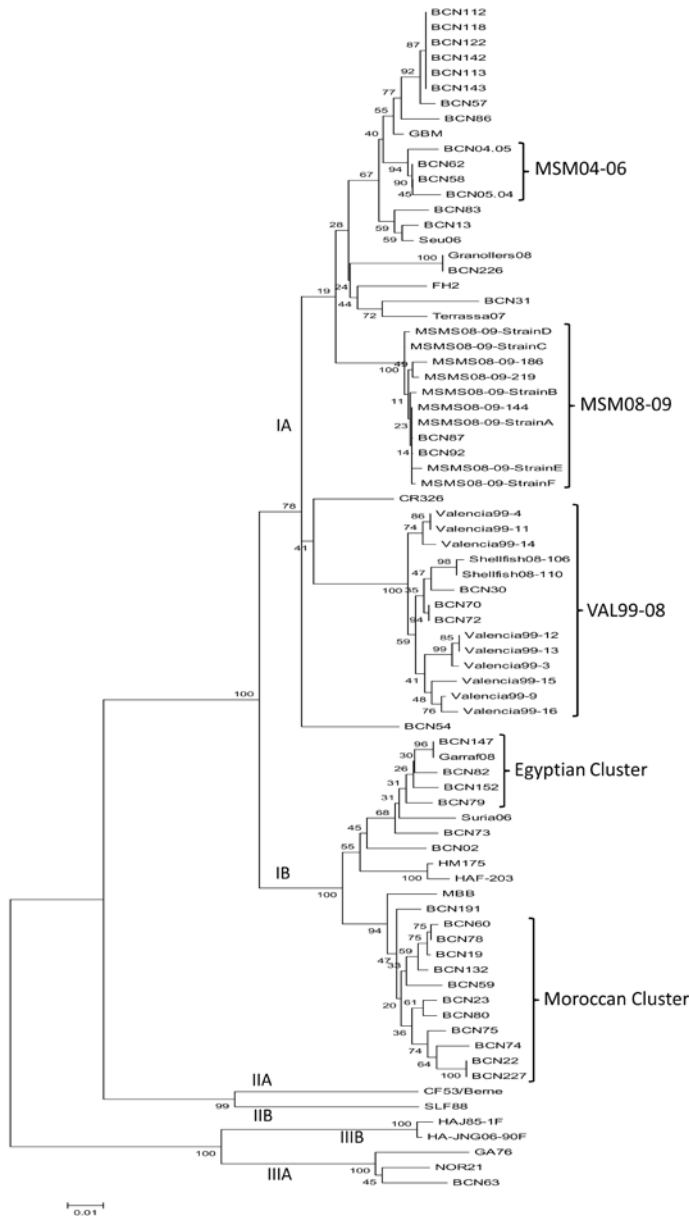
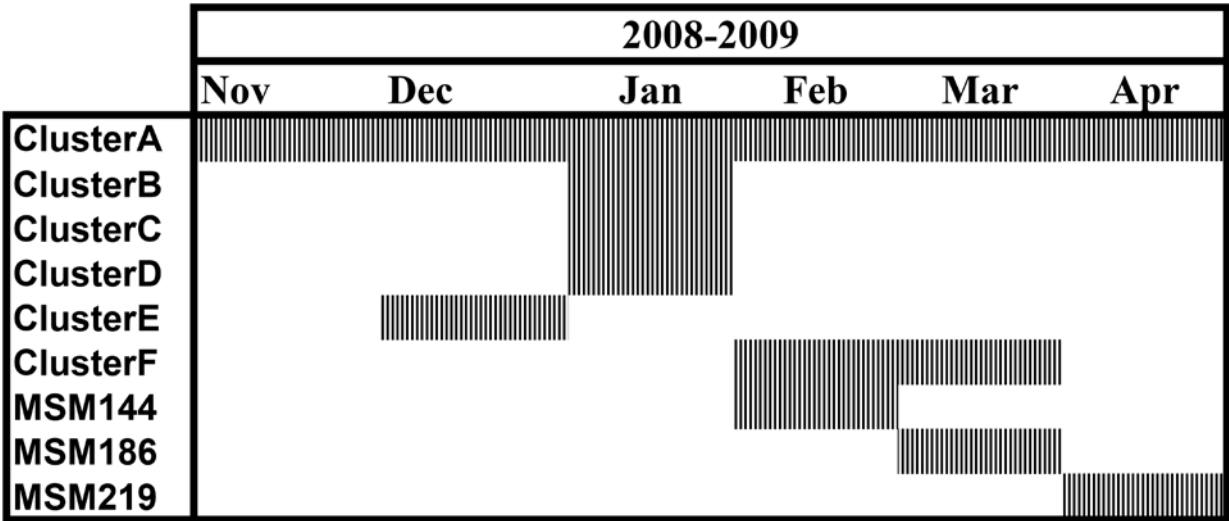


# Hepatitis A Virus Vaccine Escape Variants and Potential New Serotype Emergence

## Technical Appendix



Technical Appendix Figure 1. Phylogenetic tree based on the C-terminal fragment of viral protein 1. Neighbor-joining, Kimura 2-parameter, bootstrap 1,000 replicates (GenBank accession nos: HQ401214–HQ401267).187 × 252 mm.



Technical Appendix Figure 2. Temporal distribution of strain isolation during the 2008–2009 hepatitis outbreak among men who have sex with men (MSM). Nine distinguishable strains were isolated. Cluster E and strains MSM08-09-144, MSM08-09-186, and MSM08-09-219 are antigenic variants that evolved from the original and most abundant cluster A. 189 × 81 mm.