

OIE Collaborating Centres Reports Activities

Activities in 2021

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Title of collaborating centre:	Viral Genomics and Bioinformatics
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E-mail address:	Massimo.Palmarini@glasgow.ac.uk
Website:	https://bioinformatics.cvr.ac.uk
Name of Director of Institute (Responsible Official):	Prof Massimo Palmarini
Name (including Title and Position) of Head of the Collaborating Centre (formally OIE Contact Point):	Prof David L Robertson, Head of CVR Bioinformatics, MRC-University of Glasgow Centre for Virus Research
Name of writer:	David Robertson

ToR: To provide services to the OIE, in particular within the region, in the designated specialty, in support of the implementation of OIE policies and, where required, seek for collaboration with OIE Reference Laboratories

ToR: To identify and maintain existing expertise, in particular within its region

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

Zoonoses	
Title of activity	Scope
Understanding SARS-CoV-2 origins & spillover risk	Prof Robertson participated in online OIE ad hoc group calls on COVID-19 at the human-animal interface.
Understanding SARS-CoV-2 origins & spillover risk	CVR Bioinformatics team members contributed presentations, research articles and to discussions on animal the origins of SARS-CoV-2.
Other (Name the category)	
Title of activity	Scope
Viral Genomics and Bioinformatics	Development of bioinformatics pipelines for assembly and analysis of high-throughput viral sequence data
Viral Genomics and Bioinformatics	Investigation of the temporal and spatial characteristics of epidemics using viral epidemiology
Viral Genomics and Bioinformatics	Application of transcriptomics to study viral and host gene transcription during infection

ToR : To propose or develop methods and procedures that facilitate harmonisation of international standards and guidelines applicable to the designated specialty

2. Proposal or development of any procedure that will facilitate harmonisation of international regulations applicable to the surveillance and control of animal diseases, food safety or animal welfare

Proposal title	Scope/Content	Applicable area
Bioinformatics resources	Development of bioinformatics tools for processing and analysis of virus NGS data	<input checked="" type="checkbox"/> Surveillance and control of animal diseases <input type="checkbox"/> Food safety <input type="checkbox"/> Animal welfare

ToR: To establish and maintain a network with other OIE Collaborating Centres designated for the same specialty, and should the need arise, with Collaborating Centres in other disciplines

ToR: To carry out and/or coordinate scientific and technical studies in collaboration with other centres, laboratories or organisations

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

No

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

Yes

Name of OIE CC/RL/other organisation(s)	Location	Region of networking Centre	Purpose
Makerere University	Uganda	<input checked="" type="checkbox"/> Africa <input type="checkbox"/> Americas <input type="checkbox"/> Asia and Pacific <input type="checkbox"/> Europe <input type="checkbox"/> Middle East	Analysis of African Swine Fever virus genome sequence data
Pirbright Institute	United Kingdom	<input type="checkbox"/> Africa <input type="checkbox"/> Americas <input type="checkbox"/> Asia and Pacific <input checked="" type="checkbox"/> Europe <input type="checkbox"/> Middle East	Analysis of key animal virus data sets, e.g., Bluetongue virus and FMDV.
Peru	Americas	<input type="checkbox"/> Africa <input checked="" type="checkbox"/> Americas <input type="checkbox"/> Asia and Pacific <input type="checkbox"/> Europe <input type="checkbox"/> Middle East	Study of bat-transmitted rabies virus.

ToR: To place expert consultants at the disposal of the OIE.

5. Did your Collaborating Centre place expert consultants at the disposal of the OIE?

No

ToR: To provide, within the designated specialty, scientific and technical training to personnel from OIE Member Countries

6. Did your Collaborating Centre provide scientific and technical training, within the remit of the mandate given by the OIE, to personnel from OIE Member Countries?

No

ToR: To organise and participate in scientific meetings and other activities on behalf of the OIE

7. Did your Collaborating Centre organise or participate in the organisation of scientific meetings on behalf of the OIE?

No

ToR: To collect, process, analyse, publish and disseminate data and information relevant to the designated specialty

8. Publication and dissemination of any information within the remit of the mandate given by the OIE that may be useful to Member Countries of the OIE

a) Articles published in peer-reviewed journals: 17

Amat JAR, Patton V, Chauché C, Goldfarb D, Crispell J, Gu Q, Coburn AM, Gonzalez G, Mair D, Tong L, Martinez-Sobrido L, Marshall JF, Marchesi F, Murcia PR. Long-term adaptation following influenza A virus host shifts results in increased within-host viral fitness due to higher replication rates, broader dissemination within the respiratory epithelium and reduced tissue damage. *PLoS Pathog.* 2021 Dec 17;17(12):e1010174. doi: 10.1371/journal.ppat.1010174. eCollection 2021 Dec. PMID: 34919598

Bergner LM, Mollentze N, Orton RJ, Tello C, Broos A, Biek R, Streicker DG. Characterizing and Evaluating the Zoonotic Potential of Novel Viruses Discovered in Vampire Bats. *Viruses.* 2021 Feb 6;13(2):252. doi: 10.3390/v13020252.

Bergner LM, Orton RJ, Broos A, Tello C, Becker DJ, Carrera JE, Patel AH, Biek R, Streicker DG. Diversification of mammalian deltaviruses by host shifting. *Proc Natl Acad Sci U S A.* 2021 Jan 19;118(3):e2019907118. doi: 10.1073/pnas.2019907118.

Coffin J, Blomberg J, Fan H, Gifford R, Hatzioannou T, Lindemann D, Mayer J, Stoye J, Tristem M, Johnson W, ICTV Report Consortium. ICTV Virus Taxonomy Profile: Retroviridae 2021. *J Gen Virol.* 2021 Dec;102(12):001712. doi: 10.1099/jgv.0.001712.

Cotten M, Robertson DL, Phan MVT. Unique protein features of SARS-CoV-2 relative to other Sarbecoviruses. *Virus Evol.* 2021 Jul 23;7(2):veab067. doi: 10.1093/ve/veab067.

Davis CA, Haywood B, Vattipally S, Da Silva Filipe A, AlSaeed M, Smollet K, Baylis SA, Ijaz S, Tedder RS, Thomson EC, Abdelrahman TT. Hepatitis E virus: Whole genome sequencing as a new tool for understanding HEV epidemiology and phenotypes. *J Clin Virol.* 2021 Jun;139:104738. doi: 10.1016/j.jcv.2021.104738. Epub 2021 Jan 27. PMID: 33933822

Gallo G, Caignard G, Badonnel K, Chevreux G, Terrier S, Szemiel A, Roman-Sosa G, Binder F, Gu Q, Da Silva Filipe

A, Ulrich RG, Kohl A, Vitour D, Tordo N, Ermonval M. Interactions of Viral Proteins from Pathogenic and Low or Non-Pathogenic Orthohantaviruses with Human Type I Interferon Signaling. *Viruses*. 2021 Jan 19;13(1):140. doi: 10.3390/v13010140.

Gatherer D, Depledge DP, Hartley CA, Szpara ML, Vaz PK, Benkő M, Brandt CR, Bryant NA, Dastjerdi A, Doszpoly A, Gompels UA, Inoue N, Jarosinski KW, Kaul R, Lacoste V, Norberg P, Origgi FC, Orton RJ, Pellett PE, Schmid DS, Spatz SJ, Stewart JP, Trimpert J, Waltzek TB, Davison AJ. ICTV Virus Taxonomy Profile: Herpesviridae 2021. *J Gen Virol*. 2021 Oct;102(10):001673. doi: 10.1099/jgv.0.001673.

Holmes EC, Goldstein SA, Rasmussen AL, Robertson DL, Crits-Christoph A, Wertheim JO, Anthony SJ, Barclay WS, Boni MF, Doherty PC, Farrar J, Geoghegan JL, Jiang X, Leibowitz JL, Neil SJD, Skern T, Weiss SR, Worobey M, Andersen KG, Garry RF, Rambaut A. The origins of SARS-CoV-2: A critical review. *Cell*. 2021 Sep 16;184(19):4848-4856. doi: 10.1016/j.cell.2021.08.017.

Hosie MJ, Epifano I, Herder V, Orton RJ, Stevenson A, Johnson N, MacDonald E, Dunbar D, McDonald M, Howie F, Tennant B, Herrity D, Da Silva Filipe A, Streicker DG; COVID-19 Genomics UK (COG-UK) consortium, Willett BJ, Murcia PR, Jarrett RF, Robertson DL, Weir W. Detection of SARS-CoV-2 in respiratory samples from cats in the UK associated with human-to-cat transmission. *Vet Rec*. 2021 Apr;188(8):e247. doi: 10.1002/vetr.247.

Hufsky F, Lamkiewicz K, Almeida A, Aouacheria A, Arighi C, Bateman A, Baumbach J, Beerenwinkel N, Brandt C, Cacciabue M, Chuguransky S, Drechsel O, Finn RD, Fritz A, Fuchs S, Hattab G, Hauschild AC, Heider D, Hoffmann M, Hölzer M, Hoops S, Kaderali L, Kalvari I, von Kleist M, Kmiecinski R, Kühnert D, Lasso G, Libin P, List M, Löchel HF, Martin MJ, Martin R, Matschinske J, McHardy AC, Mendes P, Mistry J, Navratil V, Nawrocki EP, O'Toole AN, Ontiveros-Palacios N, Petrov AI, Rangel-Pineros G, Redaschi N, Reimering S, Reinert K, Reyes A, Richardson L, Robertson DL, Sadegh S, Singer JB, Theys K, Upton C, Welzel M, Williams L, Marz M. Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. *Brief Bioinform*. 2021 Mar 22;22(2):642-663. doi: 10.1093/bib/bbaa232.

Lytras S, Xia W, Hughes J, Jiang X, Robertson DL. The animal origin of SARS-CoV-2. *Science*. 2021 Aug 27;373(6558):968-970. doi: 10.1126/science.abh0117.

MacLean OA, Lytras S, Weaver S, Singer JB, Boni MF, Lemey P, Kosakovsky Pond SL, Robertson DL. Natural selection in the evolution of SARS-CoV-2 in bats created a generalist virus and highly capable human pathogen. *PLoS Biol*. 2021 Mar 12;19(3):e3001115. doi: 10.1371/journal.pbio.3001115.

Rihn SJ, Merits A, Bakshi S, Turnbull ML, Wickenhagen A, Alexander AJT, Baillie C, Brennan B, Brown F, Brunner K, Bryden SR, Burness KA, Carmichael S, Cole SJ, Cowton VM, Davies P, Davis C, De Lorenzo G, Donald CL, Dorward M, Dunlop JL, Elliott M, Fares M, da Silva Filipe A, Freitas JR, Furnon W, Gestuevo RJ, Geyer A, Giesel D, Goldfarb DM, Goodman N, Gunson R, Hastie CJ, Herder V, Hughes J, Johnson C, Johnson N, Kohl A, Kerr K, Leech H, Lello LS, Li K, Lieber G, Liu X, Lingala R, Loney C, Mair D, McElwee MJ, McFarlane S, Nichols J, Nomikou K, Orr A, Orton RJ, Palmarini M, Parr YA, Pinto RM, Raggett S, Reid E, Robertson DL, Royle J, Cameron-Ruiz N, Shepherd JG, Smollett K, Stewart DG, Stewart M, Sugrue E, Szemiel AM, Taggart A, Thomson EC, Tong L, Torrie LS, Toth R, Varjak M, Wang S, Wilkinson SG, Wyatt PG, Zusinaite E, Alessi DR, Patel AH, Zaid A, Wilson SJ, Mahalingam S. A plasmid DNA-launched SARS-CoV-2 reverse genetics system and coronavirus toolkit for COVID-19 research. *PLoS Biol*. 2021 Feb 25;19(2):e3001091. doi: 10.1371/journal.pbio.3001091.

Schultz V, Cumberworth SL, Gu Q, Johnson N, Donald CL, McCanney GA, Barrie JA, Da Silva Filipe A, Linington C, Willison HJ, Edgar JM, Barnett SC, Kohl A. Zika Virus Infection Leads to Demyelination and Axonal Injury in Mature CNS Cultures. *Viruses*. 2021 Jan 11;13(1):91. doi: 10.3390/v13010091.

Shaw AE, Rihn SJ, Mollentze N, Wickenhagen A, Stewart DG, Orton RJ, Kuchi S, Bakshi S, Collados MR, Turnbull ML, Busby J, Gu Q, Smollett K, Bamford CGG, Sugrue E, Johnson PCD, Da Silva AF, Castello A, Streicker DG, Robertson DL, Palmarini M, Wilson SJ. The antiviral state has shaped the CpG composition of the vertebrate interferome to avoid self-targeting. *PLoS Biol*. 2021 Sep 7;19(9):e3001352. doi: 10.1371/journal.pbio.3001352. eCollection 2021 Sep.

Walker PJ, Siddell SG, Lefkowitz EJ, Mushegian AR, Adriaenssens EM, Alfenas-Zerbini P, Davison AJ, Dempsey DM, Dutilh BE, García ML, Harrach B, Harrison RL, Hendrickson RC, Junglen S, Knowles NJ, Krupovic M, Kuhn JH, Lambert AJ, Łobocka M, Nibert ML, Oksanen HM, Orton RJ, Robertson DL, Rubino L, Sabanadzovic S, Simmonds P, Smith DB, Suzuki N, Van Dooerslaer K, Vandamme AM, Varsani A, Zerbini FM. Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021). *Arch Virol*. 2021 Sep;166(9):2633-2648. doi: 10.1007/s00705-021-05156-1.

b) International conferences: 0

c) National conferences: 0

d) Other

(Provide website address or link to appropriate information): 1

COVID-19 Research Response: <https://www.gla.ac.uk/researchinstitutes/iii/cvr/impact/covid-19researchresponse/>

9. Additional comments regarding your report:

In February 2020, the MRC-University of Glasgow Centre for Virus Research (CVR) redirected all of its research activity to the SARS-CoV-2 outbreak. The CVR's genomics and bioinformatics teams have made major contributions to understanding the natural origins of SARS-CoV-2, tracking virus spread as part of COG-UK in collaboration with public health bodies and global partners, and contributed online tools: <http://cov-glue.cvr.gla.ac.uk> and <https://sars2.cvr.gla.ac.uk/cog-uk/>. Due to the disruption caused by the pandemic, and our efforts in responding to it, we were unable to host training visits during 2021 and annual OIE Genomics and Bioinformatics training workshop was canceled in 2021. We anticipate being able to host visits and run the OIE Genomics and Bioinformatics training course in 2022.