

Classic Human Astrovirus 4, 8, MLB-3 and likely new genotype 5 sub-lineage in stool samples of children with Acute Flaccid Paralysis (AFP) in Nigeria

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Abstract

Introduction: Acute viral gastroenteritis is a common illness especially in developing countries. Globally, the role of human astroviruses (HAstV) in gastroenteritis among children and elderly is well documented. But there exists a substantial dearth of information on HAstV strains circulating in Nigeria. **Method:** Viral like particles (VLPs) were purified from stool samples from children diagnosed with acute flaccid paralysis (AFP) between January and December 2020 from five states in Nigeria, using the NetoVIR protocol. Extracted viral RNA and DNA were subjected to a reverse transcription step, and subsequent random PCR amplification. Library preparation and Illumina sequencing were performed. Using the Virome Paired-End Reads (ViPER) pipeline, raw reads were processed into genomic contigs. Phylogenetic and pairwise identity analysis of the recovered HAstV genomes was performed. **Results:** Six near complete genome sequences of HAstV were identified and classified as HAstV 4 (n=1), HAstV5 (n=1), HAstV8 (n=1) and MLB-3 (n=3). The HAstV5 belonged to a yet unclassified sub-lineage which we tentatively named HAstV-5d. Phylogenetic analysis of ORFs 1a, 1b and 2 suggested recombination events inside the MAstV1 species. Furthermore, phylogenetic analysis implied a geographic linkage between the HAstV5 strain from this study with two strains from Cameroon across all the genomic regions. **Conclusion:** We report for the first time the circulation of HAstV genotypes 4, 8 and MLB-3 in Nigeria and present data suggestive for the existence of a new sub-lineage of HAstV5. To further understand the burden, diversity, and evolution of HAstV increased research interest as well as robust HAstV surveillance in Nigeria is essential.

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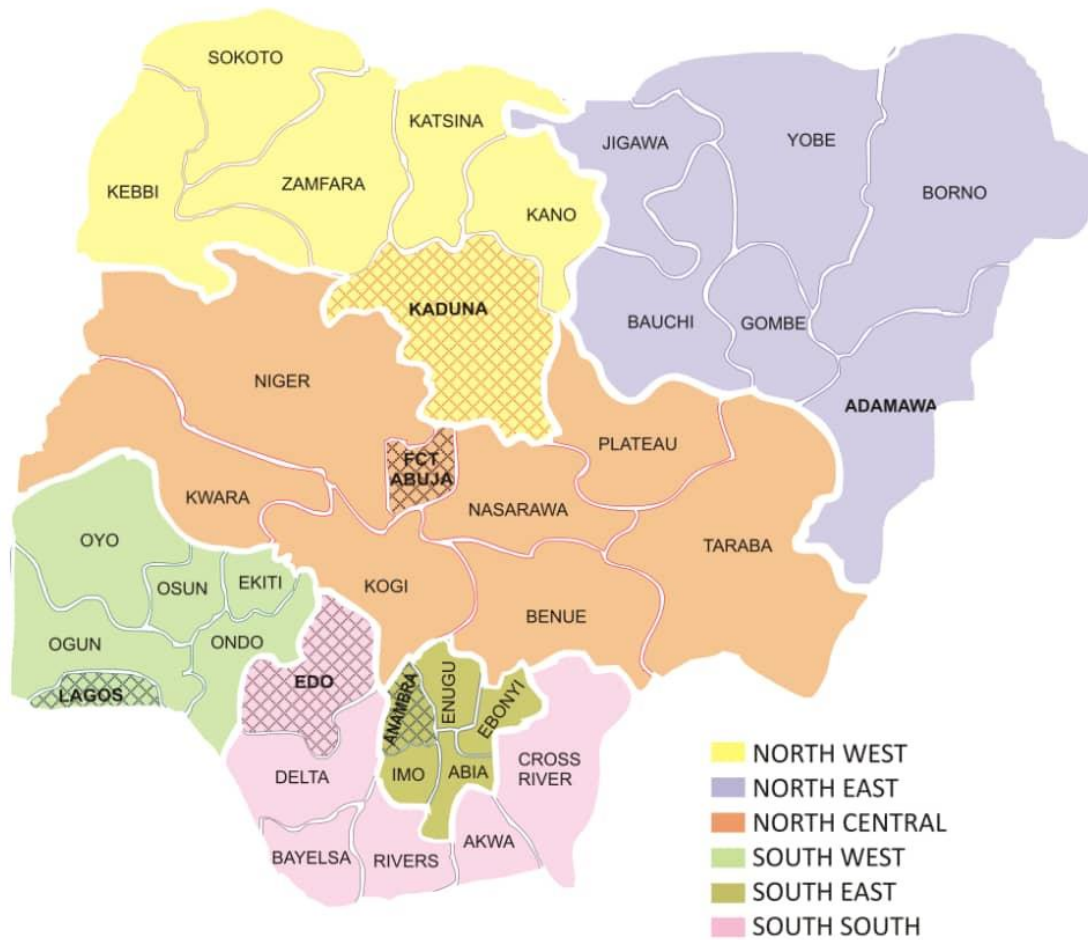


Figure 1 : Map of Nigeria showing the six geopolitical zones and indicating the states (checkedered) from where samples analyzed in this study were collected.

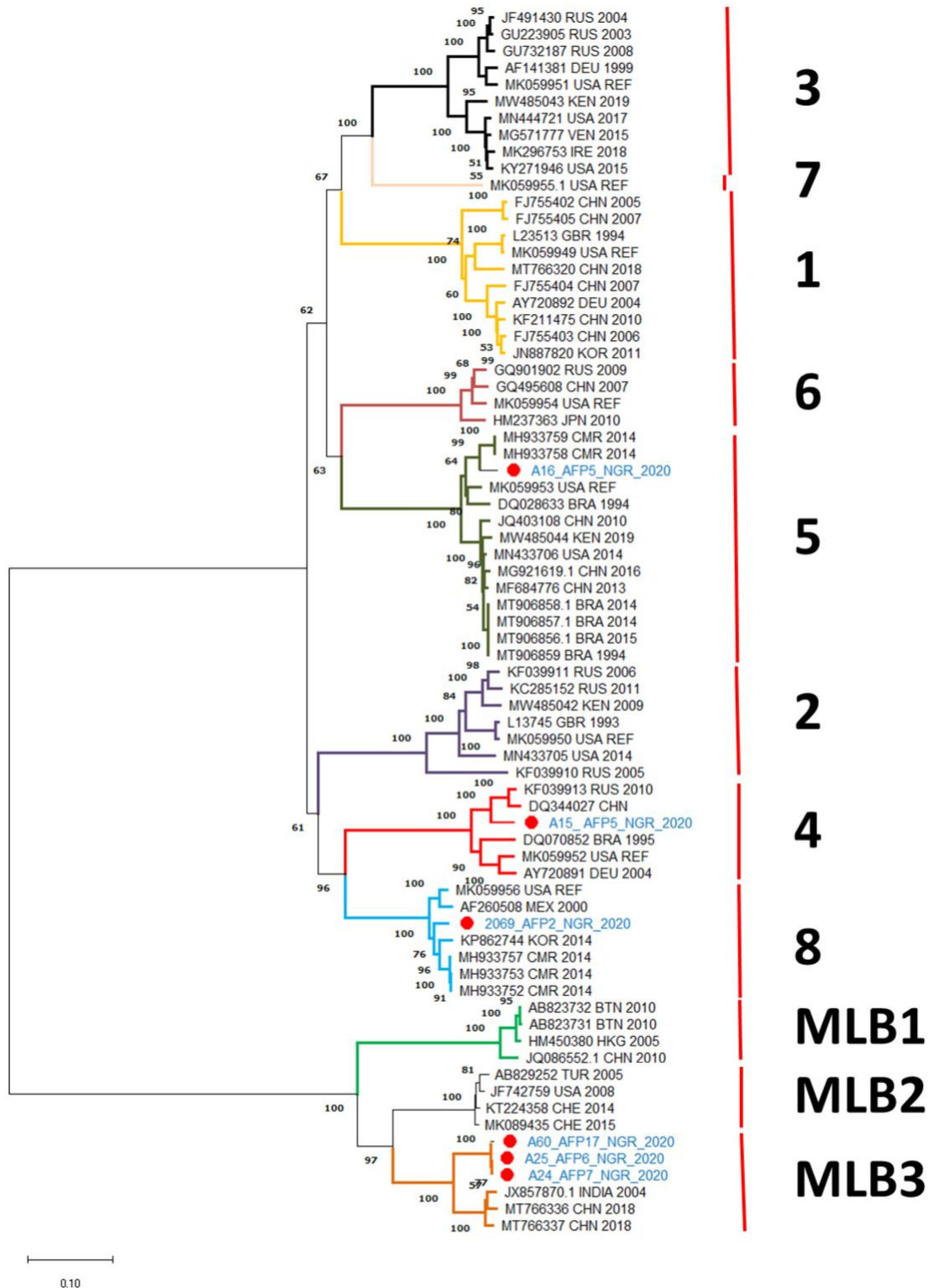


Figure 2: Phylogenetic tree of ORF2. HAdV contigs detected in this study are indicated with red circles and blue taxa labels. Bootstrap supports are shown if >50%.

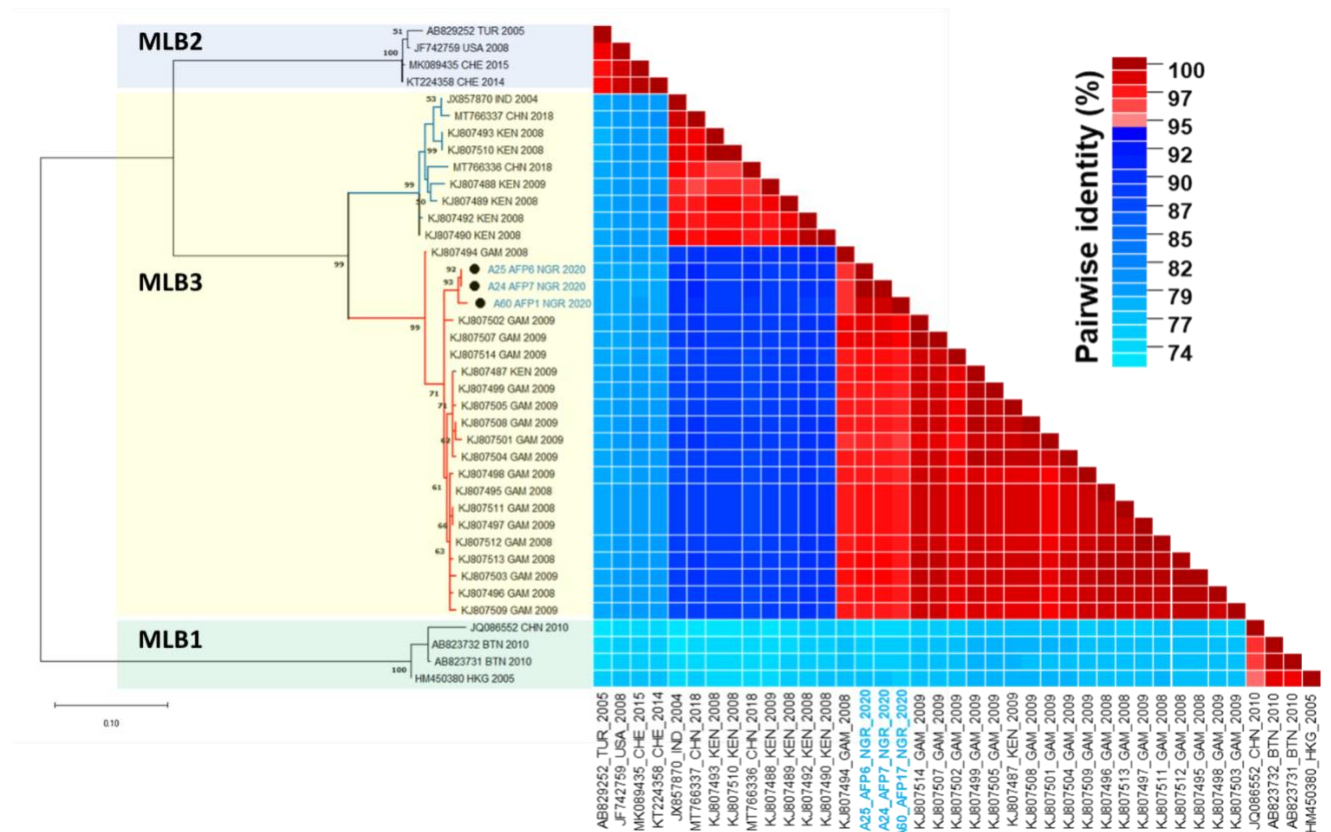


Figure 3: Partial ORF1b phylogeny and pairwise identity analysis of MLB-3 contigs detected in this study alongside others from sub-Saharan Africa. MLB-3 contigs detected in this study are indicated with blue IDs. The right side of the image shows pairwise identity as indicated.

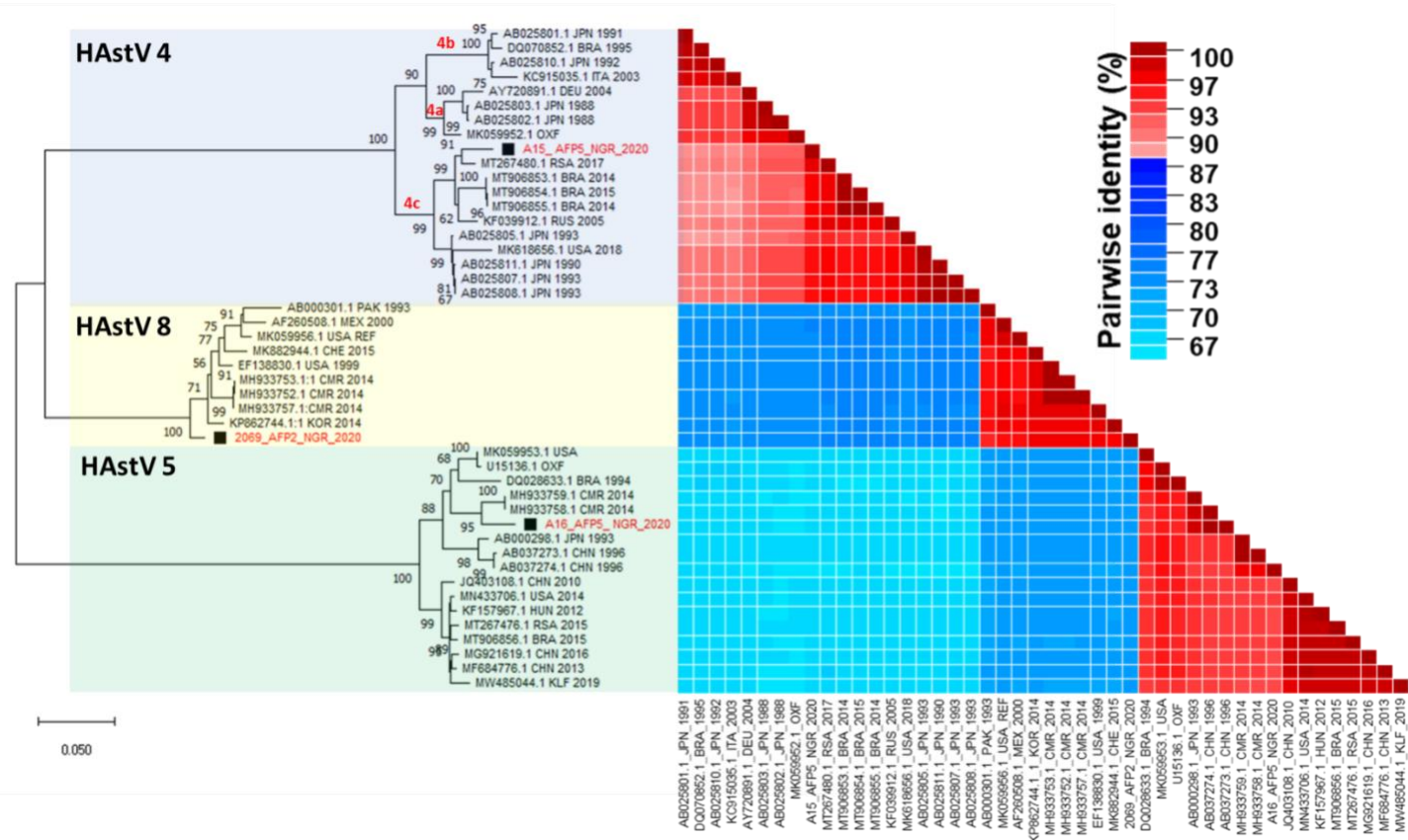


Figure 4: Sub-lineage classification of the three classical HAsV types detected in this study. HAsV contigs detected in this study are indicated with black squares.

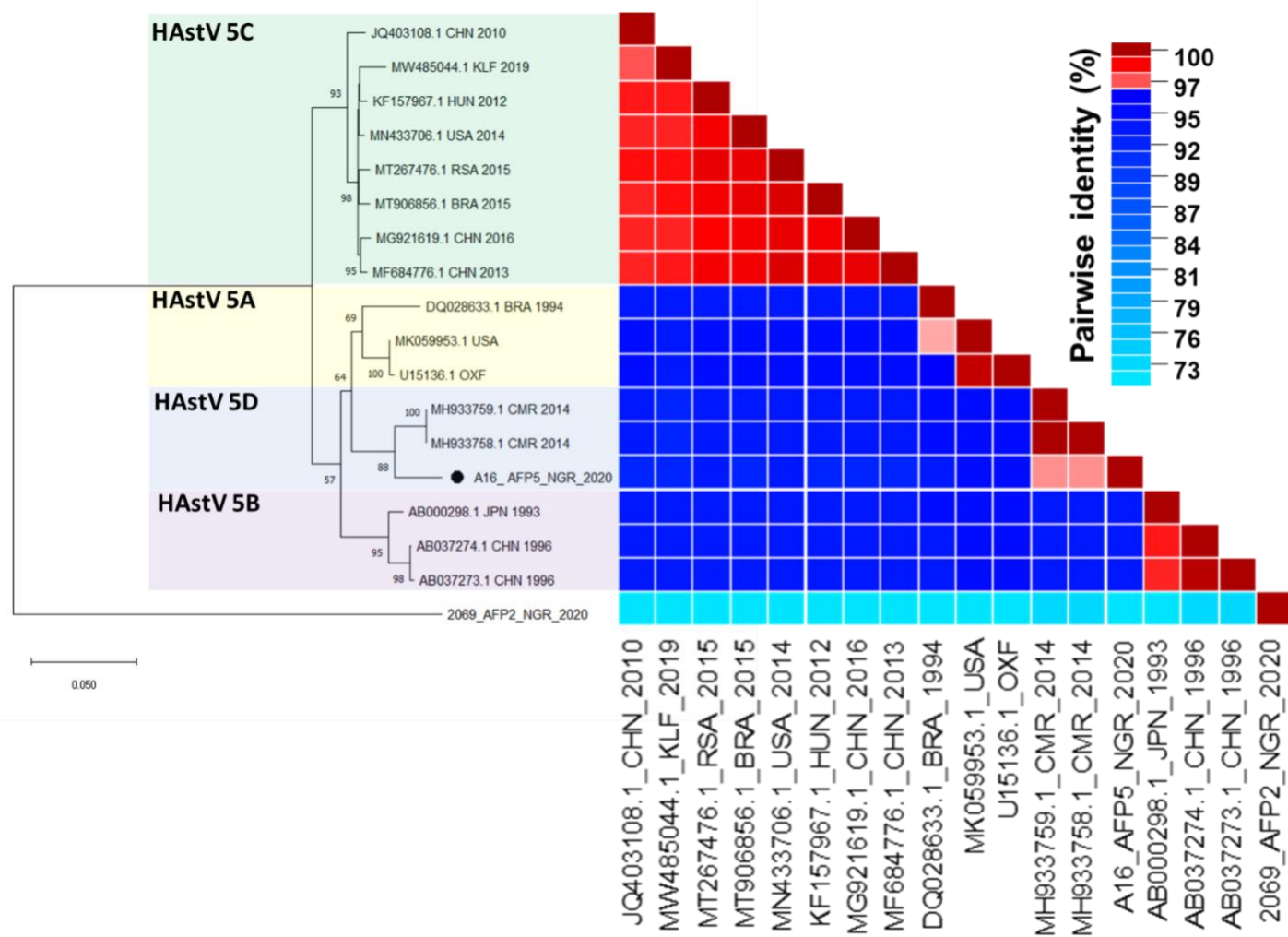


Figure 5: Sub-lineage classification of HAstV-5 showing evidence a possible new sub- lineage. HAstV-5 contigs detected in this study are indicated with black circle.

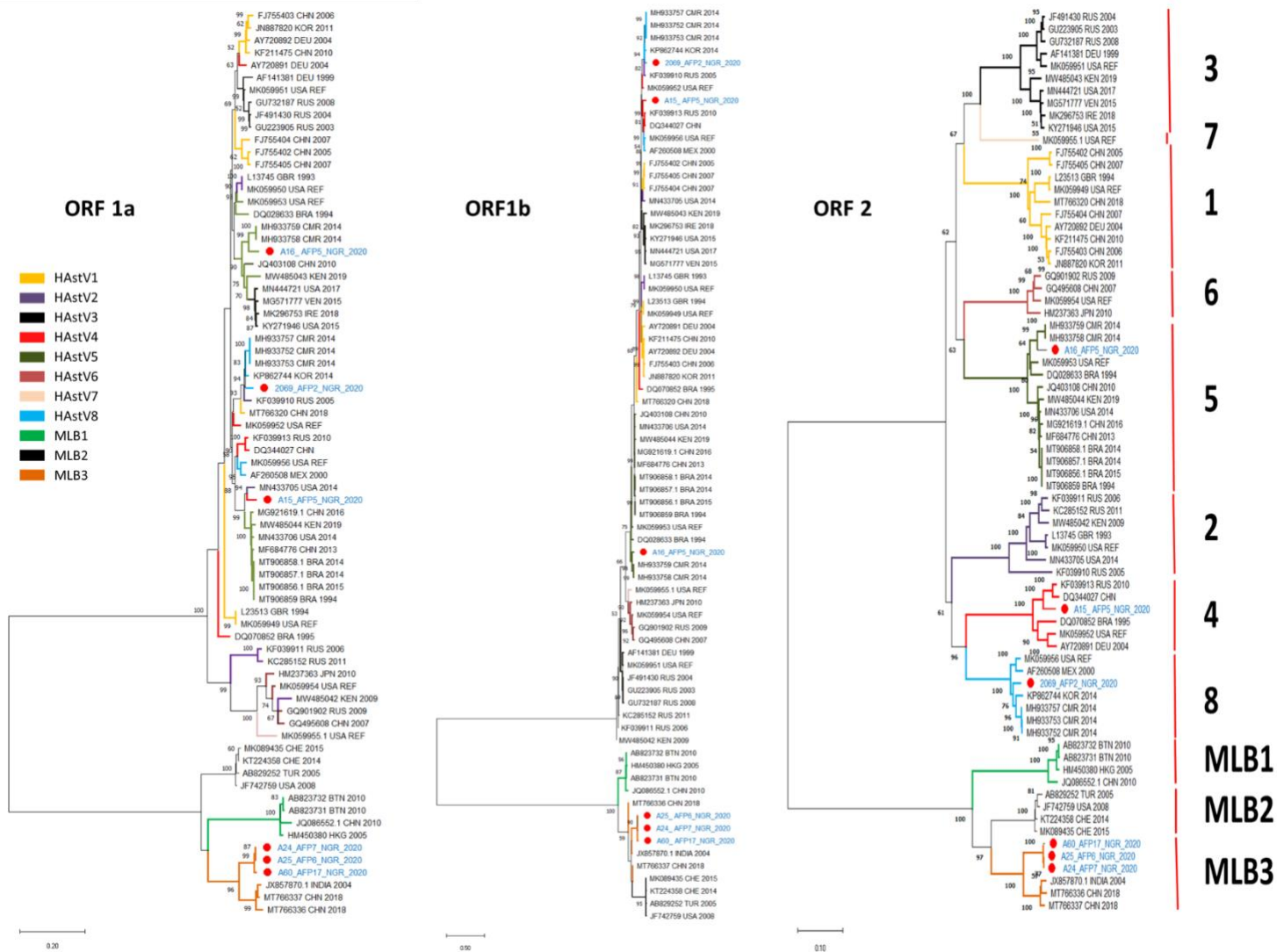


Figure 6: Phylogenetic trees of the three major ORFs in AstV genomes. The sequences described in this study are highlighted in red circles. Classification is based on ORF2 and is color-coded. Trees are arranged in accordance with the organization of the genome