Simultaneous outbreak of Dengue and Chikungunya in Al Hodayda, Yemen (epidemiological and phylogenetic findings)

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Background

Yemen, which is located in the southwestern end of the Arabian Peninsula, is one of the countries most affected by recurrent epidemics of dengue.

We conducted a study on individuals hospitalized with dengue-like syndrome in Al Hodayda, with the aim of identifying viral agents responsible of febrile illness (i.e., dengue [DENV], chikungunya [CHIKV], Rift Valley [RVFV] and hemorrhagic fever virus Alkhurma).

Methods

The study site was represented by five hospital centers located in Al-Hodayda, United Republic of Yemen. Patients were recruited in 2011 and 2012. Serum samples were analysed by ELISA for the presence of IgM antibody against DENV and CHIKV by using commercial assays. Nucleic acids were extracted by automated method and analyzed by using specific PCR for the presence of sequences of DENV, RVF virus, Alkhurma virus and CHIKV. To confirm the results, DENV positive sera underwent specific NS1 gene amplification and sequencing reaction. Similarly, CHIKV positive sera were thoroughly investigated by amplification and sequencing the gene encoding the E1 protein. The sequences were aligned using Clustal X. Maximum likelihood (ML) phylogenetic trees were estimated using appropriate models.

Results

Overall, 400 individuals were enrolled in the study. Median age was 30 (range 1-60) years. The median time interval between fever onset and sample collection was 4 days (range 2-9 days). Of the 400 study participants, 116 were lgM or PCR positive for DENV RNA. Of them, 55 were PCR positive (of 43 typed strains, 41 were DENV-2). None of the samples was positive for RVF or AHF virus. The ML tree for Dengue virus showed that Yemen isolates belonged to the lineage 2 Cosmopolitan subtype (Figure 1). All the isolates clustered in the same clade. Phylogenetic analysis for Chikungunya virus (Figure 2) showed that all the sequences form Yemen belonged to the ECSA genotype similar to the one identified in the Indian Ocean outbreak.

Fig.1

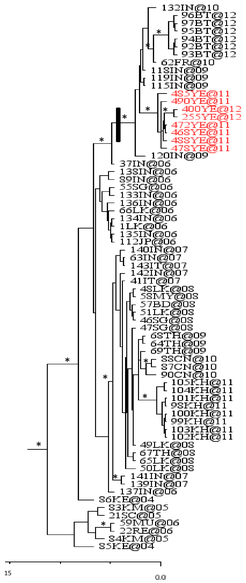
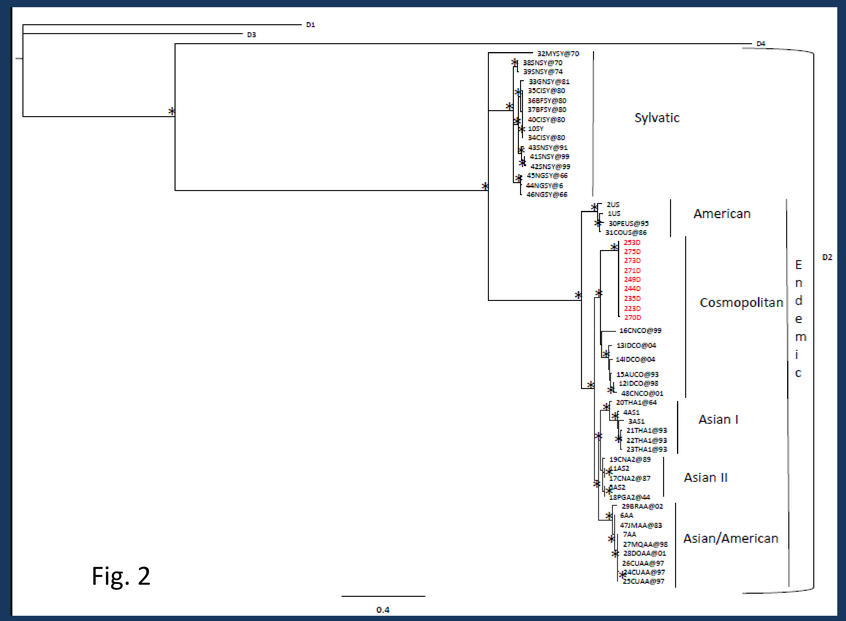


Fig. 2



Conclusions

We found co-circulation of DENV and CHIKV in the district of Al-Hodayda, Yemen, in the years 2011-2012. DENV-2 was largely predominant, with scarce circulation of other serotypes. We did not find any case of RVFV or Alkhurma in our case series.

Although climate conditions in the Middle East are not favorable for mosquitoes, increasing migration, travel, and increased urbanization, are all risk factors for the introduction and spread of these infections. Mosquito control activities are needed in order to reduce the public health impact of mosquito-borne infections in the area

References

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