

Chandipura Virus Genome Mapping: Key Findings and Impact on Healthcare

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What's in today's article?

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- Key Findings from GBRC's Genome Mapping of CHPV

Why in News?

The Gujarat Biotechnology Research Centre (GBRC) in Gandhinagar has successfully published the first fully mapped genome of the Chandipura Vesiculovirus (CHPV).

This virus is responsible for causing encephalitis or brain swelling, which accounted for a significant portion of cases during the outbreak in Gujarat in July-August.

Genome mapping

- **About**

- Genome mapping refers to the process of identifying the locations of genes and important sequences on a genome.
- Genome mapping provides important clues on where a virus comes from, how it is changing, and whether it has any mutations that are likely to make it more transmissible or deadly.
- Genome maps are of two types:
 - **genetic maps**, which show the relative positions of genes based on recombination frequency, and
 - **physical maps**, which show the absolute positions of genes based on DNA base pairs.

- **Significance**

- **Understanding Genetic Disorders:** Genome mapping helps identify genes associated with genetic diseases, facilitating early diagnosis, targeted treatment, and genetic counseling.
- **Personalized Medicine:** Mapping can lead to customized treatment plans based on an individual's genetic makeup, improving the effectiveness of therapies.
- **Agriculture:** In crops and livestock, genome mapping allows the identification of desirable traits, aiding in breeding programs for higher yield, disease resistance, and quality.
- **Vaccine and Drug Development:** Understanding the genomic structure of pathogens like viruses helps develop effective vaccines and drugs, as seen in the fight against infectious diseases like **COVID-19** and CHPV.
 - **Evolutionary Studies:** Genome maps provide insights into evolutionary relationships between species by comparing genetic sequences across organisms.

- **Challenges**

- **Complexity of Genomes:** Larger genomes, such as those in plants and animals, are highly complex and contain repetitive sequences, making accurate mapping difficult.
- **Ethical Concerns:** Genome mapping can raise privacy and ethical issues, especially regarding how genetic information is used and who has access to it.
- **Cost and Resources:** Although costs have reduced, genome mapping, particularly for large-scale projects, still requires significant financial investment and technological resources.
- **Data Interpretation:** Even after mapping, interpreting the significance of various genes and sequences remains a challenge due to gaps in our understanding of their functions.

Chandipura

- **About**

- Chandipura is a viral infection that can lead to outbreaks of Acute Encephalitis Syndrome (AES) or brain swelling.
- It is known to cause fever, headache, and encephalitis leading to convulsions, coma, and death, usually within a few days of the symptoms showing up.

- **Family and Vectors**

- Chandipura virus (CHPV) belongs to the ***Rhabdoviridae family***, which includes viruses like the lyssavirus (rabies).
- Several sandfly species, such as ***Phlebotomine sandflies*** and ***Phlebotomus papatasi***, along with *Aedes aegypti* mosquitoes (also responsible for dengue), act as vectors.
- The virus resides in the salivary glands of these insects and is transmitted to humans or other vertebrates through bites.

- **Transmission and Progression of Infection**

- Once transmitted, CHPV can spread to the central nervous system, leading to encephalitis (brain inflammation).
- Symptoms begin with flu-like signs such as fever, body aches, and headaches, and may escalate to altered mental status, seizures, and encephalitis.
- Other symptoms may include respiratory distress, bleeding tendencies, or anemia.
- The infection often progresses rapidly, leading to death within 24-48 hours of hospitalization.

- **Most Affected Population**

- The **virus** predominantly affects children under 15 years of age.
- The infection tends to be seasonal, with outbreaks often reported during periods when the sandfly population increases, particularly in monsoon seasons.

- **Historical Outbreaks and Endemic Regions**

- CHPV was first identified in 1965 during a dengue/chikungunya investigation in Maharashtra.
- Significant outbreaks occurred in 2003-2004 in Maharashtra, northern Gujarat, and Andhra Pradesh, resulting in over 300 deaths among children.
- The case fatality rate (CFR) during the 2004 Gujarat outbreak reached 78%, while Andhra Pradesh reported a CFR of 55% in 2003.
 - The infection remains endemic in central India, where the vector population is more concentrated.
 - Outbreaks are most commonly reported in rural, tribal, and peripheral areas.

Key Findings from GBRC's Genome Mapping of CHPV

- **No Major Change in Genetic Makeup**

- The CHPV virus from the recent Gujarat outbreak is highly similar to the 2012 strain, with only a single amino acid mutation in the glycoprotein-B gene.
- This gene is crucial for the virus's ability to bind to human cell receptors and trigger an immune response.
 - Unlike COVID-19, the virus has not needed to change much, possibly due to low population-wide antibody development and the absence of a vaccine.

- **Low Viral Load but Severe Impact**

- Despite the high Cycle Threshold (Ct) value in RT-PCR tests, indicating a low viral load, the virus still caused severe symptoms.

- **Indigenous Virus, Not Imported**

- Genome sequencing revealed that the current virus strain is closely related to those from previous Indian outbreaks in 2003-04 and 2007.
 - The virus was not imported from abroad and is distinct from strains found in Europe and Africa, confirming that it is circulating within India.
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Q.1. What is genome mapping, and why is it significant for healthcare?

Genome mapping helps locate genes on a genome, offering insights into virus mutations and aiding vaccine development, as seen in the Chandipura virus case.

Q.2. What were the key findings from the Chandipura virus genome mapping?

The Chandipura virus from the Gujarat outbreak closely resembled earlier strains, with minimal genetic changes, highlighting its low mutation rate.

Source: [Genome mapping of Chandipura virus: what researchers found | Indian Express](#)

Source: <https://vajiramandravi.com/current-affairs/chandipura-virus-genome-mapping/>

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