

We don't know why you're sick. It must be a virus...

Metagenomics may provide the answer

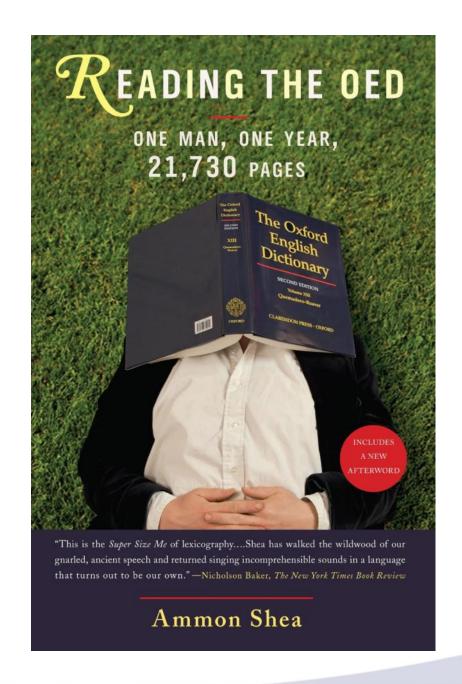
Dr Richard Hall

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apocryphal

Line breaks: apoc|ryph|al

Pronunciation: /əˈpɒkrɪf(ə)l •)) /

ADJECTIVE

(Of a story or statement) of doubtful authenticity, although widely circulated as being true: 'an apocryphal story about a former president' 'his alleged description of opera as 'fat gits singing' is probably apocryphal'







Mystery virus sidelines Stoner

NATIONAL | REGIONAL | SPORT | ELECTION 2014 | WOF

NATIONAL

CONC

2272 Shares

NEWS

Updated at 7:42 am on 12 August 2009

HOME

The battle for motor cycling's MotoGP championship has been reduced to a tw Australia's 2007 champion Casey Stoner to sit out the next three rounds of the

His world tour gigs on May 18 and 19 were postponed as doctors ordered "comple 3.03pm, Friday, 19 April 2013 rest" in his hotel room while he recuperated



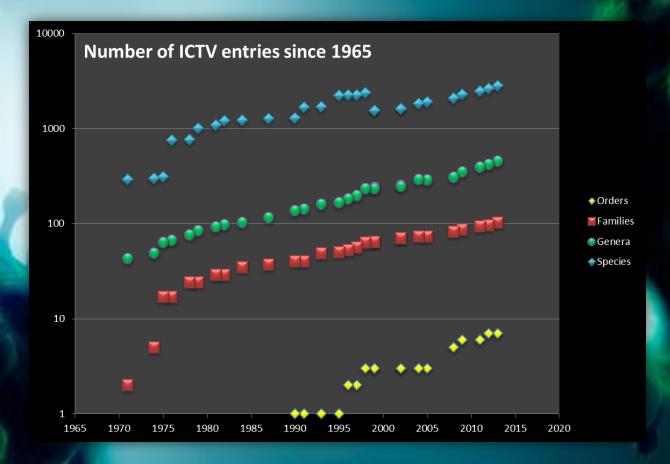
16° 7° Auckland •



coronation Street's Michelle Keegan has been signed off sick with a 'mystery' virus.

W 3 NEWS

Viruses: Discovery



"...estimate that there are a minimum of 320,000 mammalian viruses awaiting discovery..."

Anthony et al. (2013) mBio 4(5): e00598-13.

Viruses: Detection

- Clinical acumen
- Pathology
- Epidemiology
- Viral culture
- Electron microscopy
- qPCR





Metagenomic pipeline for virus discovery

Sample collection

Pre-processing or enrichment

Extract RNA / DNA







Illumina MiSeq



Oxford Nanopore (MinION)

Submission to NGS platform

NCBI Genbank

171 million known sequences

Mouse AGTCGTGTATATTTAGATCTCTCGTCTATAGATCGCTGCTATC...
Human GGTGCTCGCTATATAGCTCGCCTGCGTCTGCT...
E.Coli CCTCTGATGAGCTCTAGATATCGCTCGCGCGCGCTCTGGCGCTATG...
Bovine GGGTCGCTTCGCGCTCGCTATAGACTCTGCGCGGCGCT...
Ovine GCTCGGCTATAGGTTTTCGCTCTTCTCGATAGCTGATCTCGATC...
Ebola GGGTCTGCTCGCTAAATATATGATAATAGATATAGTAG...

Giardia GCTCGCGATTATAGAGATAGGAGAGGGCTCTCGCTCGCT...

Pairwise Comparison
Bioinformatics

Candidate Pathogen List

>5 million reads per sample

Read 1 AGATAGGATGAGAGAT

Read 2 ATAGATGGATAGAGGAGAGGATGAT Read 3 GCTCGTAGATAGATTAGAGAT

Read 4 AGATAGAGNNANATTAT Read 5 NNAGATAGGATAGGAT

Read 6 GGGATAGATATTAAATAGATATAG

Read 7 ACACACACACACACACACACACACACACA

Specific Assays for confirmation of identity of agent







"The FDA learned about the contamination after an academic research team using a novel technique to look for viruses in a range of vaccines found the material in GlaxoSmithKline's product and told the company" - CNN



Examples of viral metagenomics

- Detection of viruses in the air
- Application to unsolved outbreaks of gastroenteritis
- Trial on wastewater samples



Metagenomic detection of viruses in aerosol samples from workers in animal slaughterhouses

<u>Richard Hall¹</u>, Mily Leblanc-Maridor², Jing Wang¹, Una Ren¹, Nicole Moore¹ Colin Brooks², Matthew Peacey¹, Jeroen Douwes² and David McLean².





- 1. Institute of Environmental Science & Research, National Centre for Biosecurity & Infectious Disease, Wallaceville, Upper Hutt, New Zealand.
- 2. Centre for Public Health Research, Massey University, Wellington Campus, Wellington, New Zealand.



Mortality and cancer incidence in NZ Meat Workers

McLean et al. Occup Environ Med 2004;61:541-7

Cause of death (ICD-9)	Observed	Expected	SMR	95% CI
All Causes	227	203.6	1.12	0.98 - 1.27
All Cancer (140-208)	69	61.4	1.12	0.88 - 1.42
Lung (162)	23	12.9	1.79	1.13 – 2.68
Haematologic (200-208)	6	6.3	0.96	0.35 – 2.09

$$(n = 6,647)$$



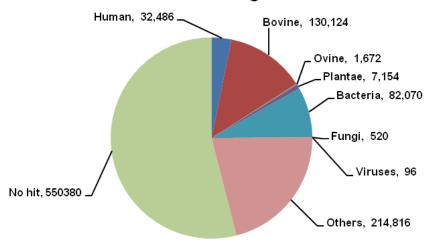


Metagenome of an aerosol sample

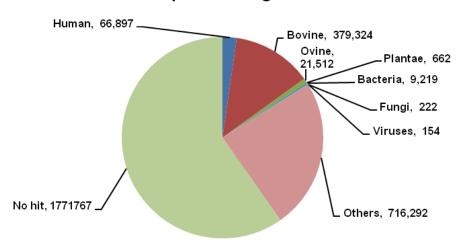
- PTFE aerosol filters
- Pooled samples (n = 9)
- Extracted DNA
 - Illumina HiSeq2000
 - 85bp reads (QC)
- Cattle area
 - 332 million reads
 - 145 million reads (collapsed)
- Sheep area
 - 250 million reads
 - 217 million reads (collapsed)



Cattle Processing Area



Sheep Processing Area



Identified two viruses:

WU polyomavirus

Suspected paedatric respiratory pathogen

Human papillomavirus 120

Recently discovered virus found at various sites on human skin. Role is any disease is unclear.

Hall et al. (2013) PLOS ONE 8(8): e72226



Bulk sampling

- Portable
 - 9 hour battery life
 - "Ruggedized"
- Increased sample size
 - Up to 310 litres per minute
 - 8 hour shift = 144,000 L
 - 150-fold greater than personal (960L)
- Sampled seven work areas
 - Sticking, Gutting, Boning room...
 - 24 x 8 hour shifts
 - n = 16 MiSeq, 250bp length, 170 million reads
- Metagenomic detection of veterinary pathogens
 - Adenoviruses
 - Bovine rotavirus
 - Bovine coronavirus





OPEN & ACCESS Freely available online



Enterovirus 74 Infection in Children

Matthew Peacey¹, Richard J. Hall¹, Jing Wang¹, Angela K. Todd¹, Seiha Yen¹, Jasmine Chan-Hyams¹, Christy J. Rand², Jo-Ann Stanton², Q. Sue Huang¹

1 Clinical Virology, The Institute of Environmental Science and Research, National Centre for Biosecurity and Infectious Disease, Wellington, New Zealand, 2 Department of Anatomy, University of Otago, Dunedin, New Zealand

Todd et al. Virology Journal 2013, 10:103 http://www.virologyj.com/content/10/1/103



RESEARCH

Open Access

Detection and whole genome sequence analysis of an enterovirus 68 cluster

Angela K Todd^{1*}, Richard J Hall¹, Jing Wang¹, Mathew Peacey¹, Sharla McTavish¹, Christy J Rand², Jo-Ann Stanton², Susan Taylor³ and Q Sue Huang¹

Journal of Virological Methods 195 (2014) 194-204



Contents lists available at ScienceDirect

Journal of Virological Methods





Evaluation of rapid and simple techniques for the enrichment of viruses prior to metagenomic virus discovery*



Richard J. Hall*, Jing Wang, Angela K. Todd, Ange B. Bissielo, Seiha Yen, Hugo Strydom, Nicole E. Moore, Xiaoyun Ren, Q. Sue Huang, Philip E. Carter, Matthew Peacey

Institute of Environmental Science and Research, at the National Centre for Biosecurity & Infectious Disease, 66 Ward Street, Wallaceville, Upper Hutt 5018, New Zealand

New Alphacoronavirus in Mystacina tuberculata Bats, New Zealand

Richard J. Hall, Jing Wang, Matthew Peacey, Nicole E. Moore, Kate McInnes, and Daniel M. Tompkins

Because of recent interest in bats as reservoirs of emerging diseases, we investigated the presence of viruses in *Mystacina tuberculata* bats in New Zealand. A novel alphacoronavirus sequence was detected in guano from roosts of *M. tuberculata* bats in pristine indigenous forest on a remote offshore island (Codfish Island).







Metagenomic analysis of unsolved outbreaks of gastroenteritis in New Zealand

Nicole Moore¹, Jing Wang¹, Joanne Hewitt², Dawn Croucher², Deborah Williamson¹, Shevaun Paine¹, Seiha Yen¹, Gail Greening², <u>Richard Hall</u>¹.

ESR, at National Centre for Biosecurity & Infectious Disease (NCBID), Upper Hutt, NZ.
 Norovirus Reference Laboratory, ESR, Porirua, NZ.



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"No specific pathogen or condition was identified in the remaining 25.1% (180/716) of outbreaks, all of which were recorded as gastroenteritis outbreaks."

Annual Summary of outbreaks in New Zealand 2012, ESR, Page 16



Table 2. Outbreaks and associated cases by pathogen, 2012

		Outbreaks ¹	Cases ¹		
Pathogen or condition	Total	% of outbreaks (n=716)	Median cases per outbreak	Total	% of cases (n=10 491)
Enteric ¹	656	91.6	7.0	9474	90.3
Norovirus	249	34.8	19.0	6097	58.1
Giardia spp.	69	9.6	3.0	284	2.7
Cryptosporidium spp.	47	6.6	3.0	164	1.6
Campylobacter spp.	32	4.5	3.0	282	2.7
Salmonella spp.	27	3.8	3.0	149	1.4
Rotavirus	23	3.2	15.0	360	3.4
Shigella spp.	12	1.7	2.5	43	0.4
Clostridium difficile	6	0.8	14.5	107	1.0
Yersinia spp.	5	0.7	3.0	14	0.1
Clostridium perfringens	4	0.6	4.5	18	0.2
Escherichia coli (EPEC)	3	0.4	23.0	63	0.6
Sapovirus	3	0.4	4.0	18	0.2
Astrovirus	2	0.3	2.5	5	0.0
Aeromonas spp.	1	0.1	8.0	8	0.1
Hepatitis A	1	0.1	30.0	30	0.3
Histamine fish poisoning	1	0.1	2.0	2	0.0
Plesiomonas shigelloides	1	0.1	3.0	3	0.0
Salmonella Paratyphi	1	0.1	2.0	2	0.0
Salmonella Typhi	1	0.1	2.0	2	0.0
Staphylococcus aureus	1	0.1	3.0	3	0.0
Toxic shellfish poisoning	1	0.1	29.0	29	0.3
VTEC/STEC infection	1	0.1	3.0	3	0.0
Pathogen not identified ²	180	25.1	6.0	1996	19.0



Metagenomic Analysis of Human Diarrhea: Viral Detection and Discovery

Stacy R. Finkbeiner^{1,2,5}, Adam F. Allred^{1,2,5}, Phillip I. Tarr³, Eileen J. Klein⁴, Carl D. Kirkwood⁵, David Wang^{1,2,4}

1 Departments of Molecular Microbiology and Pathology & Immunology, Washington University School of Medicine, St. Louis, Missouri, United States of America, 2 Department of Pathology & Immunology, Washington University School of Medicine, St. Louis, Missouri, United States of America, 3 Department of Pediatrics, Washington University School of Medicine, St. Louis, Missouri, United States of America, 4 Department of Emergency Medicine, Children's Hospital and Regional Medical Center, Seattle, Washington, United States of America, 5 Enteric Virus Research Group, Murdoch Childrens Research Institute, Royal Children's Hospital, Victoria, Australia

JOURNAL OF VIROLOGY, Oct. 2009, p. 10836–10839 0022-538X/09/\$08.00+0 doi:10.1128/JVI.00998-09 Copyright © 2009, American Society for Microbiology. All Rights Reserved. Vol. 83, No. 20

Identification of a Novel Astrovirus (Astrovirus VA1) Associated with an Outbreak of Acute Gastroenteritis[∇]

Stacy R. Finkbeiner, ¹† Yan Li, ²† Susan Ruone, ² Christina Conrardy, ² Nicole Gregoricus, ² Denise Toney, ³ Herbert W. Virgin, ¹ Larry J. Anderson, ² Jan Vinjé, ² David Wang, ¹* and Suxiang Tong ²*

JOURNAL OF VIROLOGY, June 2007, p. 5978–5984 0022-538X/07/\$08.00+0 doi:10.1128/JVI.02650-06 Copyright © 2007, American Society for Microbiology. All Rights Reserved. Vol. 81, No. 11

New Adenovirus Species Found in a Patient Presenting with Gastroenteritis[∇]

Morris Saffold Jones II, 1* Balázs Harrach, 5 Robert D. Ganac, 1 Mary M. A. Gozum, 1 Wilfred P. dela Cruz, 1 Brian Riedel, 2 Chao Pan, 2 Eric L. Delwart, 3,4 and David P. Schnurr 2

DISPATCHES

New Viruses in Idiopathic Human Diarrhea Cases, the Netherlands

Saskia L. Smits, Claudia M.E. Schapendonk, Janko van Beek, Harry Vennema, Anita C. Schürch, Debby Schipper, Rogier Bodewes, Bart L. Haagmans, Albert D. M. E. Osterhaus, and Marion P. Koopmans

Emerging viral infections can be identified by using a viral metagenomics approach for clinical human material. Diarrhea samples of patients with unexplained gastroenteritis from the Netherlands were analyzed by using viral metagenomics. Novel circular DNA viruses, bufaviruses, and genogroup III picobirmaviruses were identified. These data expand our knowledge of the human virome.

Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 20, No. 7, July 2014

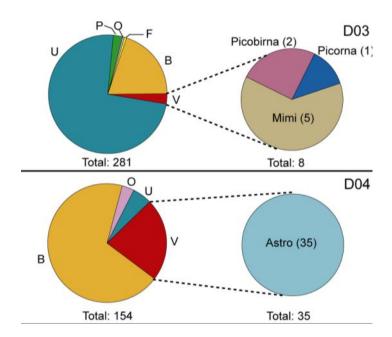


Metagenomic analysis of unsolved gastroenteritis outbreaks in New Zealand

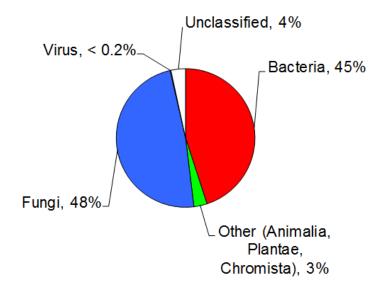
- 31 anonymous faecal samples from unsolved outbreaks
- Taken from 26 outbreaks occurring in 2011 / 2012
 - 5 outbreaks were subsequently resolved by public health investigations
- Illumina MiSeq
 - Pre-processing (spin, filter, nuclease)
 - NZGL / Massey Genome Service
 - Total of 193 million reads
 - Average of 3.1 million reads per sample
- BLASTN / BLASTX comparison to Genbank
- Eight viruses and one parasite identified







Adapted from FIGURE 1 in Finkbeiner et al. (2008) PLOS Pathogens 4(2):e1000011.



Hall et al. 2010. unpublished data



Candidate pathogenic organisms detected in metagenomic data from unsolved outbreaks of gastroenteritis, and results of independent confirmatory testing.

Metagenomic data		Independent test				
Candidate pathogen	Number of samples	% of total number of samples	Method	Result	Diseases already known to be associated with the candidate pathogen	
Adenovirus	1	3%	qPCR	Confirmed	Gastroenteritis, respiratory illness	
Human enterovirus B	2	7%	qPCR	Confirmed ¹	Paralysis; gastrointestinal symptoms ² ; HFMD ³	
Human parechovirus type 3	1	3%	RT-PCR	Confirmed	Neonatal sepsis, encephalitis, paralysis	
Human picobirnavirus	10	33%	-	-	Gastroenteritis	
Influenza A virus	1	3%	RT-PCR	Not confirmed	Respiratory illness, gastrointestinal symptoms ¹	
Pepper mild mottle virus	3	10%	-	-	Plant virus; link to abdominal pain in humans⁴	
Rotavirus	1	3%	Immunoassay, qPCR	Confirmed	Gastroenteritis	
Sapovirus	1	3%	qPCR	Confirmed	Gastroenteritis	
Dientamoeba fragilis	4	13%	qPCR	Confirmed	Possible link to gastroenteritis	
No candidates	11	37%	-	-	-	

¹ Confirmed in one sample only.



² Gastrointestinal symptoms are classified as vomiting and diarrhea

³ HFMD: Hand, foot and mouth disease

⁴ Colson et al. (2010) PLOS ONE 5(4):e10041

Conclusions

- No evidence for novel viruses
- Human parechovirus 3
 - Unknown role in outbreak
 - Significant pathogen causing neonatal sepsis, encephalitis, paralysis
 - First reported detection in Australasia
- Use for metagenomics as a diagnostic audit tool





Viruses in wastewater

Richard Hall¹, Jing Wang¹, Nicole Moore¹, Gail Greening², Dawn Croucher², Joanne Hewitt².

1. ESR, at National Centre for Biosecurity & Infectious Disease (NCBID), Upper Hutt, NZ.

2. Norovirus Reference Laboratory, ESR, Porirua, NZ.



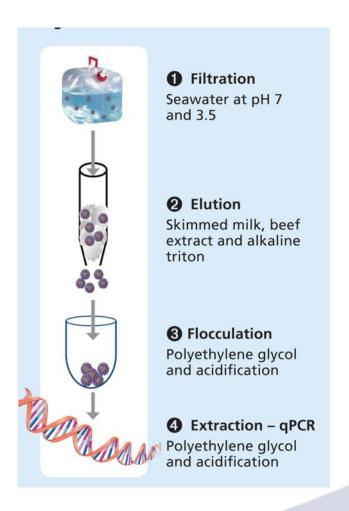
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Metagenomic analysis of New Zealand wastewater

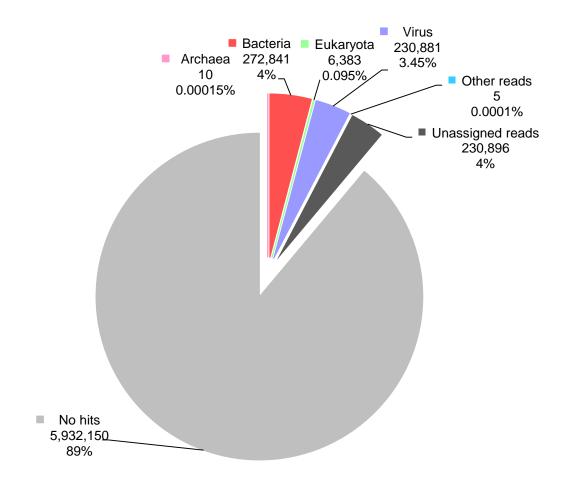
- One site (anonymous)
- Sampled 1 litre of wastewater (influent)
- 6,688,368 sequence reads x 250 bp PE
- BLASTX comparison to Genbank





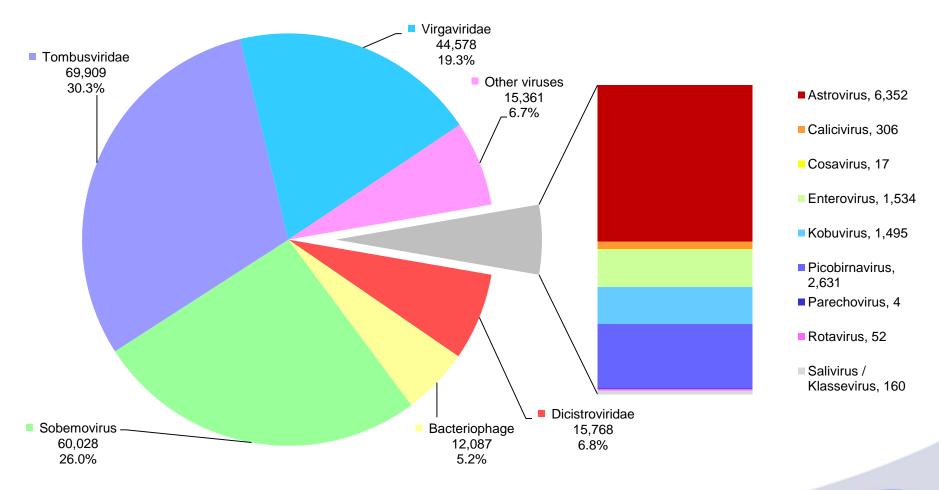


Metagenomic composition of wastewater sample





Subset of viruses present within metagenome



Hall et al. (2014) Unpublished

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- Health Research Council of New Zealand
- Ministry of Health







