

Evolution of Coxsackievirus A6: an Emerging Pathogen of Hand, Foot and Mouth Disease

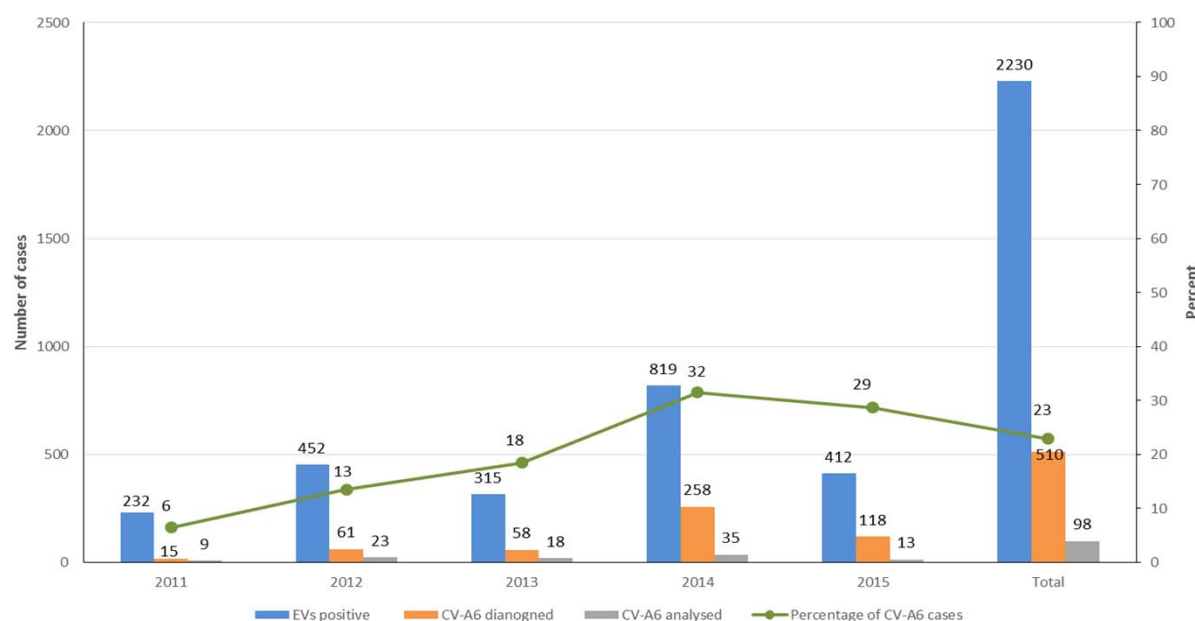
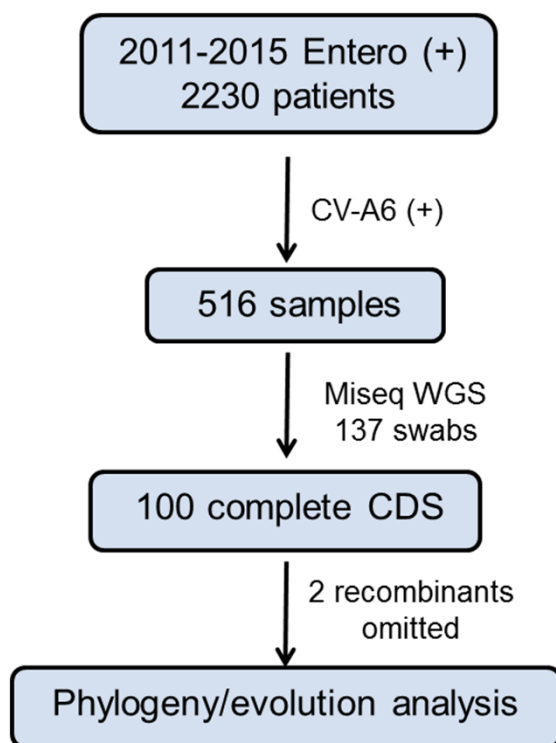


Figure 1: Temporal distribution PCR-positive HFMD cases and detection rates of CV-A6 between 2011 and 2015

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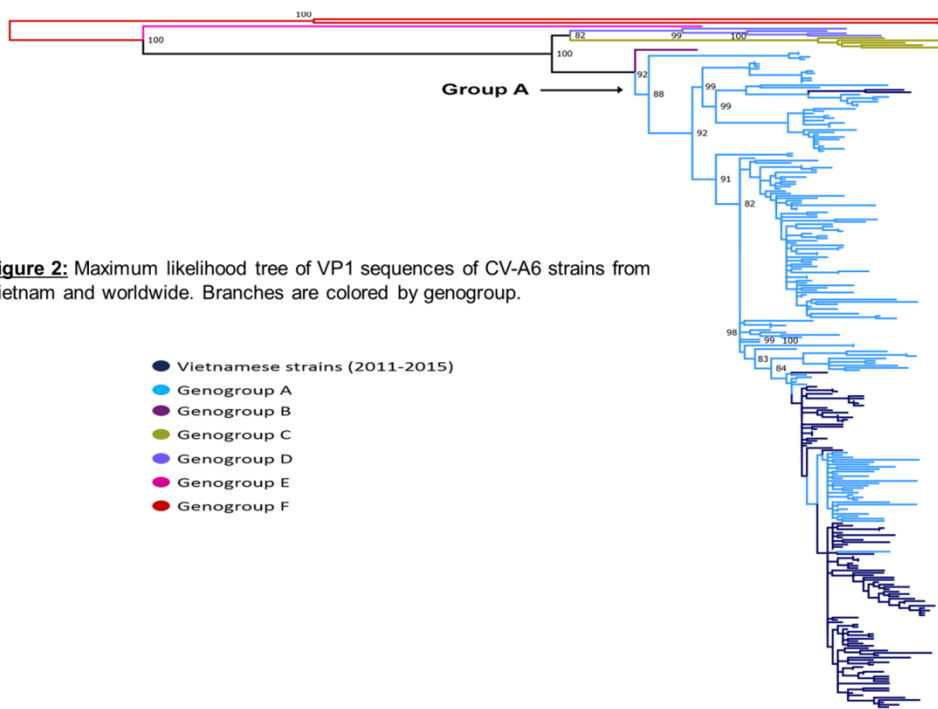


Figure 2: Maximum likelihood tree of VP1 sequences of CV-A6 strains from Vietnam and worldwide. Branches are colored by genogroup.

- Vietnamese strains (2011-2015)
- Genogroup A
- Genogroup B
- Genogroup C
- Genogroup D
- Genogroup E
- Genogroup F

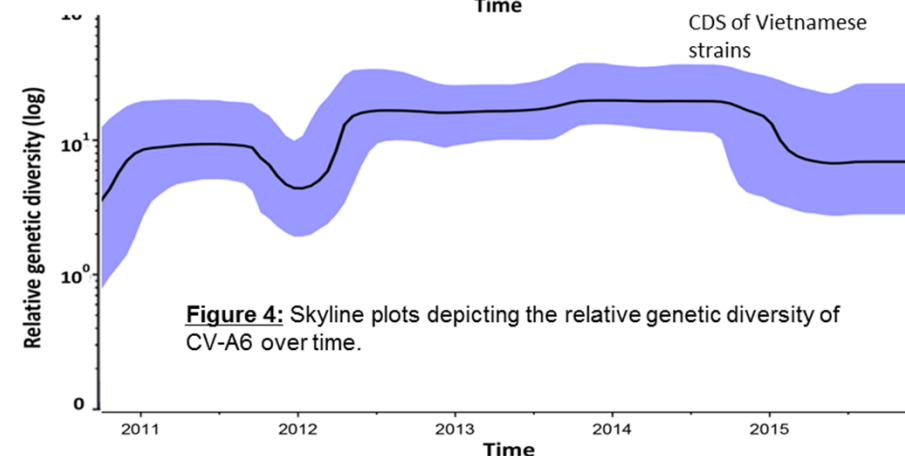
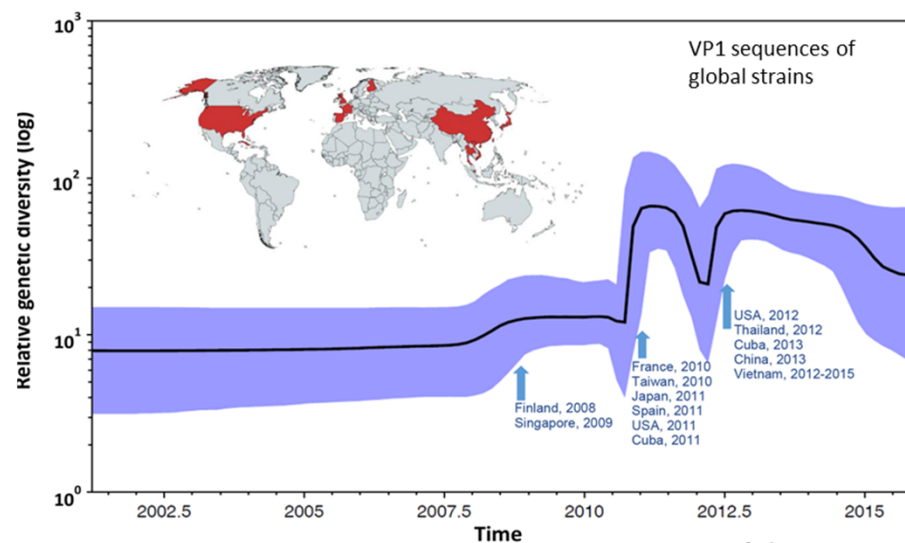


Figure 4: Skyline plots depicting the relative genetic diversity of CV-A6 over time.

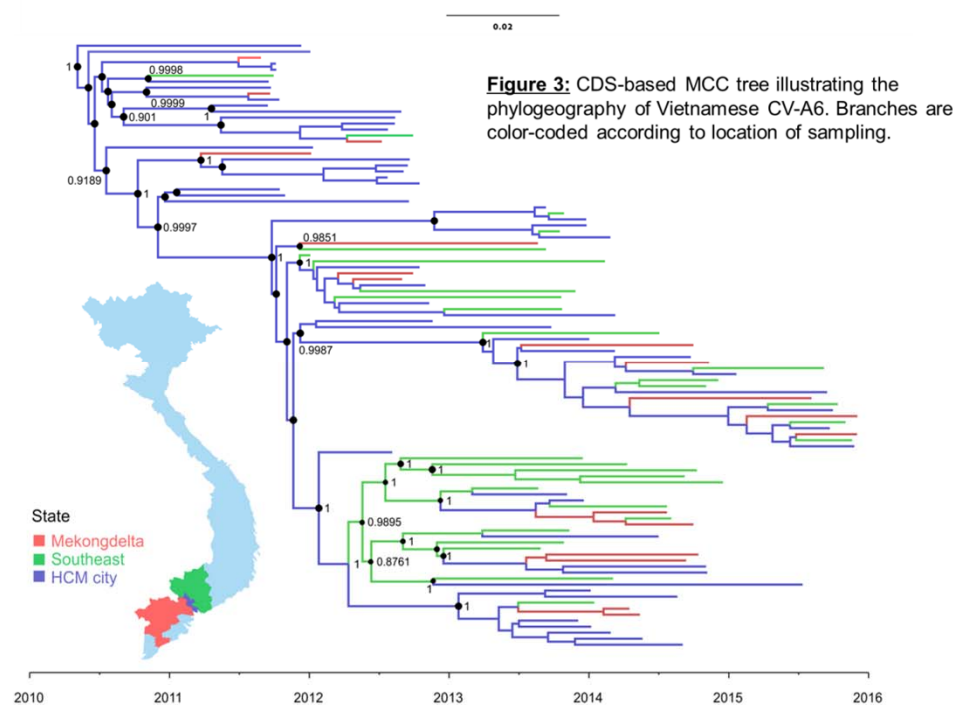


Figure 3: CDS-based MCC tree illustrating the phylogeography of Vietnamese CV-A6. Branches are color-coded according to location of sampling.

- CV-A6 has emerged and become a dominant cause of HFMD in Vietnam and worldwide.
- All isolates causing worldwide outbreaks belong to genogroup A.
- Changes in the global genetic diversity of CV-A6 strains coincided with CV-A6-associated HFMD outbreaks worldwide. But no remarkable changes in genetic diversity of Vietnamese viruses between 2011 and 2015 were observed.