WOAH Collaborative Centre Reports Activities 2025

This report has been submitted: 12 mars 2026 12:24

CENTRE INFORMATION

***Title of WOAH Collaborating Centre**	Viral Genomics and Bioinformatics
***Address of WOAH Collaborating Centre**	Medical Research Council
***Tel:**	+441413302541
***E-mail address:**	Linda.Rushworth@glasgow.ac.uk
Website:	https://www.gla.ac.uk/research/az/cvr/
***Name Director of Institute (Responsible Official):**	Prof Emma Thomson
***Name (including Title and Position) of Head of the Collaborating Centre (WOAH Contact Point):**	Prof Massimo Palmarini
***Name of the writer:**	Prof David L Robertson

TOR 1 AND 2: SERVICES PROVIDED

1. Activities as a centre of research, expertise, standardisation and dissemination of techniques within the remit of the mandate given by WOAH

Category	Title of activity	Scope
Epidemiology, surveillance, risk assessment, (true)	Bat Virus Evolution Suggests Wildlife Trade Sparked COVID-19 Virus Emergence in Humans	Researchers from UC San Diego and the CVR found that the ancestor of SARS CoV 2 likely originated in Western China or Northern Laos only a few years before COVID 19 appeared far away in Central China - too short a time for natural bat migration to account for the spread. By analysing non recombining regions of viral genomes to overcome the complications of frequent recombination in horseshoe bats, they showed that sarbecoviruses have circulated across Western China and Southeast Asia for millennia, moving at the same pace as their bat hosts. Their findings suggest the virus probably reached Central China through the wildlife trade, similar to the pathway behind the 2002 SARS outbreak, highlighting the growing risks of zoonotic spillover due to wildlife trafficking, habitat loss, and increasing human–animal contact, and underscoring the importance of continued viral surveillance in bats to anticipate future pandemics.
		Viral genomics and bioinformatics deliver bespoke training to a range of CVR trainees, including postdoctoral researchers and PhD students, as well as external training to international partners with the aim of stimulating collaborations, supporting capacity building and increasing the CVR's response capacity. The 2025 external Virus

Training, capacity building (true)	Viral Bioinformatics and Genomics Training Course	Genomics and Bioinformatics course ran in Glasgow in June. Attendees were from 10 different countries, including from New Zealand and Republic of Korea, with many participants having affiliations to WOAH. The team also play a major role in designing and delivering external Viral bioinformatics and genomics courses in collaboration with Wellcome Connecting Science. Since 2022, see https://coursesandconferences.wellcomeconnectingscience.org/our-events/global-training/
Zoonoses (true)	Tracking Adaptation of H5N1 in Dairy Cattle	H5N1 avian influenza has been infecting U.S. dairy cows since March 2024. CVR researchers found that newer virus variants infect cow cells and mammary tissue more effectively than older ones. By analysing viruses spanning 60 years of H5N1 evolution, they showed that this increasing ability results from gradual genetic changes. The study also found wide differences in how well bird flu viruses replicate in cow cells, meaning some strains may already be closer to infecting cattle and other mammals. As H5N1 continues to spread and adapt, the risk of strains emerging that could infect humans grows, highlighting the need for ongoing testing and surveillance in livestock.
Zoonoses (true)	Avian influenza viruses are resistant to fever	A team including researchers at the CVR discovered a gene that helps determine how well influenza viruses cope with high temperatures. Human flu viruses struggle to replicate at fever temperatures, but avian influenza viruses, which naturally infect birds at 40–42°C, can continue to thrive. Using mouse models, the team showed that the PB1 gene is key: viruses with an avian type PB1 could withstand fever temperatures and caused more severe illness. This matters because human and avian flu viruses can exchange genes when they infect the same host. The findings may influence future treatment approaches, although more research is needed. While fever is often reduced with drugs like ibuprofen or aspirin, some clinical evidence suggests suppressing fever may not always help recovery and could even increase influenza A transmission.
Zoonoses (true)	Understanding the Spread of Influenza in Vampire Bats	Bat flu viruses like H18N11 are mostly found in Central and South American fruit bats. CVR researchers studied how this unusual flu spreads in common vampire bats, which feed on many species, including livestock and humans. Using a 12 year dataset tracking individual bats, they modelled long term transmission and found that immunity, seasons, and even a major rabies control culling campaign affected flu spread — with influenza transmission dropping by half during culls, even though rabies didn't decline. The results suggest vampire bats are likely reservoirs for H18N11, with regular infection peaks that could allow spillover to other species. The study underscores the need to monitor animals that interact closely with vampire bats and shows that wildlife disease control can have unexpected effects.
Zoonoses (true)	Predicting the effect of mammalian adaptive mutations (supported by Trailmap funding)	The Influenza Genome Database (Flu-gDB) and its associated Flu Mutation Explorer platform constitute a platform for the identification, standardisation, and dissemination of knowledge on host adaptation mutations in influenza A viruses. The resource brings together systematically curated evidence from the scientific literature and deep mutational scanning studies, linking individual mutations to experimentally supported phenotypic effects relevant to host adaptation, pathogenicity, and emergence risk. By integrating these curated mutation datasets with large-scale, standardised genomic alignments and phylogenetic frameworks, the platform enables transparent and reproducible assessment of adaptive mutations across global influenza diversity. This will support international efforts in influenza surveillance, risk assessment, and preparedness, complementing activities undertaken by WOAH, WHO, and national

		public health agencies.
Training, capacity building (true)	Metagenomics training	Training in metagenomics at the CVR of Edoardo Giussani and Alessandro Sartori (6th - 9th May), visitors from the Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe) - WOAH Reference Laboratory for Avian Influenza and Newcastle Disease.

TOR 3: HARMONISATION OF STANDARDS

2. Proposal or development of any procedure that will facilitate harmonisation of international regulations applicable to the main fucus area for which you were designated

Proposal title	Scope/Content	Applicable Area

3. In exercising your activities, have you identified any regulatory research needs* relevant for WOAH?

No

4. Did your Collaborating Centre maintain a network with other WOAH Collaborating Centres (CC), Reference Laboratories (RL), or organisations designated for the same specialty, to coordinate scientific and technical studies?

Yes

Name of WOAH CC/RL/other organisation(s)	Location	Region of networking Centre	Purpose
The Pirbright Institute	United Kingdom	Europa	We've established an MOU with the Pirbright Institute (and UKHSA) under the umbrella of the Virus Research Institute model to work closer together around the theme of preparedness.

TOR 4 AND 5: NETWORKING AND COLLABORATION

5. Did your Collaborating Centre maintain a network with other WOAH Collaborating Centres, Reference laboratories, or organisations in other disciplines, to coordinate scientific and technical studies?

No

TOR 6: EXPERT CONSULTANTS

6. Did your Collaborating Centre place expert consultants at the disposal of WOAH?

Yes

Name of expert	Kind of consultancy	Subject
Richard Orton	Richard Orton is a member of the WOAH Emerging Diseases working group, whose activities in 2025 were focused on developing an Emerging Disease Threats Watchlist for WOAH.	Emerging diseases

TOR 7: SCIENTIFIC AND TECHNICAL TRAINING

7. Did your Collaborating Centre provide advice/services to requests from Members in your main focus area?

Yes

Provided sequencing and bioinformatics advice to the team of Isabella Monne at Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe) - WOAH Reference Laboratory for Avian Influenza and Newcastle Disease.

8. Did your Collaborating Centre provide scientific and technical training, within the remit of the mandate given by WOAH, to personnel from WOAH Members?

Yes

a) Technical visit : 6

b) Seminars : 0

c) Hands-on training courses: 32

d) Internships (>1 month) : 0

Type of technical training provided (a, b, c or d)	Content	Country of origin of the expert(s) provided with training	No. participants from the corresponding country
C	Viral bioinformatics training course 16th – 20th June. Institutes of participants with affiliations to WOAH: IRTA-CReSA (Animal Health Research Center) Animal Plant and Health Agency National Veterinary Research Institute in Pulawy IZSAM - Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise Animal and Plant Quarantine Agency Istituto Zooprofilattico Sperimentale (IZS Teramo), Italy Friedrich-Loeffler-Institut Istituto Zooprofilattico Sperimentale del Lazio e della Toscana VISAVET Health Surveillance Centre. Complutense University of Madrid (Spain)	UK, China, Croatia, Germany, Italy, Malaysia, Nigeria, Poland, Republic of Korea, Spain.	16
C	In collaboration with Wellcome Connecting Science we ran a week long Genomics and Clinical Virology course in March 2025 in Hinxton, Cambridge, UK.	UK	16
A	In collaboration with the International Atomic Energy Agency (IAEA), and collabroators from the Pirbright Institute (UK), Sciensano (Belgium), University of Freiburg (Germany) and IZSAM (Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise, Italy) we developed viral bioinformatics training material to support the IAEA's the NGS sequency service/platform GenPat-VETLAB.	UK, Belgium, Germany, Italy	6

TOR 8: SCIENTIFIC MEETINGS

9. Did your Collaborating Centre organise or participate in the organisation of scientific meetings related to your main focus area on behalf of WOAH?

Yes

National/International	Title of event	Co-organiser	Date	Location	No. Participants
Nationally	UKRI One Health	N/A	2025-04-24	University of Glasgow	100

	Computational Network Symposium				

TOR 9: DATA AND INFORMATION DISSEMINATION

10. Publication and dissemination of any information within the remit of the mandate given by WOAH that may be useful to Members of WOAH

a) Articles published in peer-reviewed journals:

14

FluMut: a tool for mutation surveillance in highly pathogenic H5N1 genomes. Giussani E, Sartori A, Salomoni A, Cavicchio L, de Battisti C, Pastori A, Varotto M, Zecchin B, Hughes J, Monne I, Fusaro A. Virus Evol. 2025 Mar 7;11(1):veaf011. doi: 10.1093/ve/veaf011

Avian-origin influenza A viruses tolerate elevated pyrexic temperatures in mammals. Turnbull ML, Wang Y, Clare S, Lieber G, Williams SL, Noerenberg M, Alexander AJT, Clohisey Hendry S, Stewart DG, Hughes J, Swingler S, Lytras S, Davies EL, Harcourt K, Smollett K, Pinto RM, Lee HM, Gaunt ER, Loney C, Jung JS, Lyons PA, Kapczynski DR, Hutchinson E, da Silva Filipe A, Taubenberger JK, Rihn SJ, Baillie JK, Fodor E, Castello A, Smith KGC, Digard P, Wilson SJ. Avian-origin influenza A viruses tolerate elevated pyrexic temperatures in mammals. Science. 2025 Nov 27;390(6776):eadq4691. doi: 10.1126/science.adq4691

The recency and geographical origins of the bat viruses ancestral to SARS-CoV and SARS-CoV-2.Pekar JE, Lytras S, Ghafari M, Magee AF, Parker E, Wang Y, Ji X, Havens JL, Katzourakis A, Vasylyeva TI, Suchard MA, Hughes AC, Hughes J, Rambaut A, Robertson DL, Dellicour S, Worobey M, Wertheim JO, Lemey P. Cell. 2025 Jun 12;188(12):3167-3183.e18. doi: 10.1016/j.cell.2025.03.035

Pathogen genomic surveillance and the AI revolution. Lytras S, Lamb KD, Ito J, Grove J, Yuan K, Sato K, Hughes J, Robertson DL. J Virol. 2025 Feb 25;99(2):e0160124. doi: 10.1128/jvi.01601-24

The potential of H5N1 viruses to adapt to bovine cells varies throughout evolution. Turnbull ML, Zakaria MK, Upfold NS, Bakshi S, Magill C, Das UR, Clarke AT, Mojsiejczuk L, Herder V, Dee K, Liu N, Folwarczna M, Ilia G, Furnon W, Schultz V, Chen H, Devlin R, McCowan J, Young AL, Po WW, Smollett K, Yaseen MA, Ross R, Bhide A, van Kekem B, Fouchier RAM, da Silva Filipe A, Iqbal M, Roberts E, Hughes J, Werling D, Murcia PR, Palmarini M. Nat Commun. 2025 Dec 15;16(1):11042. doi: 10.1038/s41467-025-67234-1

NSm is a critical determinant for bunyavirus transmission between vertebrate and mosquito hosts. Terhzaz S, Kerrigan D, Almire F, Szemiel AM, Hughes J, Parvy JP, Palmarini M, Kohl A, Shi X, Pondeville E. Nat Commun. 2025 Jan 31;16(1):1214. doi: 10.1038/s41467-024-54809-7
Multiple introductions of equine influenza virus into the United Kingdom resulted in widespread outbreaks and lineage replacement. Mojsiejczuk L, Whitlock F, Chen H, Magill C, Aranday-Cortes E, Bone J, Tong L, Da Silva Filipe A, Bryant N, Newton JR, Chambers TM, Reedy SE, Nemoto M, Yamanaka T, Hughes J, Murcia PR. PLoS Pathog. 2025 Jun 9;21(6):e1013227. doi: 10.1371/journal.ppat.1013227

Evidence of Influenza A(H5N1) Spillover Infections in Horses, Mongolia. Damdinjav B, Raveendran S, Mojsiejczuk L, Ankhanbaatar U, Yang J, Sadeyen JR, Iqbal M, Perez DR, Rajao DS, Park A, Viana M, Murcia PR. Emerg Infect Dis. 2025 Jan;31(1):183-185. doi: 10.3201/eid3101.241266

Genomic characterization of a dog-mediated rabies outbreak in El Pedregal, Arequipa, Peru. Salazar R, Brunker K, Díaz EW, Zegarra E, Monroy Y, Baldarrago GN, Borrini-Mayorí K, De la Puente-León M, Palmalux N, Nichols J, Kasaragod S, Levy MZ, Hampson K, Castillo-Neyra R. PLoS Negl Trop Dis. 2025 Mar 5;19(3):e0012396. doi: 10.1371/journal.pntd.0012396

Avian-origin influenza A viruses tolerate elevated pyrexic temperatures in mammals. Turnbull ML, Wang Y, Clare S, Lieber G, Williams SL, Noerenberg M, Alexander AJT, Clohisey Hendry S, Stewart DG, Hughes J, Swingler S, Lytras S, Davies EL, Harcourt K, Smollett K, Pinto RM, Lee HM, Gaunt ER, Loney C, Jung JS, Lyons PA, Kapczynski DR, Hutchinson E, da Silva Filipe A, Taubenberger JK, Rihn SJ, Baillie JK, Fodor E, Castello A, Smith KGC, Digard P, Wilson SJ. Science. 2025 Nov 27;390(6776):eadq4691. doi: 10.1126/science.adq4691

Pasteurisation temperatures effectively inactivate influenza A viruses in milk. Schafers J, Warren CJ, Yang J, Zhang J, Cole SJ, Cooper J, Drewek K, Kolli BR, McGinn N, Qureshi M, Reid SM, Peacock TP, Brown I, James J, Banyard AC, Iqbal M, Digard P, Hutchinson E. Nat Commun. 2025 Jan 30;16(1):1173. doi: 10.1038/s41467-025-56406-8

The recency and geographical origins of the bat viruses ancestral to SARS-CoV and SARS-CoV-2. Pekar JE, Lytras S, Ghafari M, Magee AF, Parker E, Wang Y, Ji X, Havens JL, Katzourakis A, Vasylyeva TI, Suchard MA, Hughes AC, Hughes J, Rambaut A, Robertson DL, Dellicour S, Worobey M, Wertheim JO, Lemey P. Cell. 2025 Jun 12;188(12):3167-3183.e18. doi: 10.1016/j.cell.2025.03.035

Should the equine community be concerned about the emergence of the H5N1 subtype of highly pathogenic avian influenza in US cattle? Murcia PR, Chambers TM, Daly JM, Pusterla N, Damdinjav B, Ankhanbaatar U, Mojsiejczuk L. Equine Vet J. 2025 Mar;57(2):530-531. doi: 10.1111/evj.14439

Dynamics of influenza transmission in vampire bats revealed by longitudinal monitoring and a large-scale anthropogenic perturbation. Griffiths ME, Broos A, Morales J, Tu IT, Bergner L, Behdenna A, Valderrama Bazan W, Tello C, Carrera JE, Recuenco S, Streicker DG, Viana M. Sci Adv. 2025 Feb 7;11(6):eads1267. doi: 10.1126/sciadv.ads1267

b) International conferences:

1

Rabies city dynamics (Peru) presented at RITA 2025 (rabies in the America): "Understanding canine rabies virus transmission using genomics in a decade-long epidemic in

Arequipa, Peru" Dr. Alejandra Dávila-Barclay, One Health Unit, School of Public Health and Administration, Universidad Peruana Cayetano Heredia, Lima, Peru.

c) National conferences:
0

d) Other (Provide website address or link to appropriate information):
2
Letter in the Equine Veterinary Journal to communicate to the equine community about the risks of H5N1 in horses (https://pubmed.ncbi.nlm.nih.gov/39660460/).

Perspective article in the Journal of Infectious Diseases (JID) proposing a hypothesis about the potential role of horses on the generation of the 1918 influenza pandemic virus (https://pubmed.ncbi.nlm.nih.gov/40261008/).

11. What have you done in the past year to advance your area of focus, e.g. updated technology?
Updated our IT infrastructure with GPUs for AI and training of team members in machine learning and large language models.

12. Additional comments regarding your report: