Nipah PCR Forward Primer Matches Human Genome—A Built-In Pathway to False Positives as Media Hypes 'Deadly Outbrea…

1 message

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Nipah PCR Forward Primer Matches Human Genome—A Built-In Pathway to False Positives as Media Hypes 'Deadly Outbreak'

Are PCR tests showing positive results for human genetics, not Nipah?

JON FLEETWOOD

JAN 26

Mainstream outlets are amplifying alarm over an alleged Nipah virus outbreak in India while confirming that the cases are being “confirmed” by RT-PCR testing.

But the PCR test at the center of that confirmation relies on a forward primer sequence that aligns to the human genome across numerous loci, creating a straightforward mechanism for false positives: amplification of human genetic material rather than viral RNA.

Are these tests showing positive results for human genetics, not Nipah?

Is this a false outbreak?

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BLAST Results Confirm Nipah PCR Primer Matches Human Genetics

The sequence in question is published in the World Organisation for Animal Health (OIE) Terrestrial Manual, which describes a TaqMan real-time RT-PCR assay targeting the Nipah virus N gene as a primary diagnostic method for confirming clinical cases.

- The original TaqMan 5′ nuclease PCR chemistry patent (U.S. Patent 5,210,015) explicitly states that a detectable positive signal can be generated from polymerase binding to a single primer alone—through probe cleavage—without requiring full target amplification.
- In plain terms, the chemistry used in PCR testing can produce a “positive” signal simply because a primer sticks to genetic material—even if the virus the test claims to detect is not there—raising the possibility that outbreaks defined by these tests can be created by the assay itself rather than by real infections.

The OIE manual lists the Nipah N-gene forward primer as: NiV_N_1198F: TCA-GCA-GGA-AGG-CAA-GAG-AGT-AA.

Table 2. Real-time RT PCR (Taqman) assays for the detection of HeV and NiV

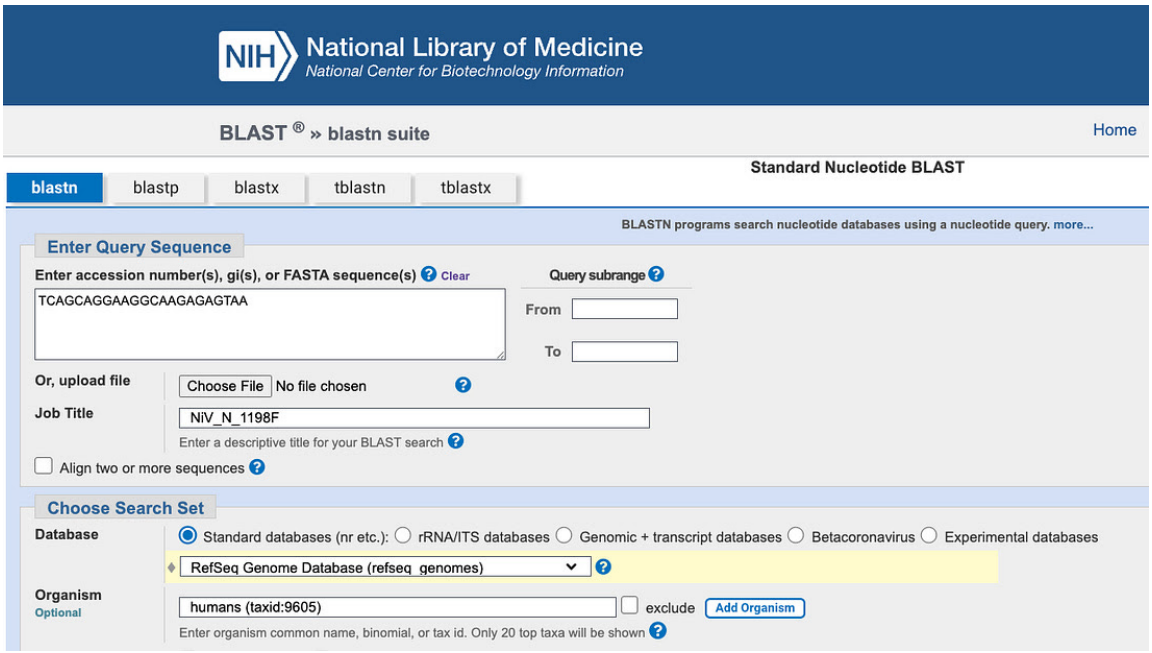
Assay	Oligo	Name	Primer sequence (5'–3')	Probe label (5'–3')
HeV_TQM_M	Forward	HeV M 5755F	CTT-CGA-CAA-AGA-CGG-AAC-CAA	
	Reverse	HeV M 5823R	CCA-GCT-CGT-CGG-ACA-AAA-TT	
	Probe	HeV M 5778P	TGG-CAT-CTT-TCA-TGC-TCC-ATC-TCG-G	FAM-TAMRA
HeV_TQM_N	Forward	HeV N119F	GAT-ATI-TTT-GAM-GAG-GCG-GCT-AGT-T	
	Reverse	HeV N260R	CCC-ATC-TCA-GTT-CTG-GGC-TAT-TAG	
	Probe	HeV N198-220P	CTA-CTT-TGA-CTA-CTA-AGA-TAA-GA	FAM-MGBNFQ
NiV_TQM_N	Forward	NiV_N_1198F	TCA-GCA-GGA-AGG-CAA-GAG-AGT-AA	
	Reverse	NiV_N_1297R	CCC-CTT-CAT-CGA-TAT-CTT-GAT-CA	
	Probe	NiV_N_1247comp	CCT-CCA-ATG-AGC-ACA-CCT-CCT-GCA-G	FAM-TAMRA

That is the primer sequence tested for in samples purportedly containing Nipah.

However, I carried out a BLAST alignment of NiV_N_1198F against the human reference genome (GRCh38) that returned high-identity matches distributed across the genome, including contiguous match lengths that meet typical priming thresholds used in PCR reactions.

In other words, the primer used to detect Nipah matches human genetics, meaning the test can amplify human DNA and generate a “positive” signal even when no virus is present.

The BLAST alignments include multiple perfect and near-perfect binding sites spanning many chromosomes.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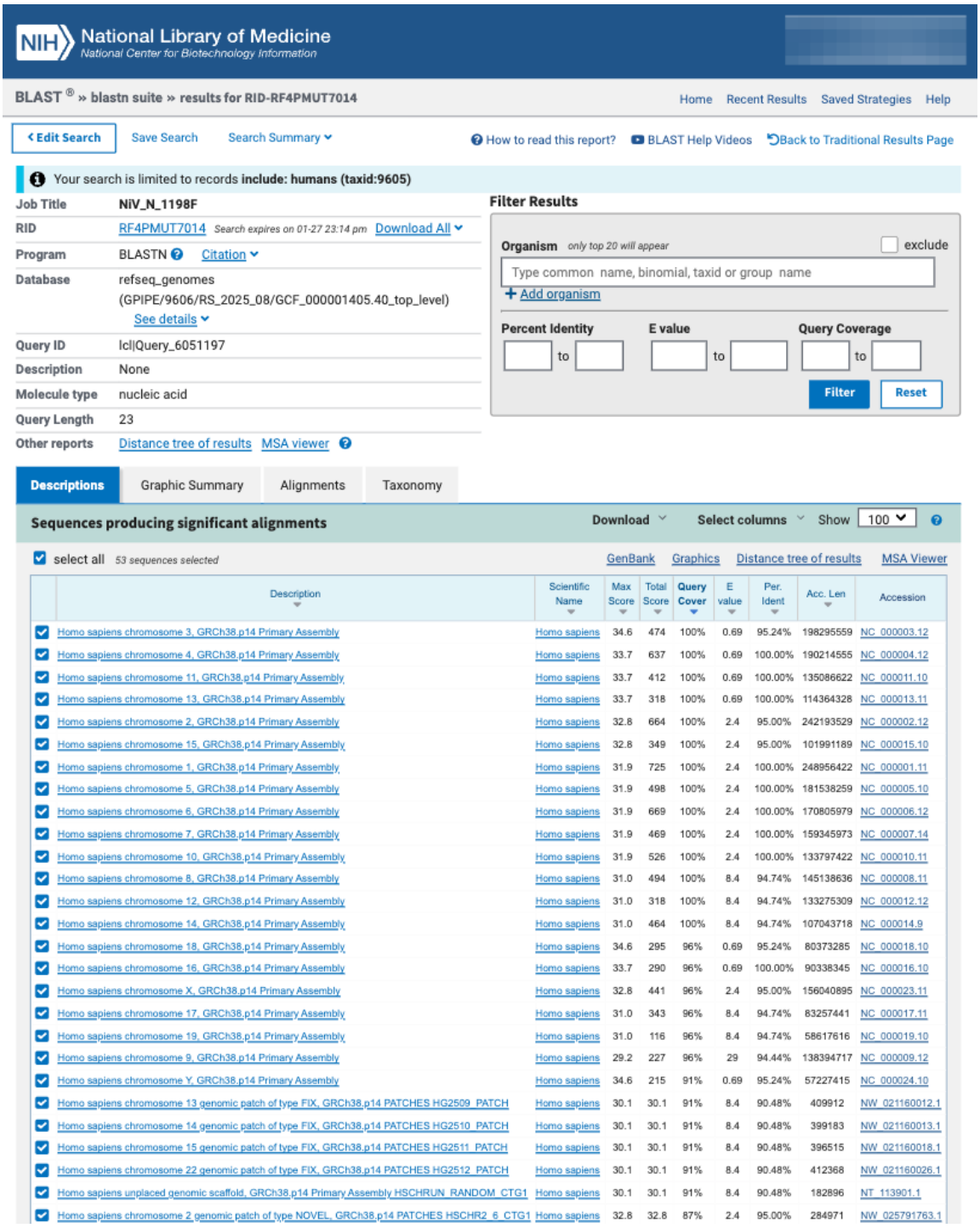

PCR amplifies whatever the primer binds to.

When a primer binds host (human) DNA at scale, the assay's output can reflect host genetics rather than a pathogen.

In practical terms, a "positive" can be created by the assay's binding behavior

alone, depending on sample composition, amplification conditions, cycle thresholds, and contamination controls.

This primer-to-human-genome alignment issue lands in the middle of a media cycle pushing the public toward fear and potential government-imposed outbreak response.

Mainstream Nipah Reporting

PEOPLE reports that two nurses near Kolkata were identified as Nipah cases, that 180 people had been tested, and that RT-PCR testing is being used in surveillance and bat screening in West Bengal.

Those headlines leave out the technical detail that determines whether a PCR “confirmed” case is meaningful: whether the primers uniquely target Nipah virus.

A primer that repeatedly aligns to human DNA introduces a simple diagnostic problem.

It creates a pathway for false positives through ordinary lab dynamics and also expands the space for manufactured outcomes, because the assay can generate a positive signal from material already present in the patient.

Are “Nipah cases” being manufactured?

PCR Test Inventor’s Warning

Dr. Kary Mullis, the late inventor of the PCR test, said in a 1997 interview (here) that his test should not be used to determine whether a subject is infected with a virus.

This is because the test “can find almost anything in anybody” if its parameters are set high enough, tainting the results, according to the Nobel Prize winner.

> “Anyone can test positive for practically anything with a PCR test. If you run it long enough… you can find almost anything in anybody,” Dr. Mullis said. “It doesn’t tell you that you’re sick.”

Mullis’ warning now appears directly relevant to a system where public health emergencies can be declared based on tests that do not require a virus to produce a positive result.

Bottom Line

Health agencies, laboratories, and media outlets reporting “PCR-confirmed Nipah” now face a basic burden: publish the primer specificity analysis, disclose the cycle threshold and control strategy used to rule out host-genome amplification, and demonstrate that the reported positives are tied to viral targets rather than to human sequence overlap.

Until that specificity question is addressed in the open, PCR-confirmed Nipah claims rest on a test design that can produce its own signal.

Public fear, quarantine measures, and international headlines are now being driven by a test that cannot be assumed to distinguish between human genetic material and the virus it is supposed to identify.