had the lowest average mutation rates.

*Zoonotic Transmission*

MCC trees were reconstructed using BEAST analyses of VP7 datasets (Figures 3, 4 & 5). Phylogenies of RVB and RVC diverged between human and non-human hosts early in their evolutionary histories and showed no signs of zoonotic transmission. However, phylogeny of RVA suggests zoonotic transmission as there was no clear separation of clades for human hosts and non-human hosts. Furthermore, a few RVA branches in humans branched off from those in non-human hosts as recent as 5-6 years ago and vice versa.