MAPPING CHANDIPURA VIRUS GENOME: SCIENCE & TECHNOLOGY

News: *The Gujarat Biotechnology Research Centre (GBRC) in Gandhinagar has achieved a significant milestone by successfully publishing the first fully mapped genome of the Chandipura Vesiculovirus (CHPV). This virus is known for causing encephalitis, a condition characterized by brain swelling. The mapping comes in the wake of a substantial outbreak that affected numerous individuals in Gujarat during July and August, highlighting the critical importance of this research in understanding and combating the virus effectively.*

What's in the news?

Genome Mapping

- **Definition and Process**: Genome mapping involves identifying gene locations and key sequences within a genome, providing insights into the origins, mutations, and potential dangers of viruses.
- **Types of Genome Maps**:
  - **Genetic Maps**: Display gene positions based on recombination frequencies.
  - **Physical Maps**: Indicate exact gene positions using DNA base pairs.

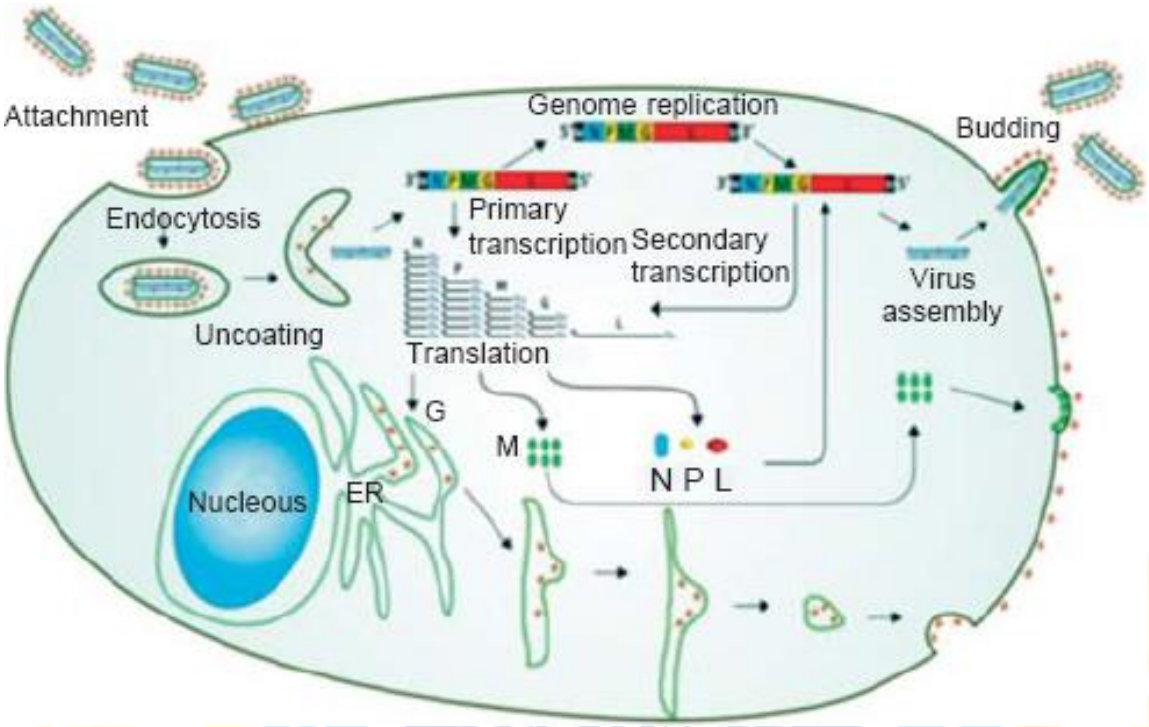
Importance of Genome Mapping

- **Medical Advancements**: Facilitates the early detection of genetic diseases, aids in creating personalized medical treatments, and enhances genetic counseling effectiveness.
- **Agricultural Benefits**: Helps in breeding programs by identifying traits that enhance yield, disease resistance, and quality in crops and livestock.
- **Virus Research**: Essential for developing vaccines by analyzing the genomic structures of pathogens, such as those causing COVID-19 and Chandipura virus (CHPV).
- **Evolutionary Biology**: Provides insights into the evolutionary relationships among species by analyzing genetic sequences.

Challenges in Genome Mapping

- **Complexity in Larger Genomes**: Genomes of plants and animals can be complex and repetitive, complicating precise mapping efforts.
- **Privacy and Ethical Concerns**: Issues arise over the use and access to genetic information.

- **Resource Intensity**: Requires significant financial and technological investment, with ongoing challenges in interpreting the relevance of various genes and sequences.



Specific Findings from GBRC's Genome Mapping of CHPV

- **Genetic Stability**: The CHPV strain from a recent outbreak in Gujarat shows minimal genetic variation from the 2012 strain, except for a single mutation in the glycoprotein-B gene, crucial for the virus's interaction with human cell receptors.
- **Impact Despite Low Viral Load**: Despite low viral load indicated by high Cycle Threshold values in RT-PCR tests, the virus caused severe symptoms.
- **Indigenous Strain Confirmation**: Sequencing confirms that the current strain is similar to those identified in previous outbreaks within India (2003-04, 2007), distinct from strains outside India, indicating no external introduction.

Chandipura Virus

- **Nature of the Virus**: Chandipura virus is an infectious agent known to cause Acute Encephalitis Syndrome (AES), which can lead to severe brain swelling and is potentially lethal.
- **Symptoms and Impact**: It manifests as fever, headache, and encephalitis, leading to severe neurological symptoms like convulsions, coma, and often death within days after the onset.

Transmission Vectors

- **Virus Classification**: The Chandipura virus is part of the Rhabdoviridae family, akin to the rabies virus.

- **Vectors**: The virus is transmitted to humans through bites from Phlebotomine sandflies and Phlebotomus papatasi, with Aedes aegypti mosquitoes also serving as carriers.
- **Infection Mechanism**: It resides in the salivary glands of these vectors and infects vertebrates via bites.

Progression and Clinical Presentation

- **Infection Spread**: Post-bite, the virus rapidly invades the central nervous system, causing encephalitis characterized by brain inflammation.
- **Symptomatology**: Initial symptoms include flu-like effects, progressing to more severe conditions such as altered mental status, seizures, respiratory issues, and bleeding tendencies.
- **Disease Course**: The progression is swift, typically resulting in fatality within 24-48 hours post-hospitalization.

Demographics and Epidemiology

- **High-Risk Group**: Mainly affects children under the age of 15.
- **Seasonality**: Peaks during monsoon seasons when sandfly populations increase, leading to more frequent outbreaks.

Historical Data and Epidemiological Patterns

- **Discovery**: Identified in 1965 during investigations for dengue and chikungunya in Maharashtra, India.
- **Notable Outbreaks**: Significant outbreaks were recorded in 2003-2004 in Maharashtra, northern Gujarat, and Andhra Pradesh, with over 300 child fatalities.
- **Case Fatality Rates**: Notably high fatality rates, with 78% during the Gujarat outbreak in 2004 and 55% in Andhra Pradesh in 2003.
- **Endemic Areas**: The virus remains endemic in central India, predominantly affecting rural, tribal, and peripheral regions where vector populations are dense.

Source: https://indianexpress.com/article/explained/explained-health/genome-mapping-chandipura-virus-9550092/