

**Next Generation Sequencing –
The Role of New Sequence Technologies in Shaping the
Future of Veterinary Science**

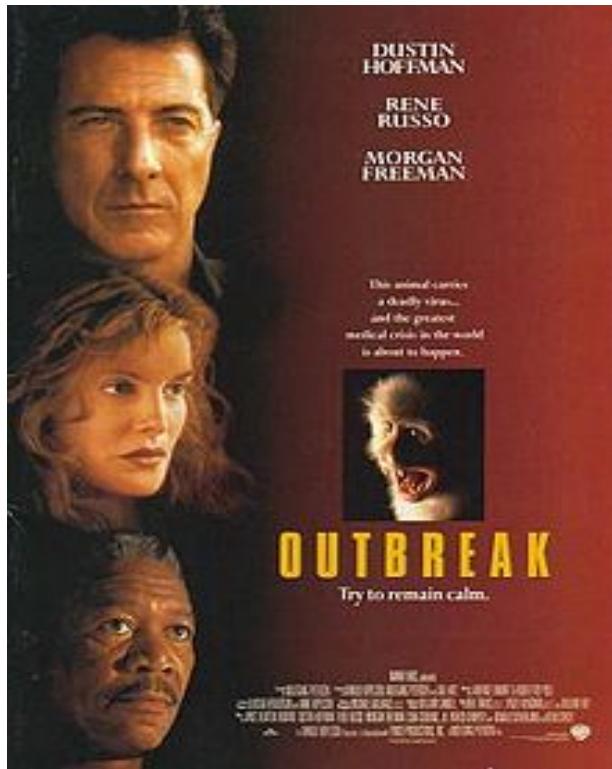
Hosted by the RCVS Charitable Trust





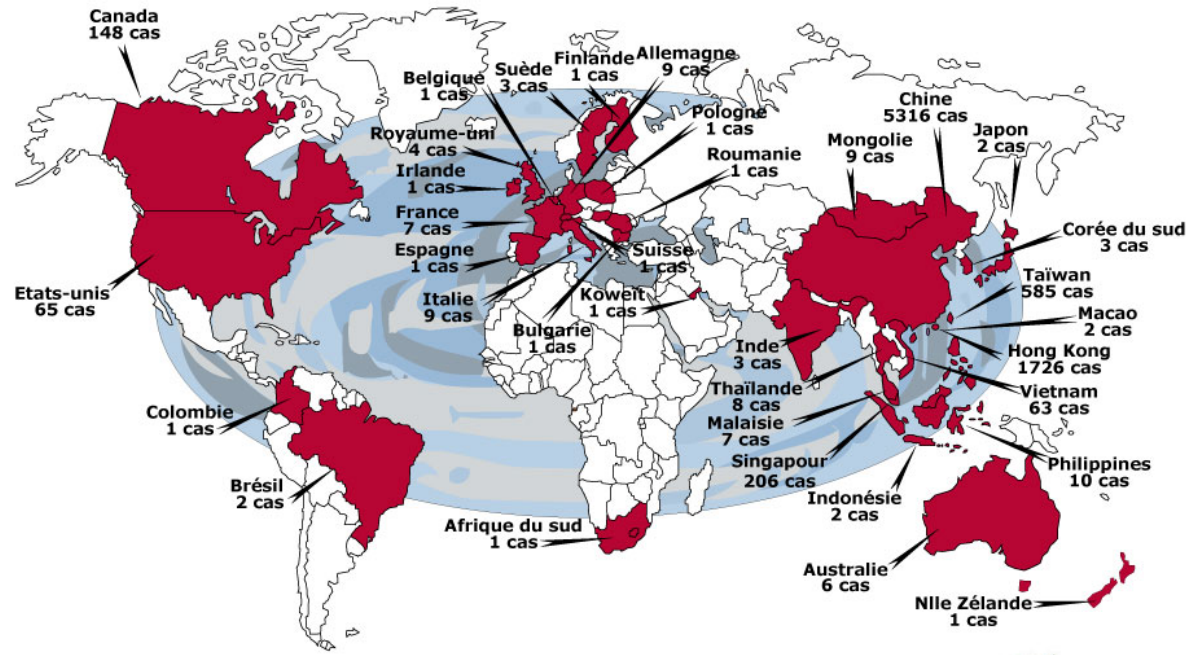
Discovery





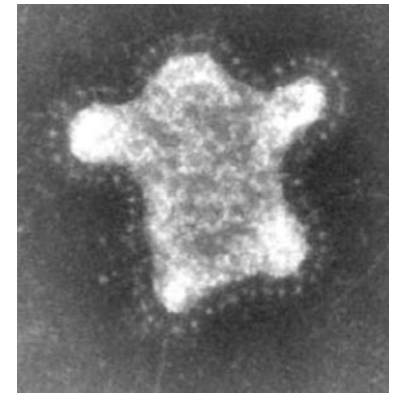
LE SRAS DANS MONDE

au 26 Mai 2003 on dénombre
au total : 8202 cas



■ Pays touchés par le SRAS et recensés par l'OMS

travelsante.com
la planète santé







World Health Organization

Home

Media centre

About WHO

[WHO](#) > [Programmes and projects](#) > [Media centre](#) > [News releases](#) > [News releases 2003](#)

Countries

[printable version](#)

Health topics

Coronavirus never before seen in humans is the cause of SARS

Publications

Unprecedented collaboration identifies new pathogen in record time

Data and statistics

Programmes and projects

16 April 2003 | GENEVA -- Today, the World Health Organization announced that a new pathogen, a member of the coronavirus family never before seen in humans, is the cause of Severe Acute Respiratory Syndrome (SARS). The speed at which this virus was identified is the result of the close international collaboration of 13 laboratories from 10 countries. While many lines of evidence have found strong associations between this virus and the disease over the last weeks, final confirmation came today.

Media centre

News

"The pace of SARS research has been astounding," said Dr. David Heymann, Executive Director, WHO Communicable Diseases programmes. "Because of an extraordinary collaboration among laboratories from countries around the world, we now know with certainty what causes SARS."

Events

The successful identification of the coronavirus means that scientists can now confidently turn to other SARS challenges. For example, various laboratories continue to work to unravel the genetic information of the SARS virus and compare the sequences obtained from viruses in different parts of the world. Experts are gathering at WHO this week to map future work on SARS.

Fact sheets

"Today, the collaboration continues as top laboratory researchers have come to WHO to design the next steps, a strategy for transforming these basic research discoveries into diagnostic tools which will help us to successfully control this disease," said Heymann.

Multimedia

This collaboration has brought together leading scientific expertise, and was established after WHO issued a global alert on SARS on 12 March 2003. The priority has been to find the cause and to develop diagnostic tests. Two laboratories in China recently joined this network of laboratories from Canada, France, Germany, Hong Kong Special Administrative Region of China, Japan, the Netherlands, Singapore, the United Kingdom, and the United States of America.

Contacts

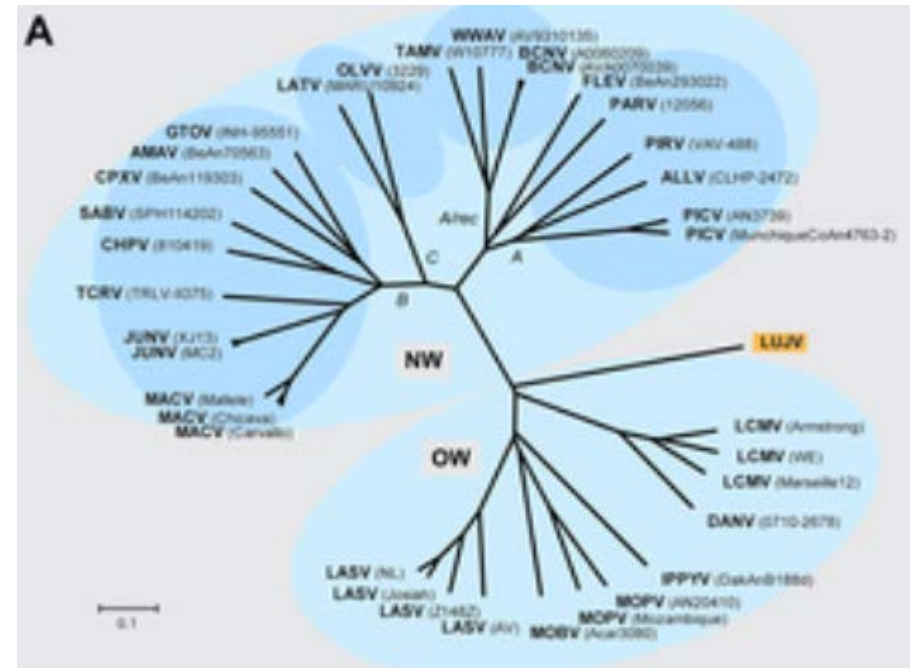
"Today, the first part of the mission of our network has been fulfilled, as researchers have both



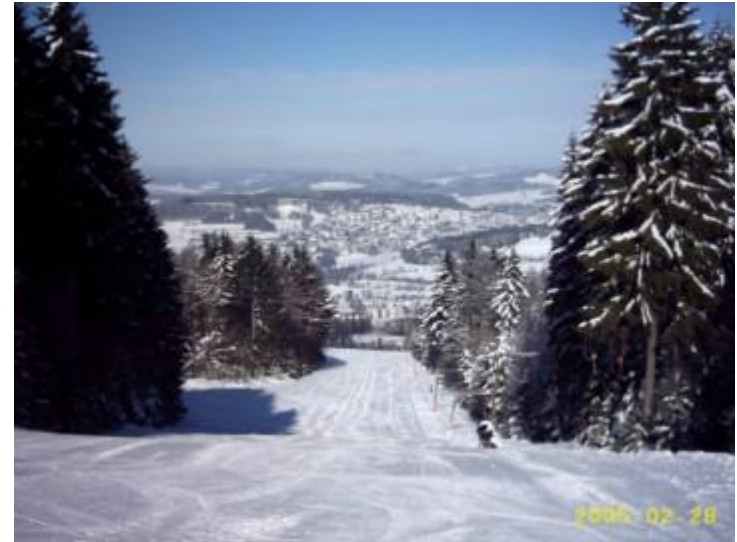
16 November 2002	N	→	First known case of atypical pneumonia occurs in Foshan City, Guangdong Province, China, but is not identified until much later.
	D		
	J		
21 February 2003	F	→	64-year-old medical doctor Guangzhou (Guangdong Province) arrives in Hong Kong to attend a wedding.
12 March	M	→	WHO issues a global alert about cases of severe atypical pneumonia following mounting reports of spread among staff at hospitals in Hong Kong and Hanoi.
27 March	A	→	Scientists in the WHO lab network identify causative agent, with results from several labs consistently pointing to a new member of the coronavirus family.
30 May	M	→	Full SARS genome sequenced.
	J		
5 July	J	→	WHO declares that SARS outbreaks have been contained worldwide, but calls for continued vigilance.



In 2008 an outbreak of unexplained hemorrhagic fever was reported in South Africa. The index patient was admitted on September 12 to a clinic in South Africa. Over the following two weeks secondary and tertiary cases were reported, with four out of the five patients dying. **Such outbreaks of haemorrhagic fever are highly emotive events, necessitating a rapid response both to control infection and to control public anxiety.** RNA extracts from two post-mortem liver biopsies (cases 2 and 3) and one serum sample (case 2) were submitted to NGS on the Roche 454. Blast analysis of the resulting sequences identified contigs corresponding to about half of a novel arenavirus ~10kb genome ([Briese et al., 2009](#)). The majority of sequences were obtained from serum rather than tissue, presumably a reflection of the higher levels of host DNA obtained from the highly cellular tissue samples.



Briese, T., Paweska, J. T., McMullan, L. K., Hutchison, S. K., Street, C., Palacios, G., Khristova, M. L., Weyer, J., Swanepoel, R., Egholm, M., Nichol, S. T. & Lipkin, W. I. (2009). Genetic detection and characterization of Lujo virus, a new hemorrhagic fever-associated arenavirus from southern Africa. *PLoS Pathog* 5, e1000455.



SCHM  Kultur- und Einkaufsstadt
LLENBERG



Novel Orthobunyavirus in Cattle, Europe, 2011

Bernd Hoffmann,¹ Matthias Scheuch,¹ Dirk Höper, Ralf Jungblut, Mark Holsteg, Horst Schirrmeier, Michael Eschbaumer, Katja V. Goller, Kerstin Wernike, Melina Fischer, Angele Breithaupt, Thomas C. Mettenleiter, and Martin Beer

Emerging Infectious Diseases 2012. Vol 8 (3), 469-72

Seven orthobunyavirus sequences were detected in the library prepared from pooled RNA from 3 animals of 1 farm



Table. Output of raw sequence data for the sequencing libraries in the analysis of a novel orthobunyavirus in cattle, Europe, 2011

Sample	Total no. reads	No. reads classified into superkingdom					No. unclassified reads
		Eukaryota	Archaea	Bacteria	Viruses	Root	
BH 80/11 RNA (3 pooled samples)	27,413	12,296	4	13,363	55 (Myoviridae, Siphoviridae, Podoviridae, Bunyaviridae, Retroviridae, Papillomaviridae)	377	1,318

Defra homepage

AHVLA home

▶ About us

▶ News

▶ Contact AHVLA

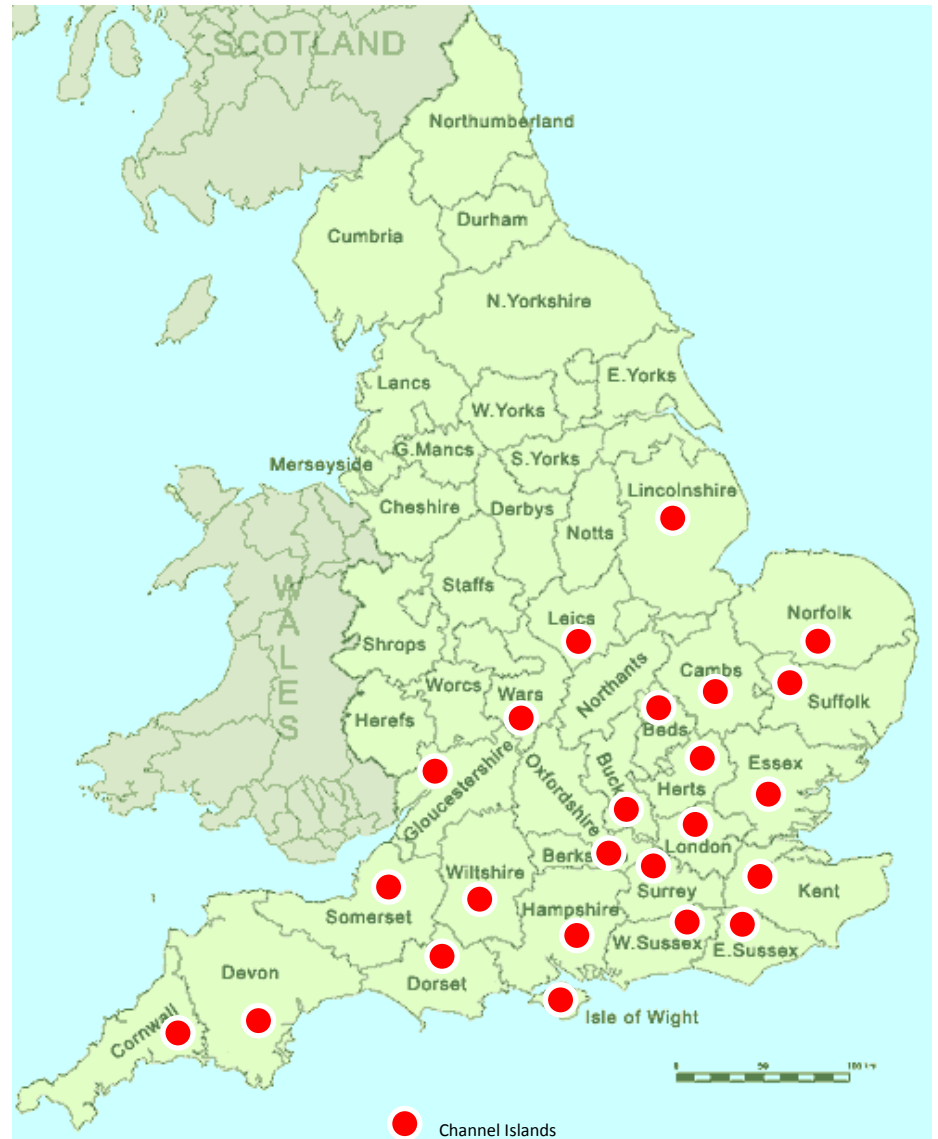
11 June – Schmallenberg virus: further update on GB testing results

There are 267 UK farms reporting SBV: 45 in cattle and 219 in sheep and 3 premises which reported sheep (earlier in the year) and are now also reporting cattle cases. There are no new reported cases since the 6 June 2012.

We have adjusted some of the current total numbers for the counties where some premises lie close to a county boundary. This has no bearing on the distribution of infection when it occurred last summer or on our assessment of the risk of incursion of potentially infected midges from Continental Europe. It is a consequence of more detailed ongoing work following up affected premises in order to assess impact.

Figures correct as of 11 June 2012

County	Positive holdings (Sheep)	Positive holdings (Cattle)	Other species	Positive holdings (cattle and sheep)	Total
Bedfordshire	1	0	0	0	1
Berkshire	2	0	0	0	2
Buckinghamshire	1	0	0	0	1
Cambridgeshire	1	1	0	0	2
Channel Islands	4	0	0	0	4
Cornwall	2	1	0	0	3
Devon	7	2	0	0	9
Dorset	5	0	0	0	5
East Sussex	39	5	0	0	44
Essex	11	2	0	0	13
Greater London	1	0	0	0	1
Hampshire	13	1	0	1	15
Hertfordshire	6	0	0	0	6
Isle of Wight	2	1	0	0	3
Kent	39	7	0	0	46
Leicestershire	1	0	0	0	1
Lincolnshire	1	0	0	0	1
Norfolk	15	5	0	1	21
North Somerset and Gloucestershire	4	0	0	0	4
Somerset excluding North Somerset	3	0	0	0	3
Suffolk	13	10	0	0	23
Surrey	5	3	0	0	8
Warwickshire	2	0	0	0	2
West Sussex	34	5	0	1	40
Wiltshire	7	2	0	0	9
Total	219	45	0	3	267





Contents lists available at ScienceDirect

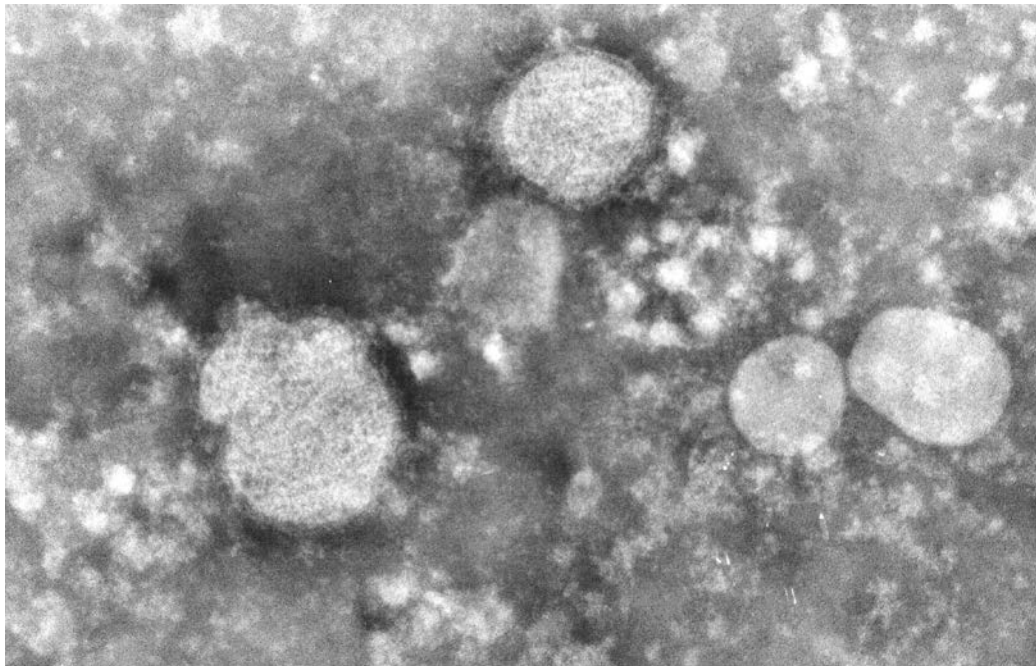
Preventive Veterinary Medicine

journal homepage: www.elsevier.com/locate/prevetmed



A case–control study of pathogen and lifestyle risk factors for diarrhoea in dogs

Jenny Stavisky^{a,*}, Alan David Radford^b, Rosalind Gaskell^b, Susan Dawson^b, Alex German^c, Bryony Parsons^b, Simon Clegg^b, Jenny Newman^b, Gina Pinchbeck^b



In 80 cases of diarrhoea..

7 CECoV

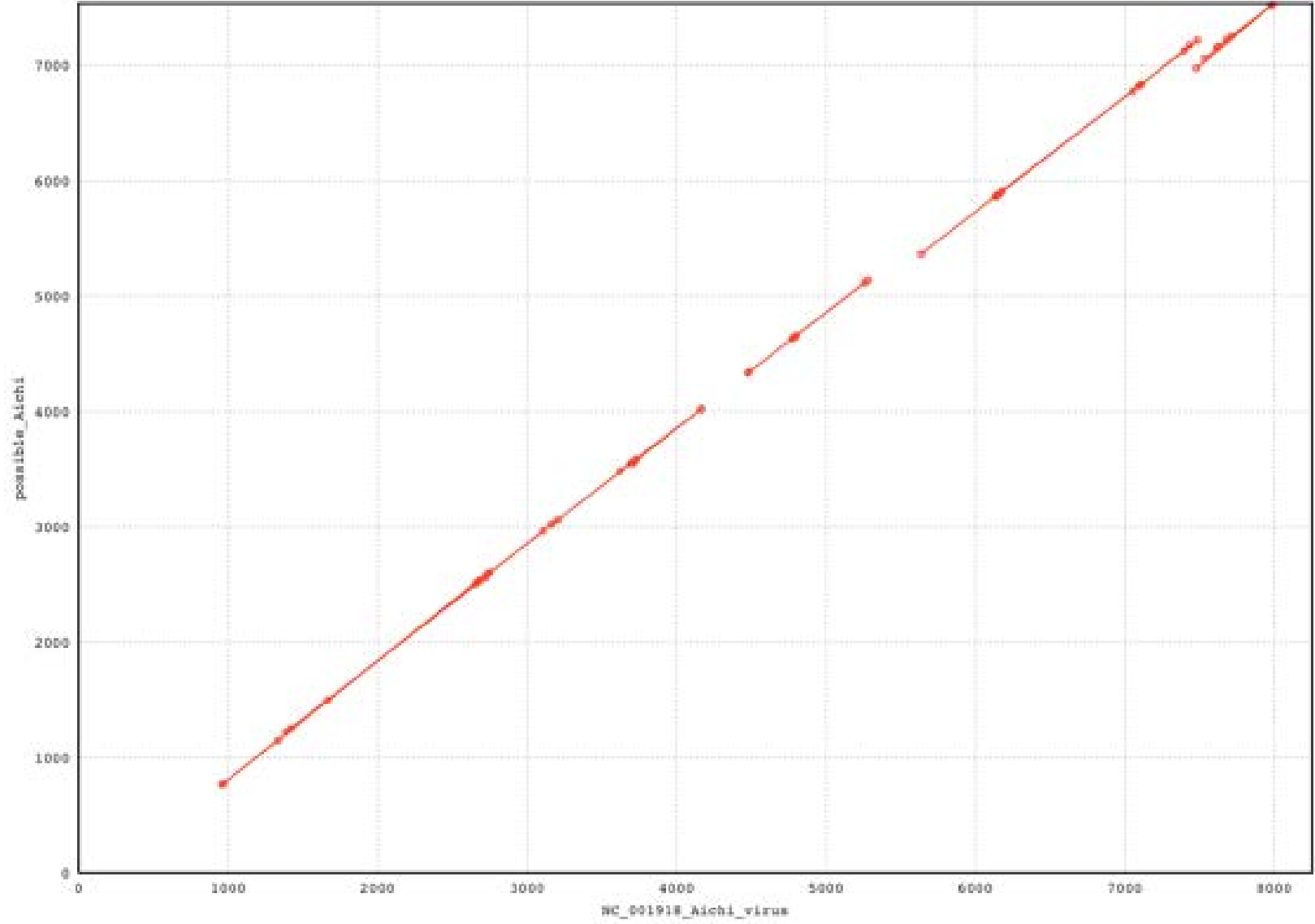
4 CPV

24 Campylobacter

1 Salmonella

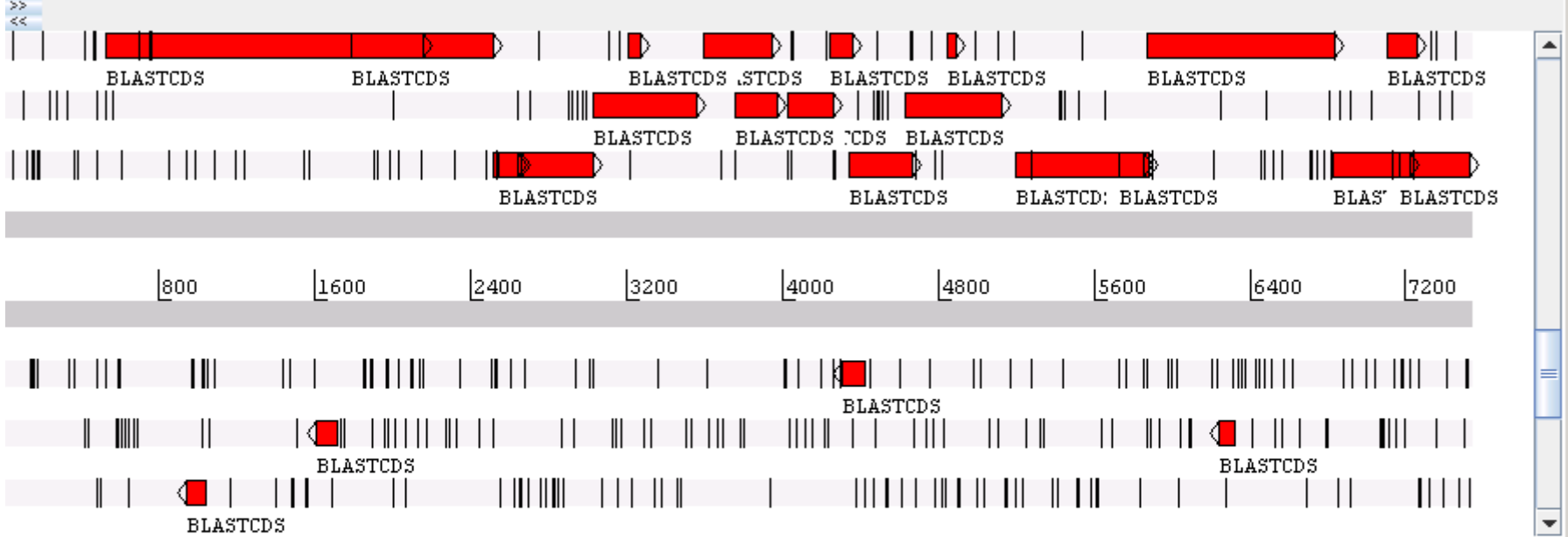
5 Helminths

39 ??



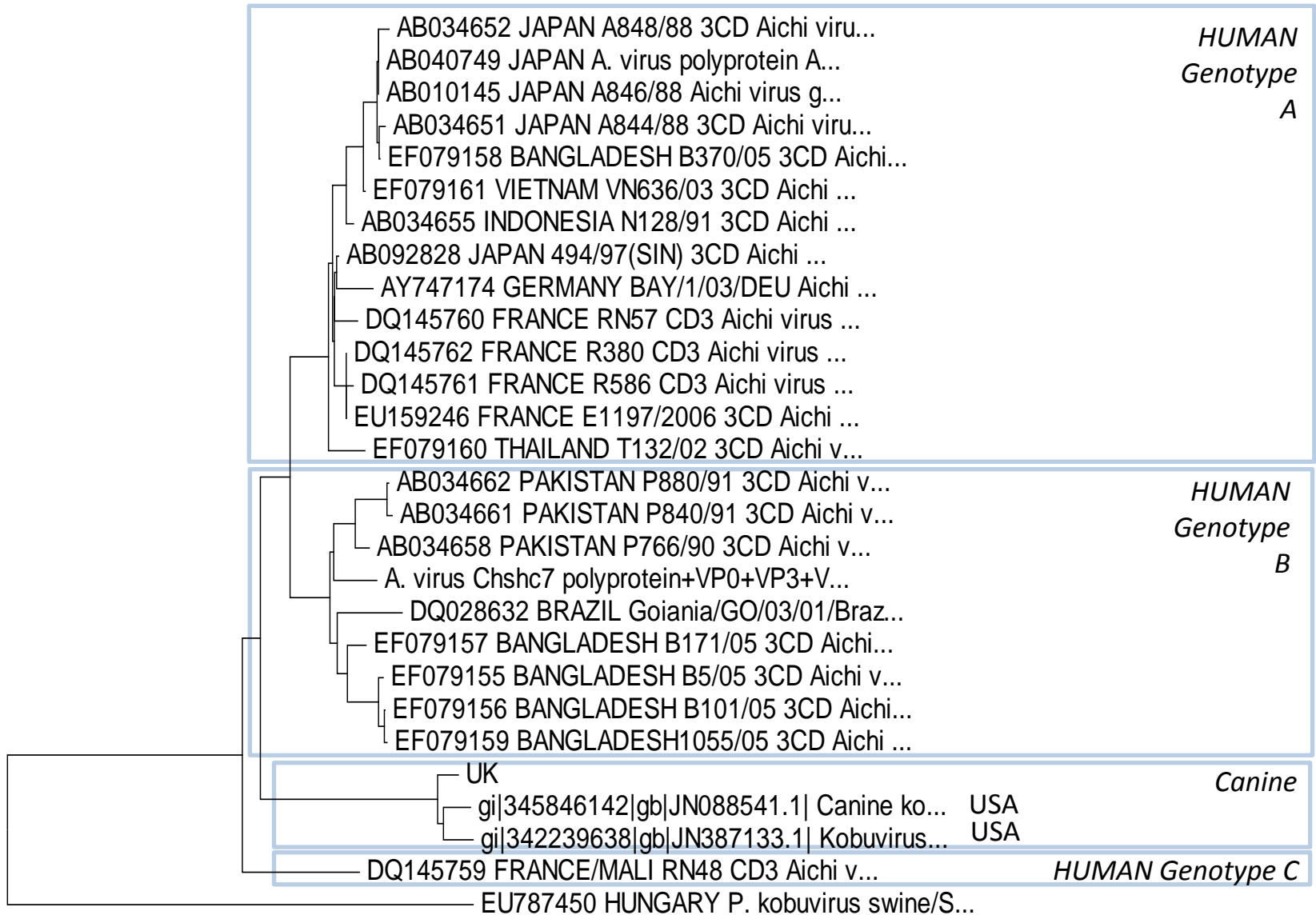
Entry: draft1.1.fna draft1.1.blastx.tab

Nothing selected



Navigation bar with left and right arrows and a vertical scrollbar.

```
+ V S L S S G L L P S S P P A * R D T G C A K T P R K L P K V A I V G S P L C K G V
R S P F P L G F C P A L P Q P D V T Q A V Q R P R E S C Q K W Q L + G L P F V K A
. G L P F L W A S A Q L S P S L T * H R L C K D P A K A A K S G N C R V S P L # R R
TAGGTCTCCCTTTCTCCTCTGGGCTTCTGCCAGCTCTCCCCAGCCTGACGTGACACAGGCTGTGCAAAGACCCCGCAAAGCTGCCAAAAGTGGCAATTGTAGGGTCTCCCTTTGTAAAGCGGT
|20 |40 |60 |80 |100 |120
ATCCAGAGGGAAAGGAGACCCGAAGACGGGTTCGAGAGGGGGTCCGACTGCACTGTGTCCGACACGTTTCTGGGGCGCTTTTCGACGGTTTTTCACCGTTAACATCCCAGAGGGGAAACATITCCGCA
P R G K R Q A E A W S E G L R V H C L S H L S G A F A A L L P L Q L T E G K Y L R
. T E R E E P S R G L E G G A Q R S V P Q A F V G R F S G F T A I T P D G R Q L P T
L D G K G R P K Q G A R G W G S T V C A T C L G R S L Q W F H C N Y P R G K T F A D
```



0.05

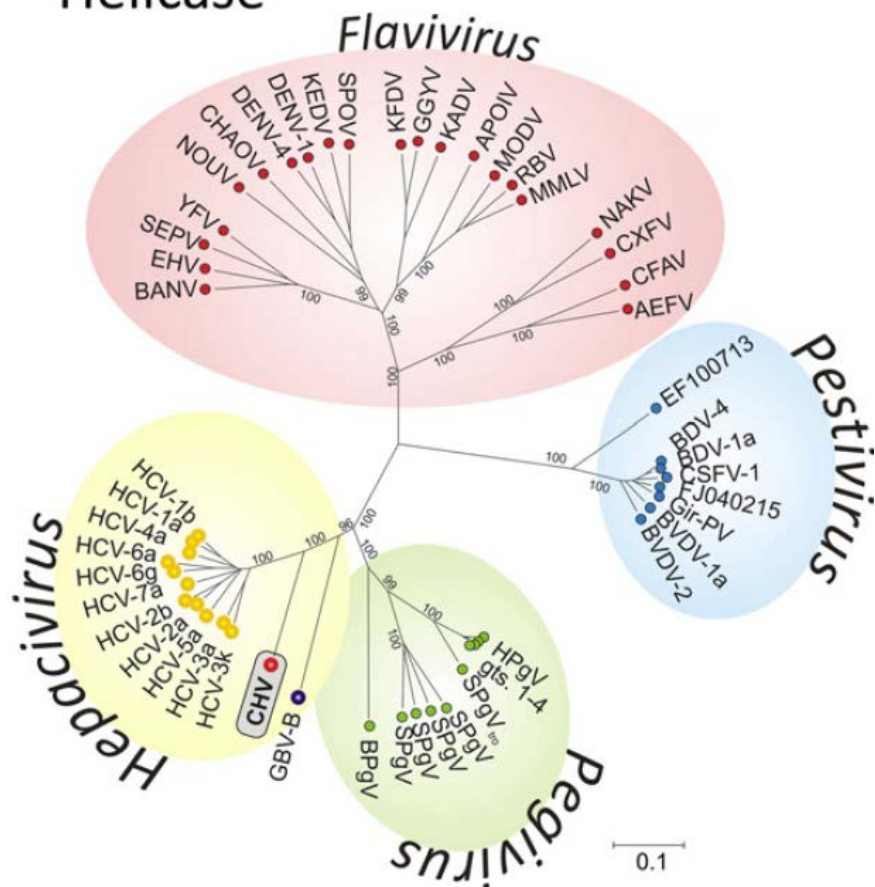
Characterization of a canine homolog of hepatitis C virus

Amit Kapoor^{a,1}, Peter Simmonds^b, Gisa Gerold^c, Natasha Qaisar^a, Komal Jain^a, Jose A. Henriquez^a, Cadhla Firth^a, David L. Hirschberg^a, Charles M. Rice^c, Shelly Shields^d, and W. Ian Lipkin^a

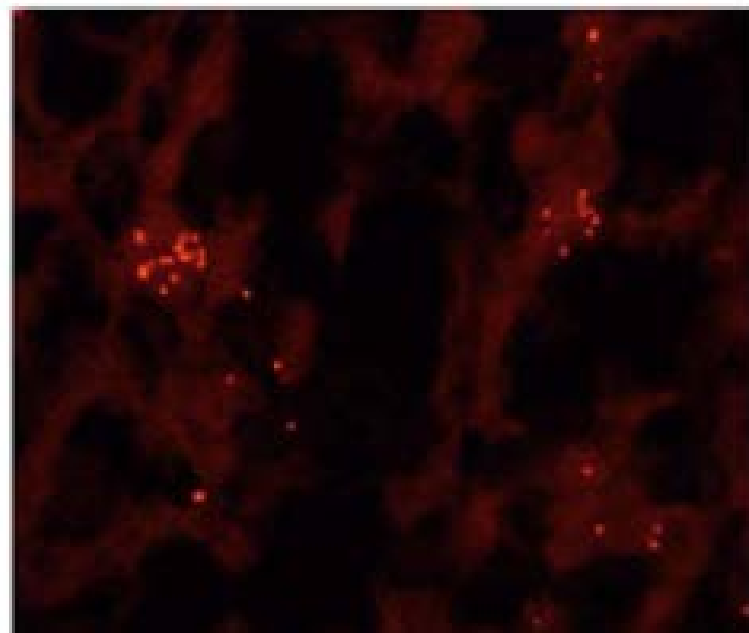
^aCenter for Infection and Immunity, Columbia University, New York, NY 10032; ^bCentre for Immunology, Infection and Evolution, Ashworth Laboratories, University of Edinburgh, Edinburgh EH9 3JT, United Kingdom; ^cCenter for the Study of Hepatitis C, Laboratory of Virology and Infectious Disease, The Rockefeller University, New York, NY 10065; and ^dPfizer Veterinary Medicine Research and Development, New York, NY 10017

Edited by Robert H. Purcell, National Institutes of Health, Bethesda, MD, and approved April 28, 2011 (received for review February 1, 2011)

Helicase



2 of 5 respiratory outbreaks
0 of 60 healthy dogs
5 of 19 livers



General principles

- Samples low in host material
 - Serum, diarrhoea, CSF
- Enrichment
 - Centrifugation, DNase / RNase digestion, filtration
- Extraction
 - RNA +/- DNA
- Amplification
 - Random
- Informatics

**Next Generation Sequencing –
The Role of New Sequence Technologies in Shaping the
Future of Veterinary Science**

Hosted by the RCVS Charitable Trust

