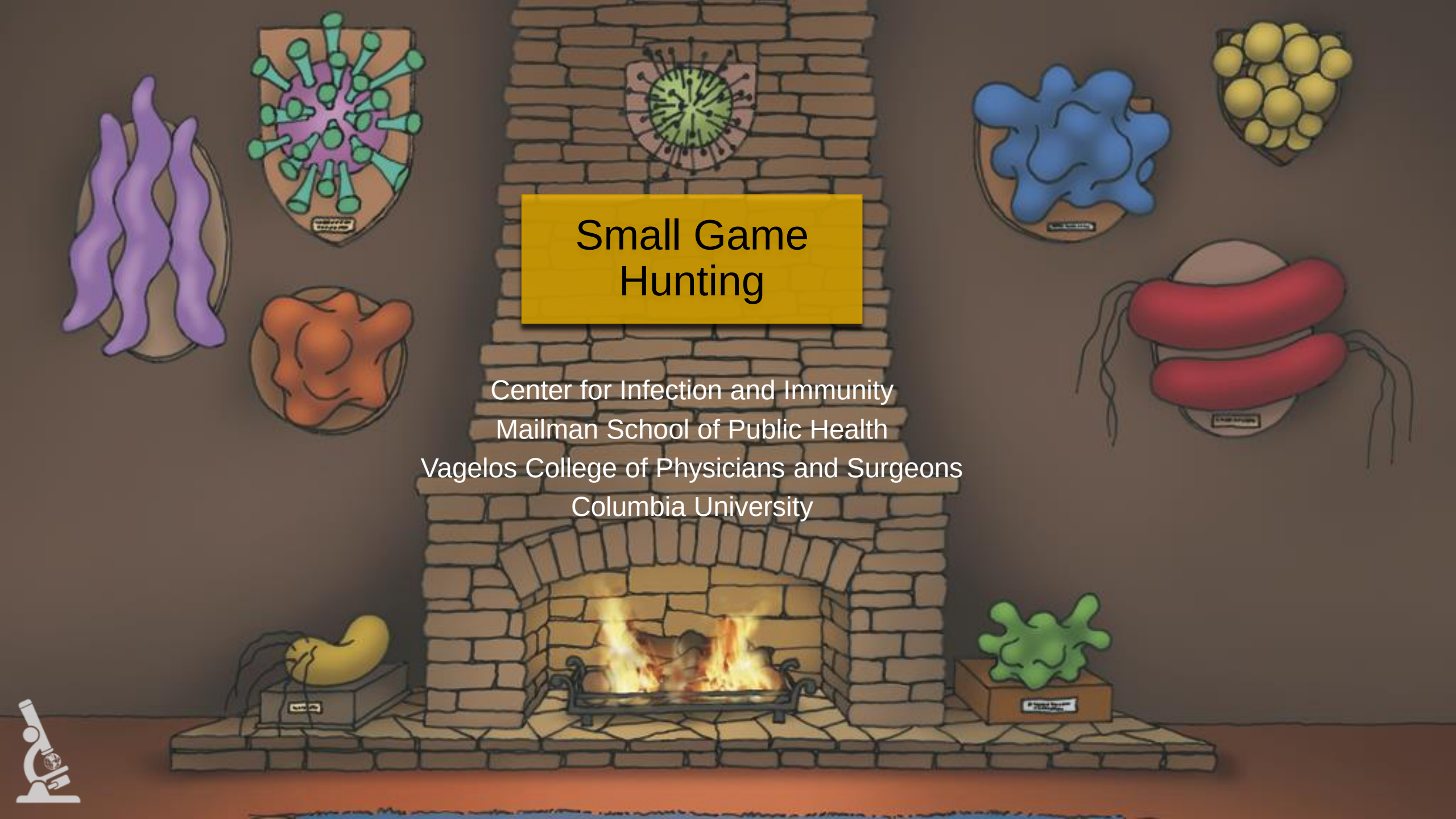

Small Game Hunting
Center for Infection and Immunity
Mailman School of Public Health
Vagelos College of Physicians and Surgeons
Columbia University

**Prediction is very difficult, especially about the future.**

**Niels Bohr**

# HIV/AIDS

Morbidity and Mortality Weekly Report (MMWR)
Weekly | June 5, 1981 | 30(21);1-3

### *Pneumocystis* Pneumonia --- Los Angeles

In the period October 1980-May 1981, 5 young men, all active homosexuals, were treated for biopsy-confirmed *Pneumocystis carinii* pneumonia at 3 different hospitals in Los Angeles, California. Two of the patients died. All 5 patients had laboratory-confirmed previous or current cytomegalovirus (CMV) infection and candida mucosal infection.

Morbidity and Mortality Weekly Report (MMWR)
Weekly | December 10, 1982 | 31(48);625-9

### Epidemiologic Notes and Reports Possible Transfusion-Associated Acquired Immune Deficiency Syndrome (AIDS) -- California

CDC has received a report of a 20-month old infant the from San Francisco area who developed unexplained cellular immunodeficiency and opportunistic infection. This occurred after multiple transfusions, including a transfusion of platelets derived from the blood of a male subsequently found to have the acquired immune deficiency syndrome (AIDS).

## Two years from recognition of disease to identification of the causative agent.

Science. 1983 May 20;220(4559):868-71.

### Isolation of T-lymphotropic retrovirus from a patient at risk for acquired immune deficiency syndrome (AIDS).

Barré-Sinoussi F, Chermann JC, Rey F, Nugeyre MR, Chamaret S, Gruest J, Dauguet C, Axler-Blin C, Vézinet-Brun F, Rouzioux C, Rozenbaum W, Montagnier L.

Science. 1984 May 4;224(4648):500-3.

### Frequent detection and isolation of cytopathic retroviruses (HTLV-III) from patients with AIDS and at risk for AIDS.

Gallo RC, Salahuddin SZ, Popovic M, Shearer GM, Kaplan M, Haynes BF, Palker TJ, Redfield R, Oleske J, Safai B, et al.

# Borna

## Five years

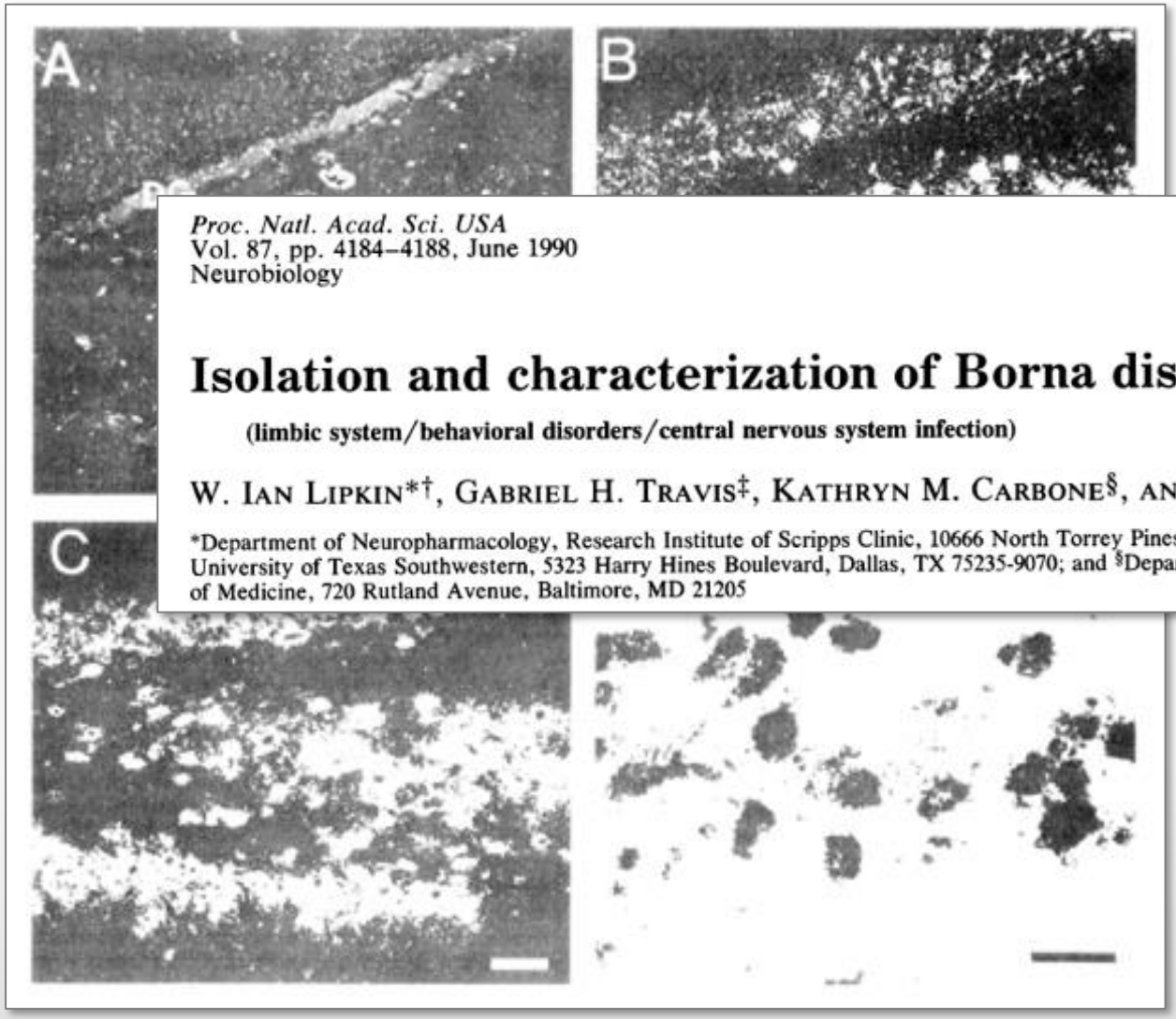
Science
10 May 1985 | Vol 228, Issue 4700 | pp. 755-756 | DOI: 10.1126/science.3922055
R. ROTT, S. HERZOG, B. FLEISCHER, A. WINOKUR, J. AMSTERDAM, W. DYSON, AND H. KOPROWSKI

**Detection of serum antibodies to Borna disease virus in patients with psychiatric disorders**

**Abstract**

Borna disease virus causes a rare meningoencephalitis in horses and sheep and has been shown to produce behavioral effects in some species. The possibility that the Borna virus is associated with mental disorders in humans was evaluated by examining serum samples from 979 psychiatric patients and 200 normal volunteers for the presence of Borna virus-specific antibodies. Antibodies were detected by the indirect immunofluorescence focus assay. Antibodies to the virus were demonstrated in 16 of patients but none of the normal volunteers. The patients with the positive serum samples were characterized by having histories of affective disorders, particularly of a cyclical nature. Further studies are needed to define the possible involvement of Borna virus in human psychiatric disturbances.

# Subtractive Cloning of BDV



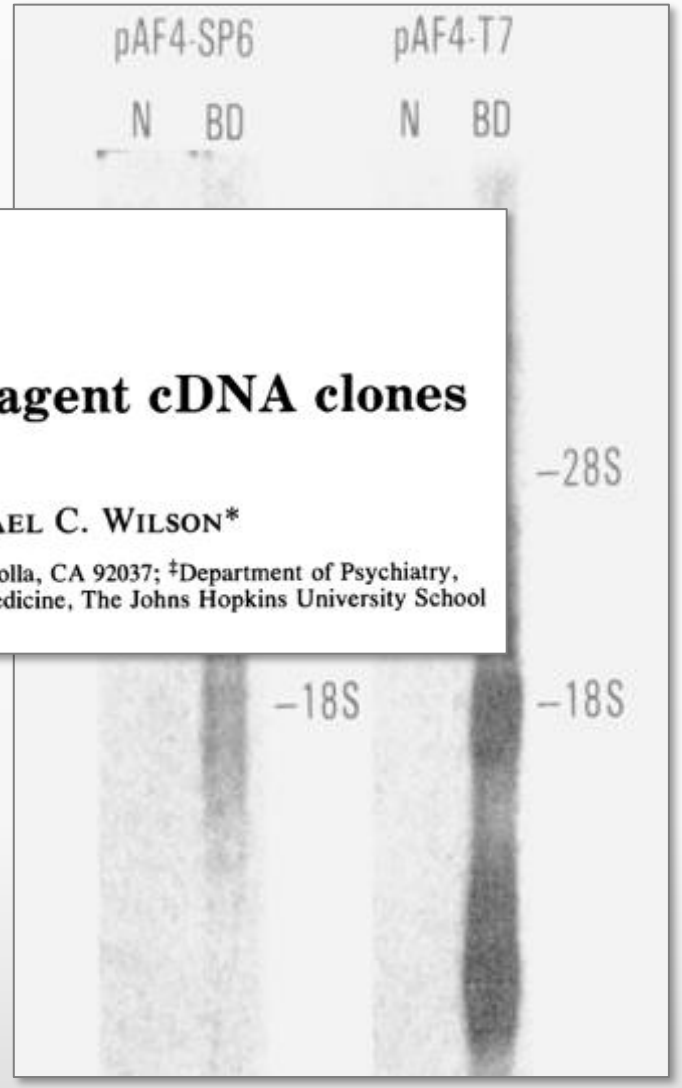

*Proc. Natl. Acad. Sci. USA*
Vol. 87, pp. 4184–4188, June 1990
Neurobiology

## Isolation and characterization of Borna disease agent cDNA clones

**(limbic system/behavioral disorders/central nervous system infection)**

W. IAN LIPKIN*†, GABRIEL H. TRAVIS‡, KATHRYN M. CARBONE§, AND MICHAEL C. WILSON*

*Department of Neuropharmacology, Research Institute of Scripps Clinic, 10666 North Torrey Pines Road, La Jolla, CA 92037; ‡Department of Psychiatry, University of Texas Southwestern, 5323 Harry Hines Boulevard, Dallas, TX 75235-9070; and §Department of Medicine, The Johns Hopkins University School of Medicine, 720 Rutland Avenue, Baltimore, MD 21205



# Dandenong Virus

**Two weeks**

The NEW ENGLAND JOURNAL of MEDICINE

**A New Arenavirus in a Cluster of Fatal Transplant-Associated Diseases**

**ORIGINAL ARTICLE** | March 6, 2008 | DOI: 10.1056/NEJMoa073785

*Palacios G, Druce J, Du L, Tran T, Birch C, Briese T, Conlan S, Quan PL, Hui J, Marshall J, Simons JF, Egholm M, Paddock CD, Shieh WJ, Goldsmith CS, Zaki SR, Catton M, Lipkin WI*

Austin Health, Victoria
CDC
Columbia
Victorian Infectious Disease Reference Laboratory
454 Life Sciences

Gustavo Palacios

# LuJo

**One week**

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From: Pr
Subject: I
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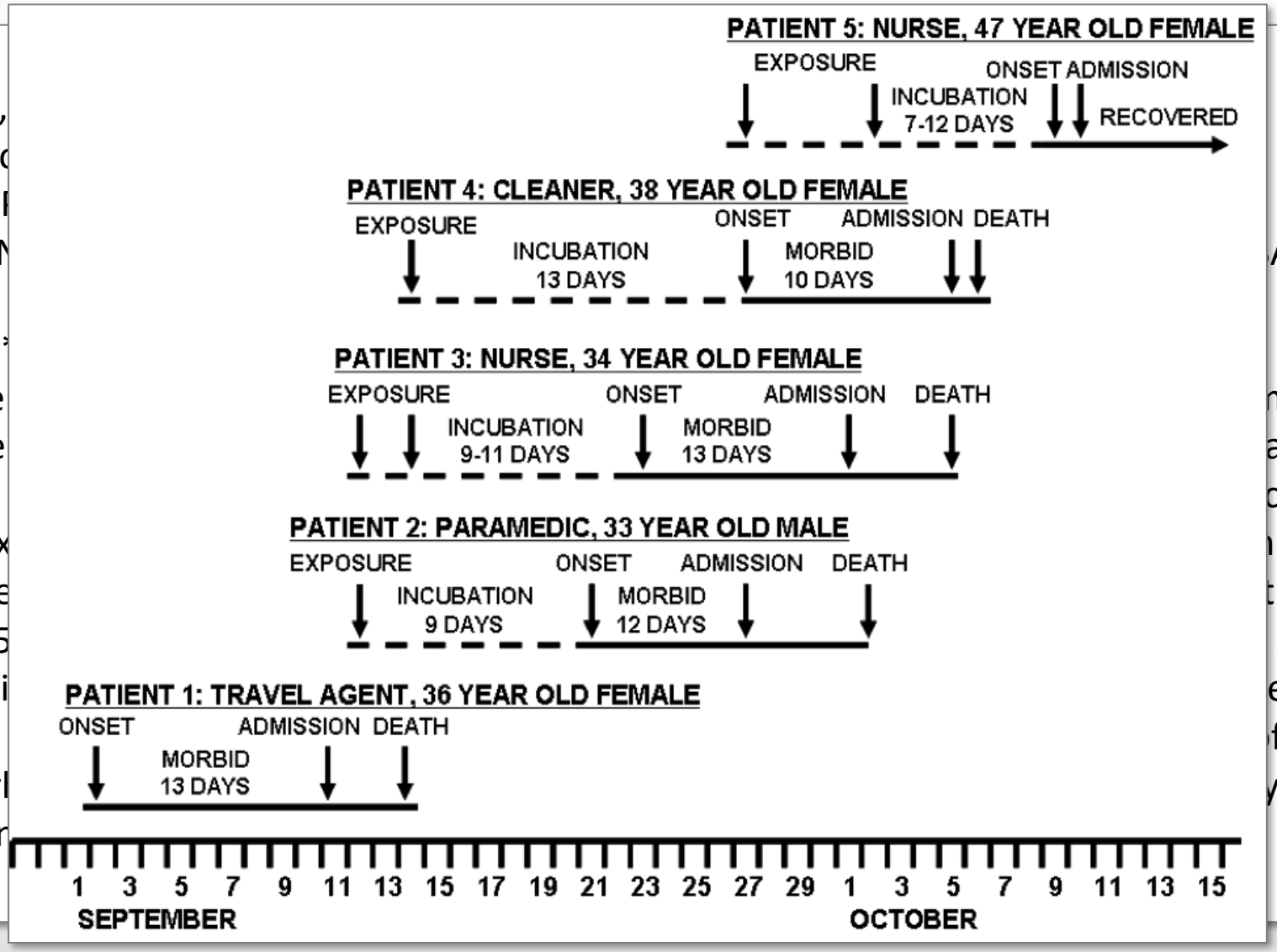
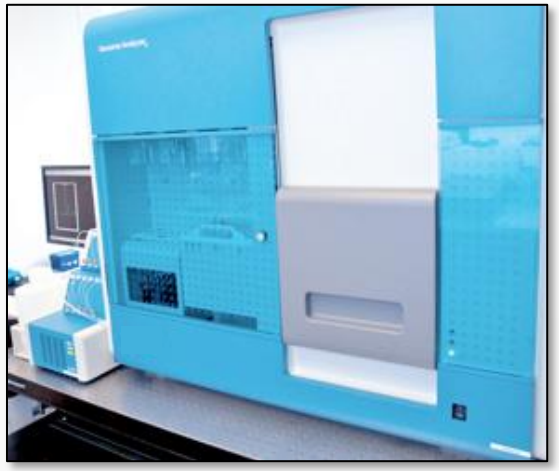


# Evolution of High-Throughput Sequencing

Roche 454



Illumina

Ion Torrent

Illumina HiSeq X Ten

Oxford Nanopore MinION

# *Prioritization?*

## >2,000 Viruses Discovered/Characterized at CII Alone

### Humans

Adenoviruses (1 species)
Astroviruses (4 species)
Bocaviruses (4 species)
Cosaviruses (4 species)
Enteroviruses (9 EVA, 15EVB, 8EVC, 1EVD (EV68),1 untyped)
Dengue Virus
LuJo Virus
Orthobunyaviruses
Parvoviruses (3 species)
Phlebovirus (7 species)
Rotaviruses (1 species)
Rhabdobirus (2 species)
Rhinovirus A, C
Polyomaviruses

### Other Mammals

Bat Adenoviruses
Bat Astroviruses
Bat Bocaviruses
Bat Coronaviruses (35+ species)
Bat Hepaciviruses and Pegiviruses
Bat Filovirus (distant relation to Ebola and Marburg)
Bat Herpesviruses
Bat Paramyxoviruses
Bat Parvoviruses
Bat Polyomaviruses
Canine Hepacivirus
Canine Kobuvirus
Cattle Orbivirus (6 species)

Cattle Orthomyxovirus (2 species)
Cetacean Influenza Virus
Cetacean Polyomavirus
Gorilla Parvovirus
Gorilla Metapneumovirus
Hedgehog Rhabdovirus
Horse Pegiviruses
Minke Whale Astrovirus
Porcine Astrovirus
Porcine Circovirus
Porcine Picobirnavirus
Rodent Hepaciviruses and Pegiviruses
Sea Lion Reovirus

### Avians

Avian Bornavirus (2 genotypes)
Avian Farmington Virus
Turkey Hepatitis Virus (4 genotypes)

### Insects

Mosquito Rhabdovirus (8 species)
Mosquito Orbivirus
Mosquito Alphavirus
Mosquito Nidovirus
Mite Rhabdovirus
Insect Phlebovirus (19 species)
Insect Negevirus
Metagenomic studies of *Apis mellifera*

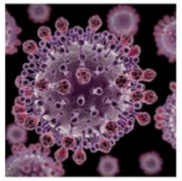
### Fish/Reptiles/Other

Piscine reovirus (Salmon)
Clam retrovirus
Snake nidovirus
Tilapia Lake virus

# *Faster, Cheaper, Easier*

## Sequence-Capture Based Diagnosis and Discovery: VirCapSeq-VERT

2015 WORLD CHANGING IDEAS



H1N1 INFLUENZA is one of many viruses snared by a single new test.

### Trawling for Viruses

A new method identifies every virus in a given sample with near-perfect accuracy

**When doctors want** to identify the virus behind an infection, they usually turn to the polymerase chain reaction (PCR), a method for "amplifying" scattered bits of DNA into a sample large enough to study. To use PCR, however, a physician must know what kind of virus to look for, and that involves guesswork.

This past September a team of Columbia University researchers described a new method that could eliminate that guesswork. The technique, which has the unfortunate name of "virome capture sequencing platform for vertebrate viruses," or VirCapSeq-VERT, can find every virus in a given drop of saliva, tissue or spinal fluid with near-perfect accuracy. The method makes it possible to simultaneously analyze 21 samples in less than 48 hours at an estimated cost of just $200 per sample. It can also detect novel or mutated viruses, so long as they are at least 40 percent identical to known ones. "When someone goes into an emergency room and winds up having all kinds of tests run, it costs thousands of dollars," says W. Ian Lipkin, John Snow Professor of Epidemiology at Columbia University's Mailman School of Public Health. "This method is very inexpensive and allows us to personalize medicine by telling you exactly what you have."

To develop the technique, Lipkin and his colleagues first created a database of more than 1,000 vertebrate viruses. Then they synthesized genetic probes to match every strain of every virus—two million of them, each a strand of DNA 25 to 50 nanometers long. When a probe encounters a matching virus, it binds to it. To extract those viruses, laboratory workers add magnetic beads measuring one to three microns in diameter to the mix; a chemical linker binds the beads to the genetic probes and the viruses they have captured. Researchers then insert a tube containing the mixture into a magnet stand, which pulls the probes to the tube's walls. After researchers isolate and wash the probe-bead-virus combos, they genetically sequence the viruses, eliminating the risk of false positives. Lipkin and his colleagues are now looking to team up with a commercial provider that can distribute the technology to hospitals and clinics around the world. They are also planning on adding probes for all known infectious bacteria and fungi.

—*R.N.*

SCIENCE SOURCE (virus)

34 Scientific American, December 2015

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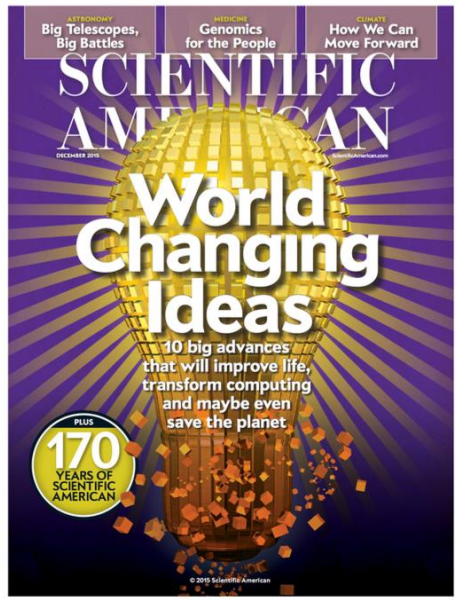
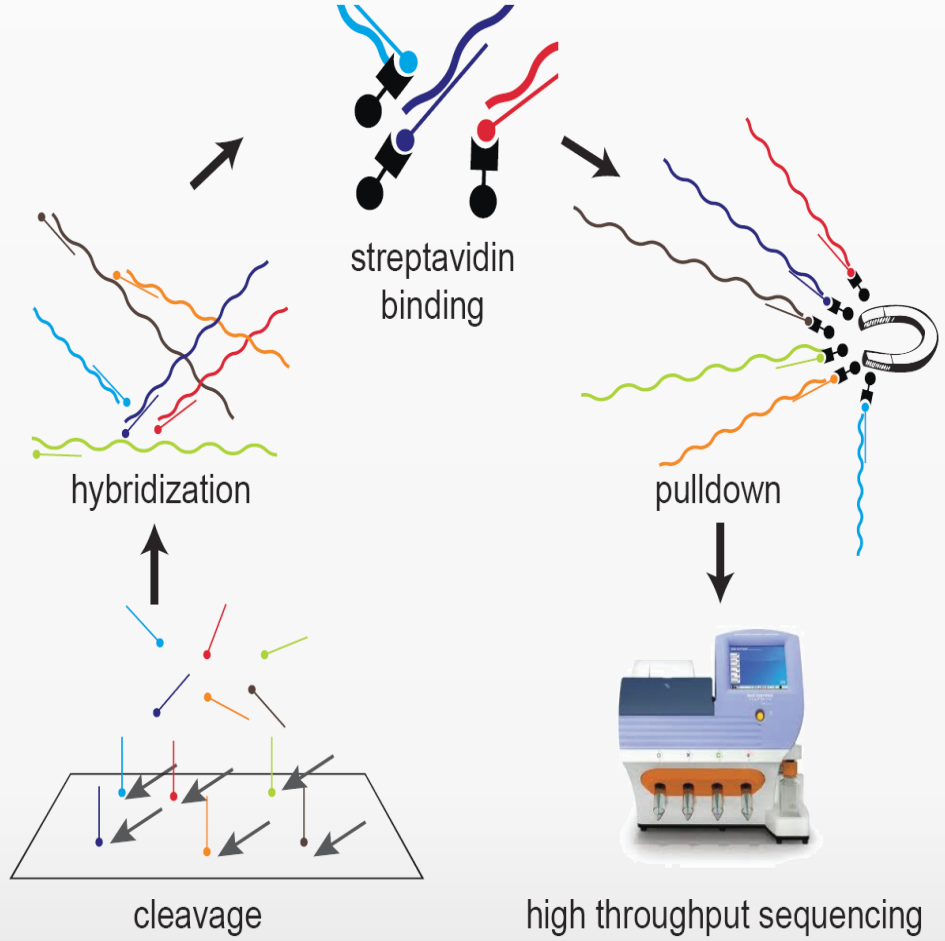
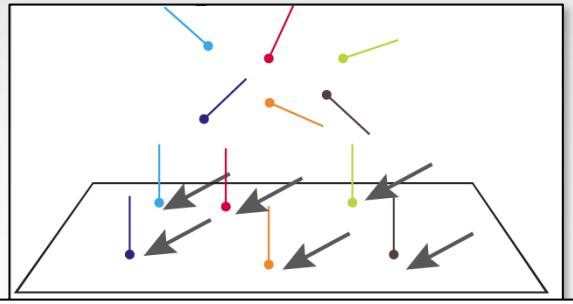


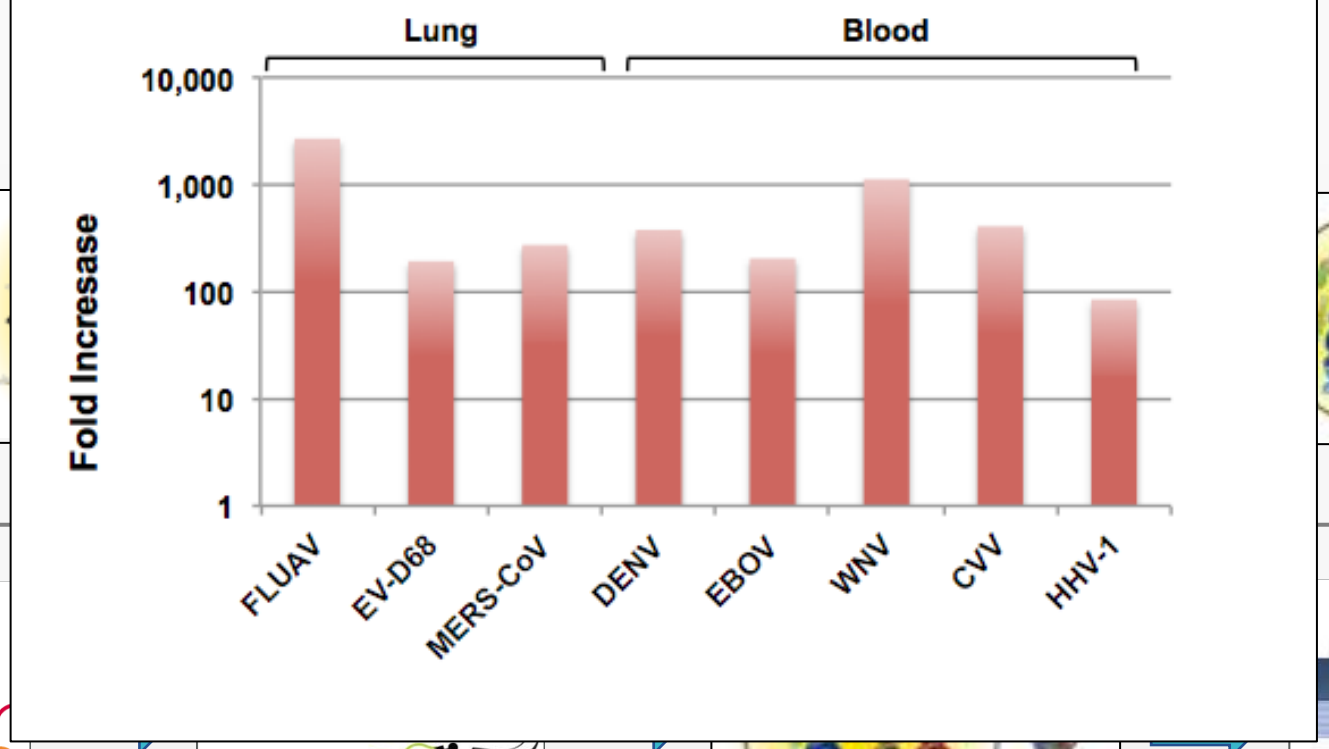
PROBE LIBRARY



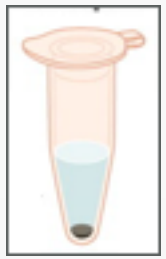
Biotinylated oligonucleotides synthesized on slide

Released from slide to generate soluble probe pool

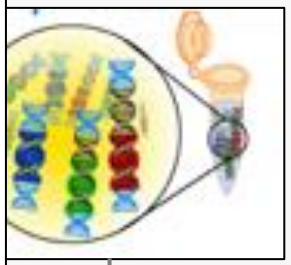
TARGET ENRICHMENT

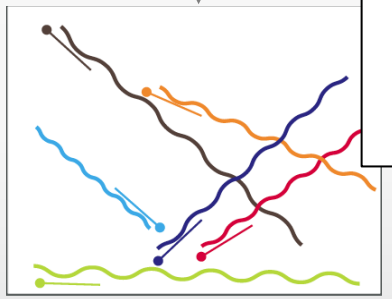



Sample



Pre-capture amplification





Hybridization

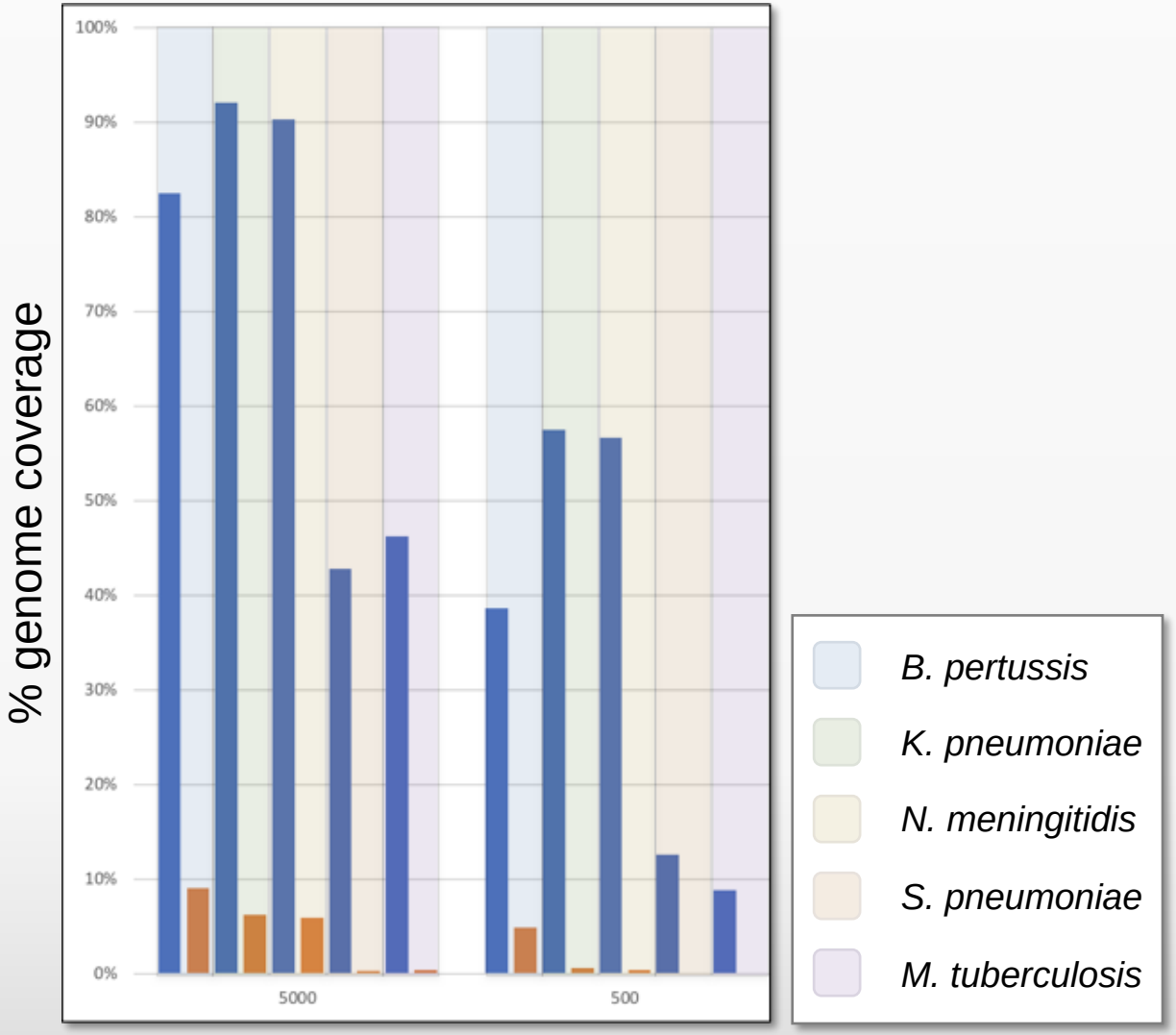

Streptavidin capture and pulldown

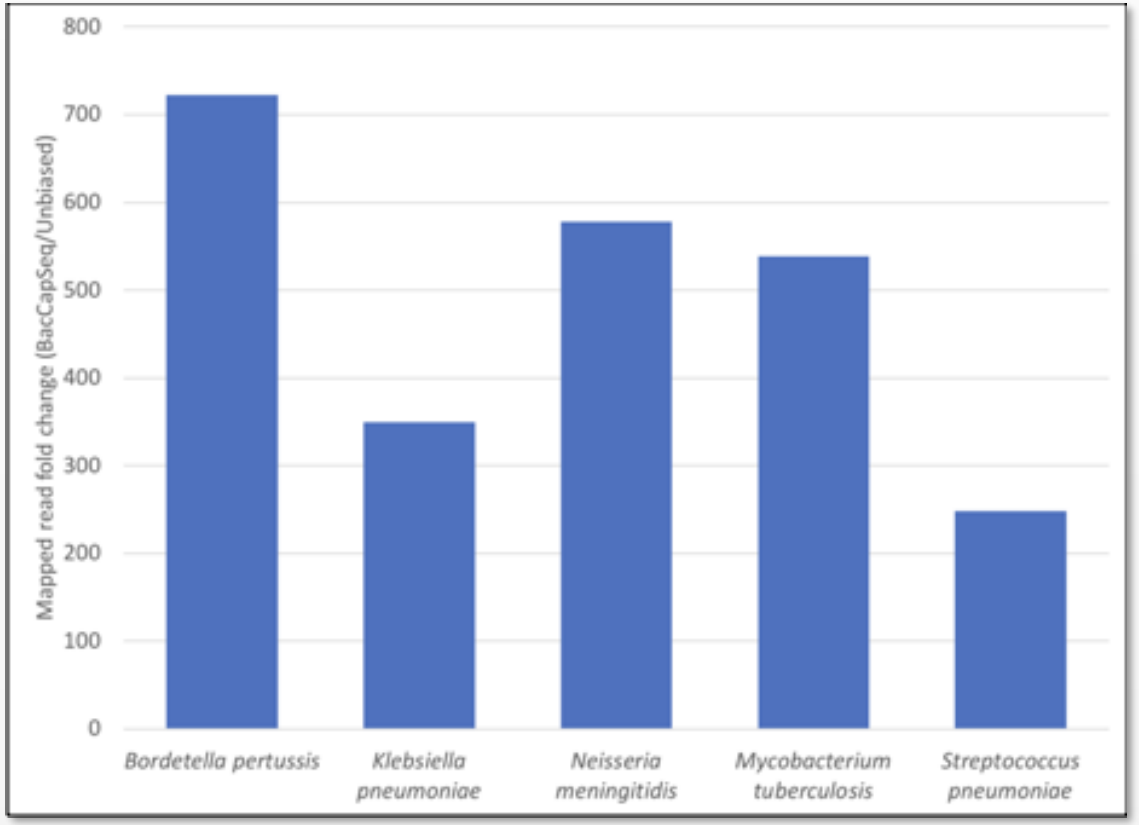
Post-capture amplification

Sequencing

# BacCapSeq

*Bacterial pathogens, antimicrobial resistance*



# Innovation is Enabling Improvements in Timeliness and Sensitivity in Sequencing

| Instrument | # of Samples | # of Reads | Read Length | Runtime |
|---|---|---|---|---|
| Illumina NextSeq 1000/2000 | 100 | 1.2 billion | 150 nt | 11h |
| Illumina NextSeq 500 | 40 | 400 million | 150 nt | 12h |
| Illumina MiSeq | 3 | 25 million | 300 nt | 5h |
| *Illumina MiniSeq* | *3* | *25 million* | *150 nt* | *4h* |
| Illumina iSeq | 1 | 4 million | 150 nt | 9.5h |
| Oxford Nanopore MinION | 1 | 5 million | 1000 nt | 8h |

| Workflow | Unbiased | Capture |
|---|---|---|
| Extraction | 1h | 1h |
| Library preparation | 6h | 6h |
| Hybridization | n/a | 1h |
| *Sequencing on MiniSeq* | *4h* | *4h* |
| Bioinformatics analysis | 8h | 2h |
| *Total turn around time* | *19h* | *14h* |
| *Sensitivity* | *1x* | *100-1000x* |

UNITED STATES PATENT AND TRADEMARK OFFICE

uspto

**Abstract:** The present invention provides novel methods, systems, tools, and kits for the simultaneous detection, identification and/or characterization of all viruses known or suspected to infect vertebrates. The methods, systems, tools, and kits described herein are based upon the virome capture sequencing platform ("VirCapSeq-VERT"), a novel platform developed by the inventors. The invention also provides methods and kits for designing and constructing of the virome capture sequencing platform.

**Filed:** September 19, 2016
**Publication Date:** September 20, 2018
**Document Identifier:** US 20180265935 A1

**Free for public health applications**

NEW YORK STATE OF OPPORTUNITY. Department of Health

KATHY HOCHUL
Governor

MARY T. BASSETT, M.D., M.P.H.
Commissioner

KRISTIN M. PROUD
Acting Executive Deputy Commissioner

January 26, 2022

Mahesh M. Mansukhani, M.D.
Columbia University Laboratory of Personalized Genomic Medicine
630 West 168th St Rm 11-453
New York, NY 10032

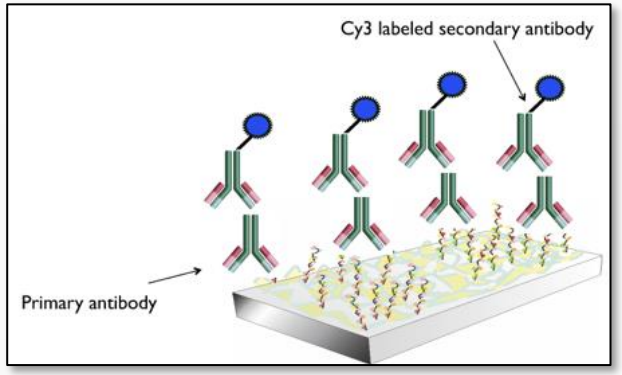
PFI: 7313
Project ID: 85920

Dear Dr. Mansukhani:

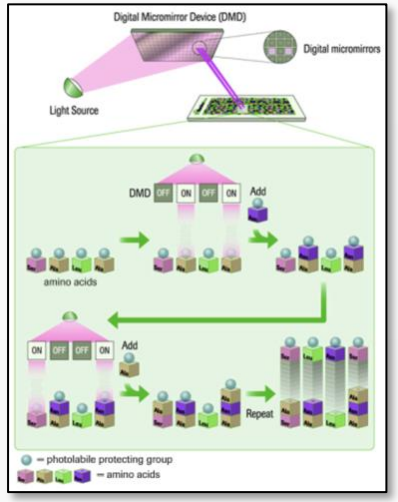
Thank you for submitting portions of your standard operating procedure manual and validation data needed to evaluate your next generation sequencing-based method for Columbia VirCapSeq-VERT in plasma specimens. After carefully evaluating all the information provided, the Clinical Laboratory Reference System's reviewers have found your validation data for this testing acceptable. You may offer this testing under your current permit in the category of Virology.

# *Indirect Methods for Microbe Discovery and Implication*

## High-Throughput Serology Using Peptide Microarrays

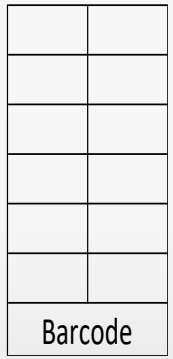



3M feature density
24M features needed to tile the vertebrate virus proteome

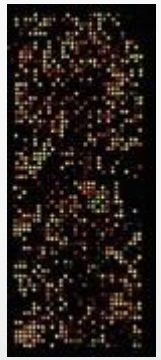



Synthesis in situ

## Data Production




Virtual image of each array, peptides are printed randomly on each sub array, and co-ordinates known for each peptide.



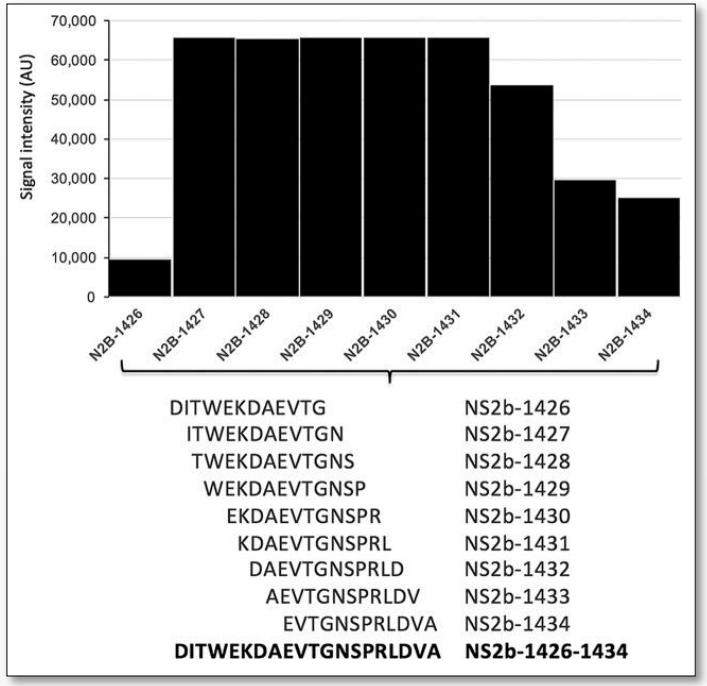
Scanned array image after secondary IgG and IgM Ab binding (Fluorescent signals)

Overlap images

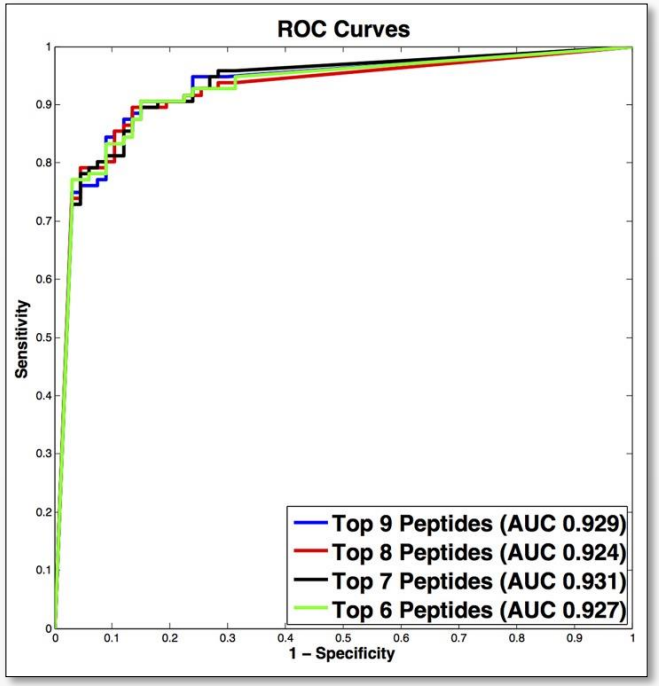
| AA position | ZIKV_AY632535 | ZC1 | ZC3 | ZC4 | ZC5 | ZC7 | ZC8 | ZC10 | ZC11 | ZC12 | ZC14 | ZC15 | CONTROL |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1426 | | 333.25 | 8182.3 | 413.29 | 12659.73 | 2017.06 | 6594.73 | 4150.09 | 9488.55 | 3633.04 | 840.34 | 348.96 | 1094.96 |
| 1427 | | 5929.83 | 65535 | 40686.59 | 65524.72 | 65533.86 | 65502.77 | 62587.86 | 65533.94 | 65516.8 | 43074.78 | 29062.1 | 2326.87 |
| 1428 | | 1167.64 | 65500.03 | 21902.73 | 65523.24 | 65127.44 | 64648.23 | 63418.59 | 65486.87 | 63716.99 | 31907.45 | 21128.54 | 1590.4 |
| 1429 | | 17833.23 | 63912.63 | 15760.5 | 65535 | 65535 | 65442.69 | 65096.3 | 65534.21 | 65518.18 | 62389.82 | 49153.83 | 3619.51 |
| 1430 | | 30032.74 | 65535 | 60224.11 | 65528.73 | 65240.54 | 65050.65 | 62511.76 | 65529.66 | 65484.65 | 58686.57 | 39390.5 | 3177.84 |
| 1431 | | 44195.73 | 65506.73 | 64752.4 | 65517.85 | 65249.55 | 65164.64 | 65275.14 | 65532.21 | 65535 | 63452.59 | 61976.44 | 3653.07 |
| 1432 | | 9107.15 | 54122.52 | 24994.3 | 63781.27 | 47079.49 | 32032.5 | 32277.86 | 53493.7 | 28045.73 | 19244.79 | 13894.04 | 773.36 |
| 1433 | | 194.26 | 36612.42 | 1403.83 | 60530.99 | 26119.84 | 26386.36 | 13440.57 | 29573.1 | 17285.55 | 6787.69 | 9720.6 | 756.19 |
| 1434 | | 193.6 | 25712.89 | 1453.79 | 41425.13 | 16979.84 | 15147.67 | 9767.21 | 24949.63 | 12211.56 | 4808.66 | 7190.39 | 916.53 |

Fluorescent signals converted to arbitrary units (data) and transferred to heat maps

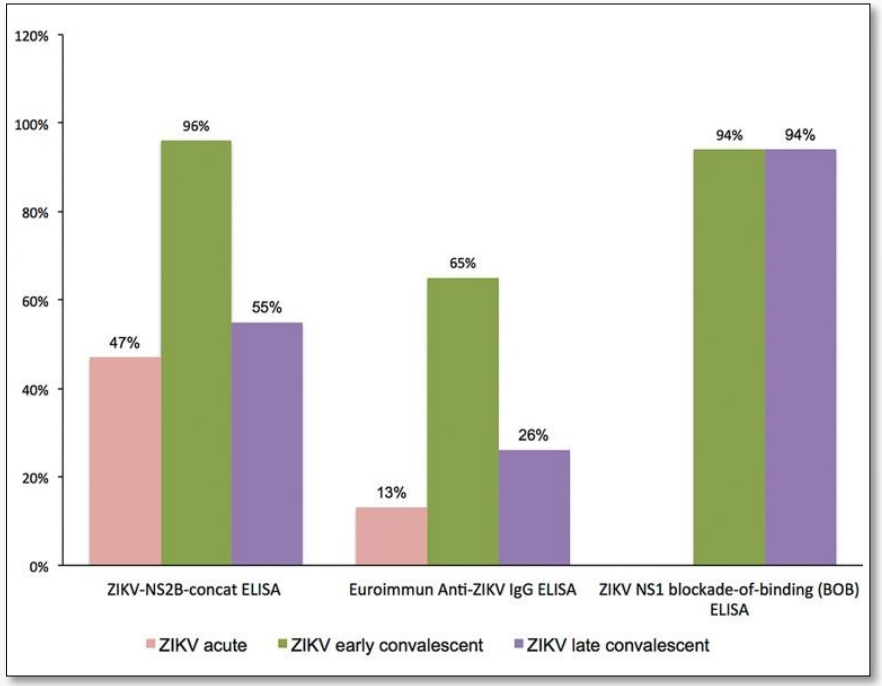
# Diagnosis of Zika Virus Infection by Peptide Array and Enzyme-Linked Immunosorbent Assay




Identification of an immunoreactive 20-amino-acid ZIKV NS2B peptide

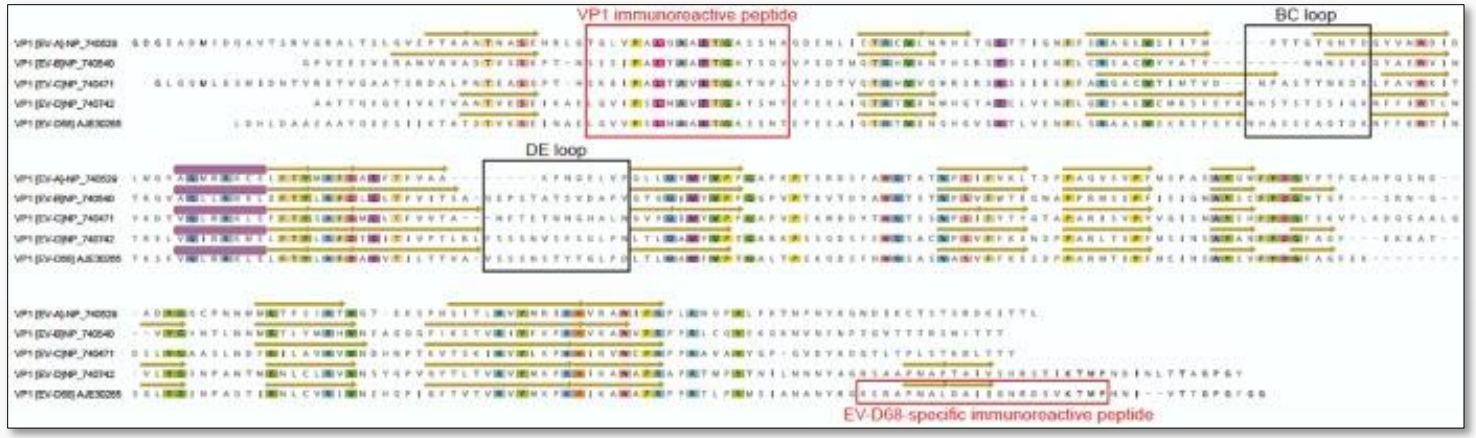



Average receiver operating characteristic (ROC) curves over 1,000 runs using the 9 overlapping peptides identified (comprising 20-aa ZIKV NS2B peptide), with an average area under the curve (AUC) of 0.931

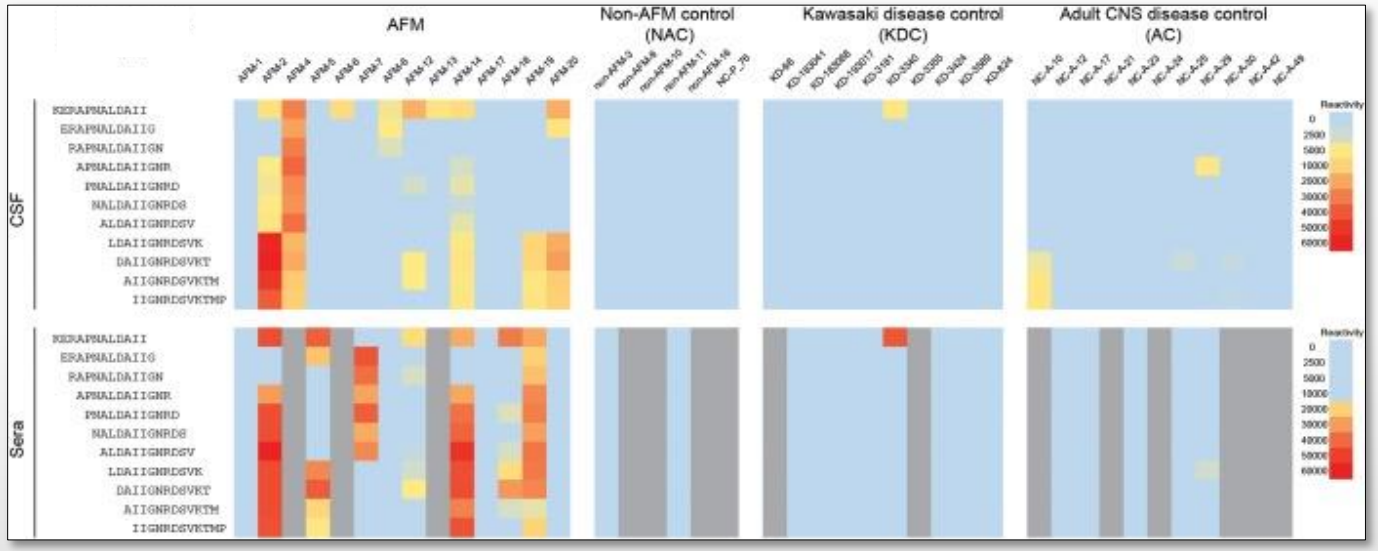



ZIKV-NS2B-concat ELISA sensitivity comparison with Euroimmun anti-ZIKV IgG ELISA and ZIKV-ELISA

# Antibodies to Enterovirus D68 in Cerebrospinal Fluid of Patients with Acute Flaccid Myelitis

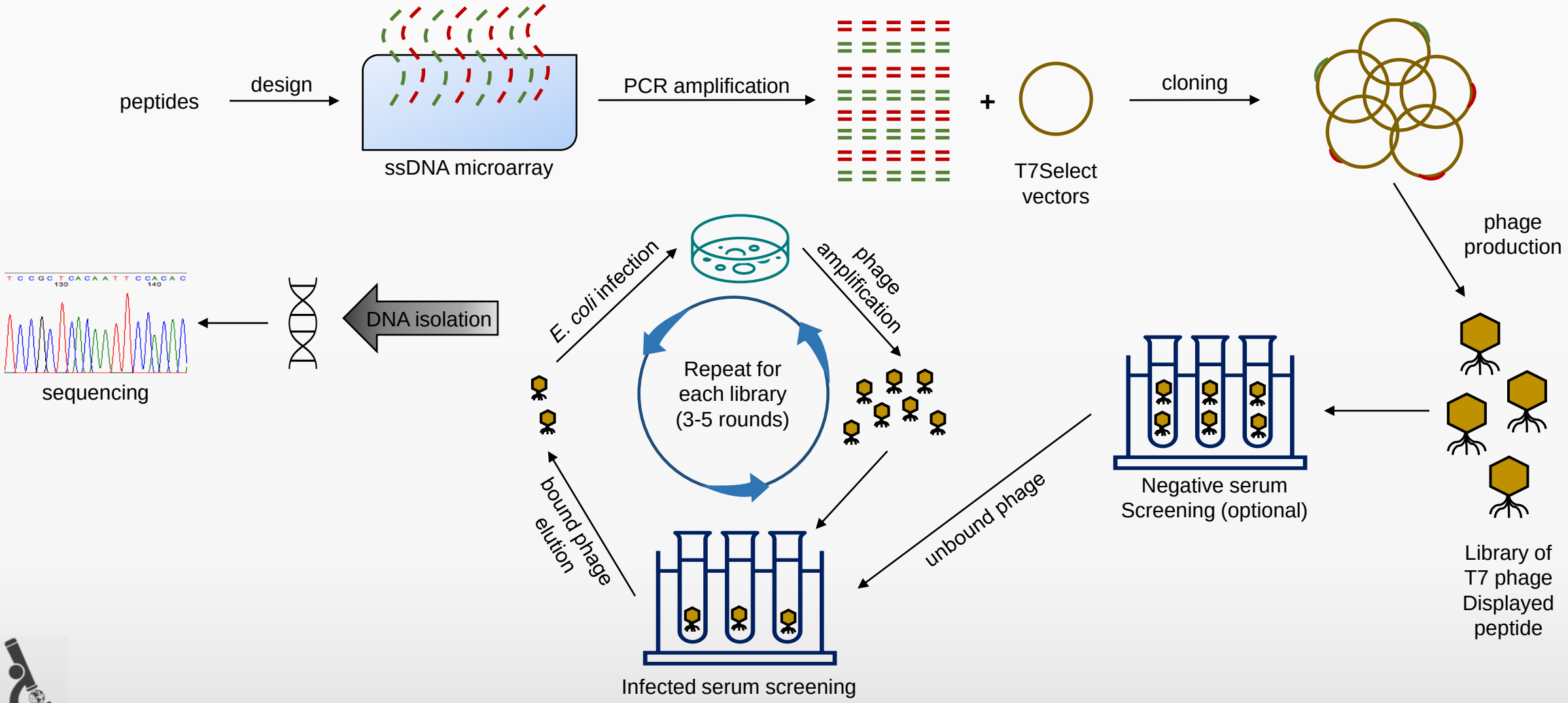



Identification of an immunoreactive peptide sequence region in VP1 protein of reference sequence entries for EV-A, EV-B, EV-C, and EV-D



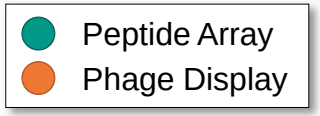

Immunoreactivity against an EV-D68-specific 22-aa VP1 capsid peptide in patients with AFM, non-AFM controls (NAC), Kawasaki disease controls (KDC), and adult CNS disease controls (AC).

# Multiplex Serology Using Phage Display



# Concordance Between Peptide Array and Granular Phage Display

*Opportunities to Discriminate Between Infections With Related Viruses and Find Evidence of Reactivation*




## Herpesvirus Reactivation in ME/CFS

| Virus | Protein | CASE1 | CASE2 | CASE3 | CASE4 | CASE5 | CASE6 | CASE7 | CASE8 |
|---|---|---|---|---|---|---|---|---|---|
| HHV4 | BZLF1 | ● | | | ● | | | | |
| HHV4 | C M protease | | | | | ● | | ● | ●● |
| HSV1 | E- Protein | ● | ●● | ●● | ●● | | | ●● | |
| HHV-6A | Helicase | ● | ●● | | ●● | | ●● | | |
| HHV3 | Large Tegument Protein | ●● | ●● | ●● | ● | ●● | ●● | ● | ● |
| HHV3 | UL32 | | | ● | ● | | ● | | ● |

## Convalescent COVID-19

| Virus | Protein | Sample1 | Sample2 | Sample3 | Sample4 | Sample5 | Sample6 |
|---|---|---|---|---|---|---|---|
| Coronavirus | NP | ● | ●● | ●● | ●● | ● | |
| | | ●● | ●● | ●● | ●● | ●● | ● |
| | GP | ● | ●● | ● | ● | ● | ● |
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# En sh

Vijay Bondre,
National Institute
of Virology, Pune

सत्यमेव जयते

**डा. सौम्या स्वामीनाथन**
एमडी, एफएएससी, एफएनएएससी, एफएएमएस
सचिव, भारत सरकार
स्वास्थ्य अनुसंधान विभाग
स्वास्थ्य एवं परिवार कल्याण मंत्रालय
एवं
महानिदेशक, आई सी एम आर

**Dr. Soumya Swaminathan**
MD, FASc, FNASc, FAMS
**Secretary to the Government of India**
Department of Health Research
Ministry of Health & Family Welfare
&
**Director-General, ICMR**

**भारतीय आयुर्विज्ञान अनुसंधान परिषद**
स्वास्थ्य अनुसंधान विभाग
स्वास्थ्य एवं परिवार कल्याण मंत्रालय
वी. रामलिंगस्वामी भवन, अंसारी नगर
नई दिल्ली-110 029 (भारत)

**Indian Council of Medical Research**
Department of Health Research
Ministry of Health & Family Welfare
V. Ramalingaswami Bhawan, Ansari Nagar
New Delhi-110 029 (INDIA)

**No. Secy.(DHR) & DG,ICMR/ 2017**
**Dated, the 17th August, 2017**

**Dear Prof. Lipkin**

I am writing to invite you to visit the ICMR Hqrs in New Delhi and the NIV field Unit at Gorakhpur, Uttar Pradesh to assist with the investigation of encephalitis outbreak.

As you are aware, AES has been claiming the lives of children in Eastern Uttar Pradesh for many years and the etiology remains unknown in 50% of the cases. Your inputs to improve the diagnosis using advanced sequencing techniques for pathogen discovery will be very useful. I look forward to meeting you in India next week.

With regards,

Yours sincerely,

( **Soumya Swaminathan** )

**Prof. W. Ian Lipkin, MD**
John Snow Professor of Epidemiology and
Director
Center for Infection and Immunity
Mailman School of Public Health
Professor of Pathology and Neurology
College of Physicians & Surgeons
Columbia University
722 West 168th Street, 17th Floor
**New York, NY 10032**

*Ran Out in an Indian Hospital*

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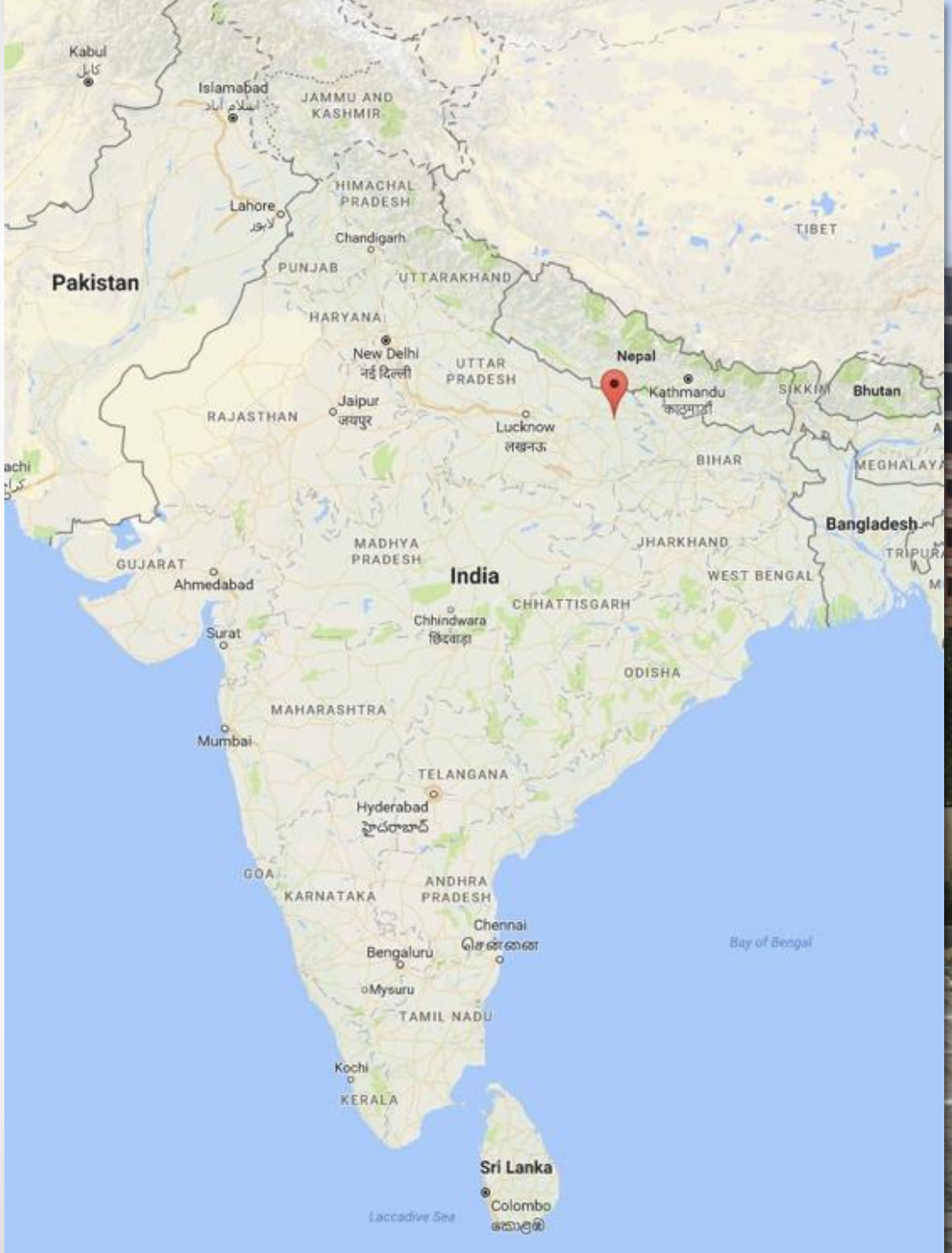
ths: Oppn demands
Yogi Adityanath, health

esh' CM Yogi Adityanath's silence in the aftermath of the children's deaths in
College that has left the state stunned.



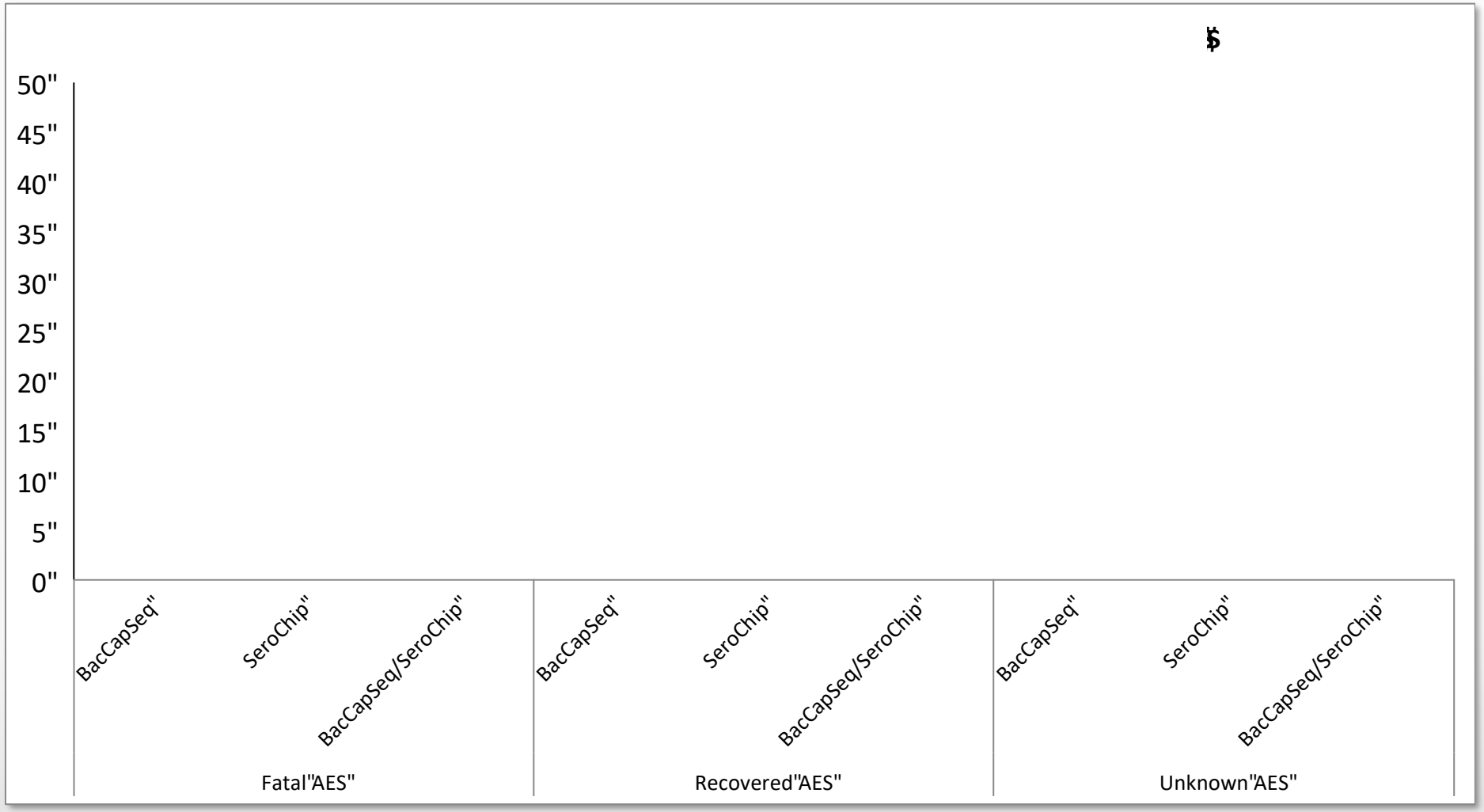

Musahar children

# Agents Detected by VirCapSeq-VERT and BacCapSeq in Cerebrospinal Fluid (CSF) of Children with Acute Encephalitis Syndrome (AES)

| | Fatal (n=223) | Discharged (n=283) | OR | 95% CI | | p-value |
|---|---|---|---|---|---|---|
| Human Herpesvirus 1 | 13 (5.8) | 6 (2.1) | 3.392 | 1.292 | 9.810 | 0.013 |
| Human Herpesvirus 3 | 0 (0.0) | 1 (0.4) | 0.003 | 0.003 | 9.530 | 0.612 |
| Human Herpesvirus 6 | 0 (0.0) | 1 (0.4) | 0.004 | 0.004 | 10.966 | .723 |
| Human Herpesvirus 7 | 0 (0.0) | 1 (0.4) | 0.006 | 0.006 | 17.262 | 0.949 |
| Human Parvovirus 4 | 8 (3.6) | 10 (3.5) | 0.389 | 0.389 | 2.694 | 0.942 |
| Human Parvovirus B19 | 3 (1.3) | 2 (0.7) | 0.626 | 0.626 | 21.181 | 0.152 |
| Human Immunodeficiency Virus | 10 (4.5) | 11 (3.9) | 0.454 | 0.454 | 2.777 | 0.790 |
| GB Virus C/Human Pegivirus | 11 (4.9) | 15 (5.3) | 0.749 | 0.749 | 4.118 | 0.189 |
| Human Papillomavirus | 6 (2.7) | 10 (3.5) | 0.362 | 0.362 | 3.028 | 0.884 |
| Torque Teno Virus | 8 (3.6) | 10 (3.5) | 0.450 | 0.450 | 3.189 | 0.695 |
| Human Coxsackievirus | 1 (0.4) | 3 (1.1) | 0.077 | 0.077 | 5.217 | 0.839 |
| Hepatitis A Virus | 4 (1.8) | 1 (0.4) | 0.844 | 0.844 | 53.399 | 0.077 |
| Human Adenovirus | 3 (1.3) | 2 (0.7) | 0.564 | 0.564 | 18.681 | 0.192 |
| Mumps Virus Genotype C | 5 (2.2) | 6 (2.1) | 0.310 | 0.310 | 3.427 | 0.937 |
| Merkel Cell Polyoma | 3 (13) | 7 (2.5) | 0.200 | 0.200 | 3.016 | 0.812 |
| Gemycircularvirus | 1 (0.4) | 7 (.25) | 0.038 | 0.038 | 1.776 | 0.235 |
| Rhinovirus | 0 (0.0) | 1 (0.4) | 0.001 | 0.001 | 3.938 | 0.293 |
| Densovirus/Ambidensovirus | 0 (0.0) | 3 (1.1) | 0.002 | 0.002 | 3.364 | 0.386 |
| Norovirus | 1 (0.4) | 0 (0.0) | 0.123 | 0.132 | 373.129 | 0.548 |
| Human Picobirnavirus | 1 (0.4) | 0 (0.0) | 0.134 | 0.134 | 379.345 | 0.540 |
| Japanese Encephalitis Virus | 3 (1.3) | 1 (0.4) | 0.446 | 0.446 | 31.185 | 0.271 |
| Measles Virus/Genotype D8 | 1 (0.4) | 0 (0.0) | 0.153 | 0.153 | 432.749 | 0.483 |
| Enterovirus/Echovirus | 0 (.0) | 3 (1.1) | 0.001 | 0.001 | 1.733 | 0.942 |
| Nilaparvata Lugens Reovirus | 76 (34.1) | 115 (40.6) | 0.474 | 0.474 | 1.006 | 0.054 |
| *Orientia tsutsugamushi* | 24 (10.8) | 31 (11.0) | 0.419 | 0.419 | 1.354 | 0.349 |
| *Rickettsiae* | 13 (5.8) | 24 (8.5) | 0.416 | 0.416 | 1.758 | 0.701 |

# Viral and Bacterial Capture Sequencing and Unbiased Serology

*AES CSF Samples Positive for Orientia tsugtsugamushi*



# Global Alliance for Preventing Pandemics

*Capacity Building*

### Mali Cohort June 2022




**CII Collaborations (2001-)**

Argentina, Australia, Brazil, Canada, Cambodia, China, Croatia, Democratic Republic of Congo, Ecuador, Germany, India, Indonesia, Israel, Kenya, Liberia, Mali, Mexico, Mongolia, New Zealand, Nicaragua, Nigeria, Norway, Peru, Russia, Saudi Arabia, Senegal, Sierra Leone, Singapore, Spain, Sweden, South Africa, Taiwan, Tanzania, The Gambia, Uganda, Zambia, Zimbabwe

### Sequencing and Serology

- Supplies (volume purchasing)
- Computational tools and databases

JCI The Journal of Clinical Investigation — DOI: 10.1172/JCI150646

**A randomized double-blind controlled trial of convalescent plasma in adults with severe COVID-19** Max R. O'Donnell, … , Andrew Eisenberger, Walter I. Lipkin

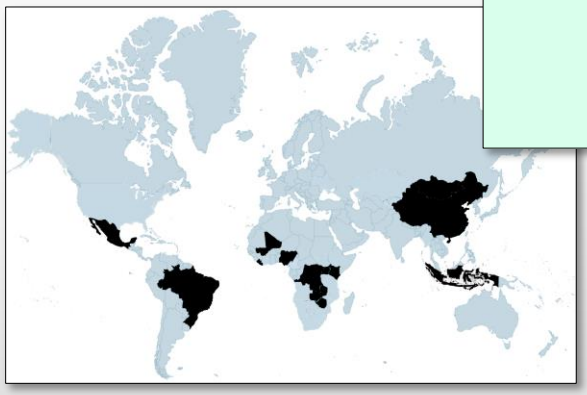
JAMA Network Open — DOI:10.1101/2021.08.11.21261915

**Molecular and serological investigation of the 2021 COVID-19 case surge in Mongolian vaccines** Dashdorj NJ, … , Lipkin WI, Mishra M

EMERGING INFECTIOUS DISEASES — DOI: 10.3201/eid2712.211818

**SARS-CoV-2 sequence analysis of respiratory samples collected from hospitalized patients during the Liberia case surge in June, 2021**
Bode Shobayo, … , W. Ian Lipkin, Nischay Mishra

**Recent/Upcoming Training Cohorts:**
**Liberia July 2021**
**Zambia September 2022**
**Nigeria November 2022**
**Mexico January 2023**



# Food Security: Piscine Reovirus

**Bloomberg** Eduardo Thomson | October 11, 2011

**Chile's Multiexport Heads to 17-Month Low on Fish Virus Concern**

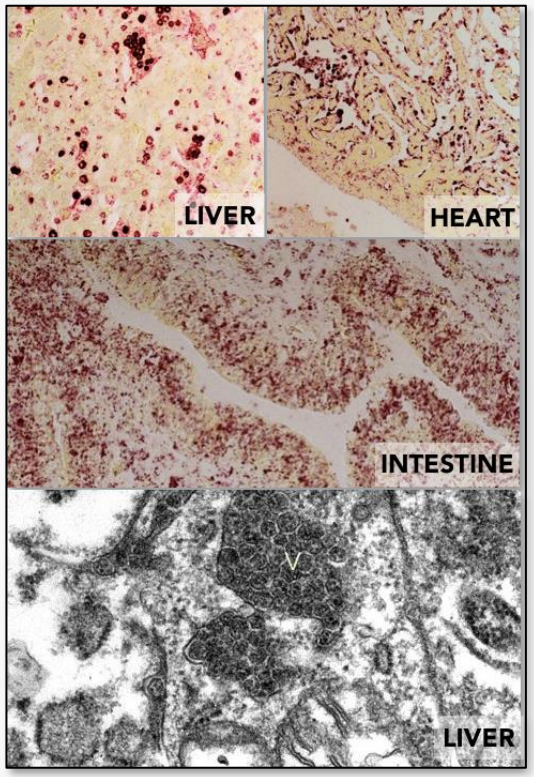
Multiexport Foods SA (MULTIFOO), the only salmon farmer on Chile's benchmark Ipsa index, headed for a 17 month low on concern a virus may effect production. Multiexport retreated 4.9% to 115.09 pesos at 4:30 pm Santiago time, the lowest price a closing basis since May 2010. The Ipsa rose 1.9%. Diario Financiero reported that regulators detected traces of "heart and skeletal inflammation," or HSMI, a virus among local farms.

Alexandra Morton

**New Norwegian virus in supermarket farm salmon**

Sointula, BC (April 13, 2012) Test results report 44 out of 45 farm salmon purchased from the Superstore and T&T markets throughout Vancouver tested positive for a newly identified Norwegian virus. The piscine reovirus weakens the fish's heart causing Heart and Skeletal Muscle Inflammation (HSMI). HSMI is considered a "major challenge" in Norway infecting over 400 farms since it's symptoms first appeared in 1999. It has spread to the U.K.

# Food Security: Tilapia Lake Virus




Food and Agriculture Organization of the United Nations

## FAO issues alert over lethal virus affecting popular tilapia fish

Though not a human health risk, Tilapia Lake Virus has large potential impact on global food security and nutrition

**26 May 2017**

Joyce Makaka tends her FAO-assisted fish farm in western Kenya.

Food and Agriculture Organization of the United Nations

**GLOBAL INFORMATION AND EARLY WARNING SYSTEM ON FOOD AND AGRICULTURE (GIEWS)**

**SPECIAL ALERT**

**No. 338**

**REGION: Global** **DATE: 26 May 2017**

**Outbreaks of Tilapia lake virus (TiLV) threaten the livelihoods and food security of millions of people dependent on tilapia farming**

**Highlights**

- Tilapia lake virus (TiLV) poses a great threat to the tilapia sector. Tilapias are farmed globally and are the second most important aquaculture species in terms of volumes produced, providing a key source of affordable animal protein, income to fishfarmers and fishers, and domestic and export earnings.
- TiLV has been confirmed in some countries in Asia, Africa and Latin America. It is likely that TiLV may have a wider distribution than is known today and its threat to tilapia farming at the global level is significant.
- While there is no public health concern for this pathogen, there is a significant risk of TiLV being translocated both inter- and intra-continentally through the movement of infected live tilapias in the absence of appropriate biosecurity measures.
- Tilapia producing countries need to be vigilant and take appropriate risk management measures (e.g. enhanced diagnostic testing of imported stocks and unexplained tilapia mortalities and reporting to biosecurity authorities, active surveillance, public information campaigns and contingency plans) to reduce the further spread and potential socio-economic impacts of this emerging disease.

**United States – Israel**
**Binational Agricultural Research and Development Fund**
**קרן דו-לאומית למחקר ולפיתוח חקלאיים של ארצות הברית וישראל**
**BARD - קמח**

September 2020

**Prof. Ian Lipkin**
Center for Infection and Immunity
Mailman School of Public Health
Columbia University

Dear Prof. Lipkin,

It is our deep pleasure to inform you that research conducted by you, together with Profs. Eran Bacharach from Tel Aviv University and Avi Eldar from the Kimron Veterinary Institute, on isolation and identification of the novel Tilapia Lake Virus, has been recognized for its outstanding scientific achievement and excellence. The research has been selected among the top 3most successful and impactful research projects in the environmental and social domains, amongst the 1,330 projects granted by the US-Israel Binational Research and Development fund over the entire 40 years of its existence. Please accept this formal letter of recognition with our warmest congratulations.

As you know, we have recently completed the BARD 40-year research impact assessment. The external review committee that oversaw the evaluation process was deeply impressed by your research approach leading to identification of the virus and establishing a first diagnostic tool, and the exceptional global implications following the elucidation of one of the primary disease concerns for tilapia farming worldwide. The findings were a stellar scientific breakthrough and have a tremendous impact on global food security, nutrition and farmers livelihoods.

The accomplishments driven from this research reflect the remarkable vision, dedication and persistence of the joint Israel-US team in pursuing and achieving ambitious scientific goals of tremendous value and the far-reaching implications for improved tilapia disease management and containment. In light of the above, we wish to recognize this research for its important social and environmental impact.

Furthermore, I would like to personally thank you for taking part in the survey and interviews. Your feedback was very much appreciated. The report is available online BARD 40-year review research impact evaluation report (Full case study featuring your research). I wish you and your colleagues much success in your further work, and, of course, wishing you all health during these times.

Sincerely yours,

**Prof. Yoram Kapulnik**
Executive Director

# Building a Global Immune System

**We have the tools needed to expedite and democratize microbial surveillance and discovery**

- Inexpensive, rapid, sensitive molecular methods for direct detection of microbial sequences

  *local outbreak investigation and surveillance of humans and potential zoonotic sources for Pathogen X*

- Multiplexed, granular methods for indirect detection and implication of infection through serology

  *early evidence of cross species transmission of Pathogen X and insights into chronic diseases like ME/CFS and PASC*

- Same tool kit can be used to broadly enhance biosecurity

  *detect threats to the food supply and the emergence of antimicrobial resistance*

**Missing components**

- Resources to build and sustain infrastructure for independent outbreak response and surveillance in low- and middle-income countries
- Commitment to sharing laboratory and clinical metadata
- International regulatory body that can facilitate clinical trials and approvals of diagnostics, drugs, and vaccines