Persistent global transmission of chikungunya from India

Context

- Studying the geographic distribution and evolution of the chikungunya virus over the period from 2005-2018, a team from ICMR-National Institute of Virology, Pune, has noted India as an endemic reservoir for the virus with persistent global transmissions from the country.
- The paper published recently in Infection, Genetics and Evolution adds that “dispersal of the strains from India was noted to neighbouring and distant countries” such as Sri Lanka, Bangladesh and China.
- The team studied newly sequenced chikungunya viruses isolated during outbreaks that happened between 2014 and 2018. During these years, the virus showed activity in India. Karnataka, Maharashtra and New Delhi accounted for a majority of the cases.

Indian Ocean lineage

- The whole-genome sequencing study revealed that the isolates belonged to the Indian subcontinent sub-lineage of the Indian Ocean lineage.
- The Indian Ocean lineage is a subgroup within the East Central South African genotype.
- It was responsible for the resurgence in the epidemic on La Reunion island and other neighbouring islands in the Indian Ocean and in the Indian sub-continent during 2004-2005.
- This study helped understand the overall evolution and epidemiology of the Indian Ocean lineage.
- Analyses of about 207 whole genomes, including the eleven whole genomes of this study and 39 additional whole genomes from India, showed two separate clusters of Indian Ocean islands sub-lineage and Indian subcontinent sub-lineage.
- It is already known that Kenya was the most likely ancestral location for both the sub-lineages, and the study further confirmed this.

Spread from clusters

- Observations from the phylogeography study (Phylogeography is the study of the historical processes that may be responsible for the contemporary geographic distributions of individuals) based on the genome sequences over the period from 2005 to 2018, showed persistent global transmissions from India.
- The strains from these clusters were noted to have spread to China, Sri Lanka, Bangladesh, and Southeast Asian countries including Indonesia, Malaysia, Singapore and Papua New Guinea beyond mid-2006.
- Transmissions to Yemen, China, Japan, Hong Kong, Pakistan, Australia, Bangladesh and Italy were also noted later on.
- Further studies of the chikungunya sequences revealed indigenous evolution in India at least at three time points over the period 2005-2018, with specific mutations that conferred viral fitness in the Aedes vector species.
- There is a possibility of further diversification as this is an RNA virus and continues to acquire mutations.