A226V mutation in virus during the 2007 chikungunya outbreak in Kerala, India

N. Pradeep Kumar,1 Rajan Joseph,2 T. Kamaraj2 and P. Jambulingam1

1Vector Control Research Centre (ICMR), Indira Nagar, Pondicherry, India
2Kerala State Institute of Virology and Infectious Disease, Alappuzha, Kerala, India

Kerala State in India was gripped by a renewed and widespread outbreak of Chikungunya virus (CHIKV) infection during 2007. Here, we report the A226V mutation in the glycoprotein envelope 1 (E1) gene of the virus among isolates collected from the three worst-affected districts of the state during this outbreak. This mutation had already been suggested to be directly responsible for a significant increase in CHIKV infectivity in Aedes albopictus. The badly affected districts in Kerala State during 2007 have abundant rubber plantations, which supported prolific breeding of Ae. albopictus mosquitoes. The abundance of Ae. albopictus in the region and molecular evolution of CHIKV may be contributing factors for the renewed epidemic of chikungunya fever during 2007.

An outbreak of Chikungunya virus infection (CHIKV; 00.073.0.01.007; family Togaviridae; genus Alphavirus (ICTV, 2006)] occurred during 2006 in 15 states or union territories in India. The official number of suspected cases in the country was 1.39 million (NVBDCP, 2007). The southern state of Kerala (Fig. 1) contributed 70,731 cases during this epidemic; these cases were mostly from Alappuzha district (82.44%), while sporadic infections were recorded from other districts. Our investigation in Alappuzha revealed that the virus involved in the outbreak was of the East, Central and South African (ECSA) genotype (Kumar et al., 2007).

Since May 2007, a renewed outbreak of fever has occurred in the state, more widespread than the earlier one (NVBDCP, 2008). About 3.6 million fever cases were recorded during 2007 (11.3% of the total population of the state), compared with about 1.8 million in 2006 and 1.2 million in 2005. These fevers were classified as either viral fever, which would have included chikungunya and dengue fever, or other fevers, such as malaria and leptospirosis (Arogyakeralam, 2008). The Department of Health and Family Welfare of the Government of Kerala reported 24052 cases as suspected chikungunya fever during 2007, distributed across all 14 administrative districts of the state. The hilly and forested districts Kottayam and Pathanamthitta were the worst affected, respectively contributing 44.33 and 14.37% of the total cases. These districts are situated immediately to the east of the coastal Alappuzha district (Fig. 1), which was badly affected during 2006. However, Alappuzha district contributed only 7.70% of the total cases during 2007.
where they were processed further. Serum from these blood samples was separated by centrifugation at 6000 r.p.m. for 15 min at 4 °C. Viral RNA was isolated using the QIAamp Viral RNA Mini kit (Qiagen) following the kit protocol. A negative control was also maintained. The diagnostic non-structural protein 1 (nsP1) gene (Hasebe et al., 2002) was amplified by RT-PCR in order to identify CHIKV infection in the samples, using the Titan One Tube RT-PCR kit (Roche). Reverse transcription was carried out at 50 °C for 30 min, followed by 35 cycles of 30 s of denaturation at 94 °C, 30 s annealing at 54 °C and 90 s extension at 68 °C following a modified protocol of Hasebe et al. (2002), according to the manufacturer’s instructions (Roche). Reaction products were separated on a 1.0% agarose gel to resolve any amplified DNA fragments. Of the samples diagnosed positive for CHIKV infection, five viral RNA extractions from each of the three districts were processed further to amplify a large section (about 900 bp) of the phylogenetically informative glycoprotein envelope 1 (E1) gene (Schuffenecker et al., 2006; Kumar et al., 2007). The amplified E1 gene was sequenced and cDNA sequences were aligned using CLUSTAL W software. Phylogenetic analysis was performed using MEGA4 software (Tamura et al., 2007) including E1 sequences of all three genotypes of CHIKV (from GenBank) and those of isolates from the 2006 outbreak in India. The neighbour-joining (NJ) method was followed using Kimura two-parameter (K2P) genetic distances (Kimura, 1980) to deduce the phylogenetic tree. The interior branch test was carried out using 1000 replications to examine the statistical significance of the branching pattern.

Of the 33 serum samples processed, 24 (seven, 12 and five, respectively, from Alappuzha, Pathanamthitta and Kottayam districts) were found to be positive for CHIKV infection (Supplementary Table S1). These yielded DNA fragments corresponding to 354 bp of the nsP1 gene, while no amplification products were observed in negative samples. The size of the amplified E1 DNA fragments of 15 isolates ranged from 891 to 957 bp. The region of E1 that was common to all these fragments (834 bp) corresponded to positions 10264–11097 of the genome of CHIKV strain LR2006_OPY1 (GenBank accession no. DQ443544).

The NJ phylogenetic tree constructed based on sequences of the E1 gene is given in Fig. 2. There was not much genetic variability (K2P genetic distance 0.001) among the 15 isolates obtained in 2007 from different districts of Kerala. The genetic distance between these isolates from Kerala and isolates from the island of Réunion (Schuffenecker et al., 2006) was only 0.003, thus denoting them to be of the ECSA genotype, closely related to CHIKV involved in the Réunion outbreak. However, the Asian and West African (WA) genotypes of CHIKV were clearly

Fig. 1. Map of Kerala State, India, showing the study area and locations of hospitals (indicated by numbers 1–5) from where samples used in the study were collected.
different from the Kerala isolates, with respective genetic distances of 0.058 and 0.171. Comparison of the sequences of the E1 gene showed that all 15 virus isolates from Kerala in 2007 had the non-synonymous mutation C/T at position 10670 of the E1 gene, resulting in a change from alanine to valine at position 226 of the deduced protein sequence (Fig. 3).

This is the first report of the A226V mutation in the E1 gene from CHIKV in India. Another non-synonymous mutation, D284E, recorded during the present investigation among 2007 isolates, was also observed among isolates from various regions of the country during 2006 (Kumar et al., 2007; Arankalle et al., 2007). Mutations A226V and D284E had been reported previously during the renewed circulation of CHIKV on Réunion in 2006, affecting about 30 % of the entire population of the island. During the initial outbreak on Réunion, both of these mutations were absent (Schuffenecker et al., 2006). This study therefore indicates that the virus may be undergoing similar microevolutionary changes in Kerala.

The A226V mutation had been proposed to provide cholesterol-independence to a Semliki Forest virus population (Vashishtha et al., 1998). Schuffenecker et al. (2006) proposed that this mutation might provide a selective advantage to the virus in mosquitoes, which are cholesterol auxotrophs. Recently, Vazeille et al. (2007) have reported a higher efficiency of replication and dissemination in the vector species *Aedes albopictus* for CHIKV with the A226V mutation, and Tsetsarkin et al. (2007) have proved that this mutation is directly responsible for CHIKV adaptation to *Ae. albopictus* mosquitoes.

Entomological investigations carried out during the 2006 outbreak of chikungunya in Kerala recorded high population densities of *Ae. albopictus* in affected areas as well as
in areas not affected by the disease (WHO, 2006). The worst affected districts in Kerala during the 2007 outbreak, Kottayam and Pathanamthitta, are hilly and heavily forested, with vast rubber plantations [109 582 ha (the largest area in the state) in the former district and 61 016 ha in the latter]. Ae. albopictus breeds profusely in rainwater that collects in the hemispherical containers fitted to the trunks of rubber trees for latex collection in the region (National Informatics Centre, Government of India, 2008; NVBDCP, 2008). The role of this mosquito species in the transmission of dengue fever has already been documented (Sumodan, 2003; NVBDCP, 2008). Surveys of immature mosquitoes carried out by the VCRC during June 2007 in the districts of Alappuzha and Kottayam showed that Ae. albopictus constituted 85–92 % of the total mosquito larvae/pupae collected. Only 0–3.6 % of the total larvae/pupae belonged to Aedes aegypti. In another survey, carried out in Alappuzha, Kottayam and Pathanamthitta districts during July 2007, Ae. albopictus was recorded to make up 58–76 % of the larvae/pupae collected, while Ae. aegypti represented only 2–17 % (VCRC, unpublished reports). These reports show that Ae. albopictus was the predominant mosquito species in the region during the renewed chikungunya outbreak.

It is clear that there was an upsurge in fever cases in Kerala during 2007 compared with previous years (Aroguyakeralam, 2008). During 2007 there was a peak of cases of fever at the beginning of the outbreak, in May–June 2007 (Supplementary Fig. S1). A similar trend was recorded in suspected cases of chikungunya fever (Supplementary Fig. S2). It may be presumed that most fever cases went undiagnosed owing to the lack of infrastructure in the state to handle such a large number of fever cases and were grouped as viral fever, which may likely include more chikungunya fever cases than were officially reported.

We conclude that the molecular evolutionary adaptation acquired by CHIKV as a result of the A226V mutation in the E1 gene and the high population density of Ae. albopictus in the region may have contributed to the widespread and renewed chikungunya fever epidemic in Kerala during 2007.

Acknowledgements

The investigators are grateful to Dr M. Kalyanasundaram, Officer-in-Charge, Vector Control Research Centre (VCRC), for his encouragement to take up the study. We also thank Mr N. Krishnamoorthy and Mr P. M. Ajithlal, VCRC, for technical assistance.

References


