

# OIE Collaborating Centres Reports Activities

## *Activities in 2018*

**This report has been submitted : 2019-02-14 16:22:50**

<b>Title of collaborating centre:</b>	Viral Genomics and Bioinformatics
<b>Address of Collaborating Centre:</b>	MRC-University of Glasgow Centre for Virus Research (CVR) 464 Bearsden Road Glasgow G61 1QH UNITED KINGDOM
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<b>Name of Director of Institute (Responsible Official):</b>	Prof. Massimo Palmarini
<b>Name (including Title and Position) of Head of the Collaborating Centre (formally OIE Contact Point):</b>	Prof. David Robertson Head Of Bioinformatics MRC-University of Glasgow Centre for Virus Research
<b>Name of writer:</b>	Prof. Massimo Palmarini

**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**

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	Development of bioinformatic tools for information exchange platforms
Viral Genomics and Bioinformatics	Investigation of the temporal and spatial characteristics of epidemics using viral epidemiology
Viral Genomics and Bioinformatics	Development of mathematical and software tools to study transmission dynamics of animal viruses during outbreaks
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
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<p>Full genome sequencing pipeline</p>	<p>The application of next generation sequencing technology and downstream bioinformatic analyses of African Swine Fever viral genomes sequenced directly from clinical samples.</p>	<p><input checked="" type="checkbox"/> Surveillance and control of animal diseases  <input type="checkbox"/> Food safety  <input checked="" type="checkbox"/> Animal welfare</p>
<p>Full genome sequencing pipeline</p>	<p>The application of next generation sequencing technology and downstream bioinformatic analyses of hepatitis E viral genomes sequenced directly from clinical samples.</p>	<p><input type="checkbox"/> Surveillance and control of animal diseases  <input checked="" type="checkbox"/> Food safety  <input type="checkbox"/> Animal welfare</p>
<p>Bioinformatic resources</p>	<p>Bioinformatic software for the organisation and processing of viral genomic sequence data within scalable computing resources</p>	<p><input checked="" type="checkbox"/> Surveillance and control of animal diseases  <input type="checkbox"/> Food safety  <input type="checkbox"/> Animal welfare</p>

***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	Sequencing and bioinformatic analyses of African Swine Fever viral isolates
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	Studies of Bluetongue and Schmallenberg virus Studies on arthropod-borne viruses Studies on foot and mouth disease virus and Infectious Bronchitis Virus
Cornell University	United States of America	<input type="checkbox"/> Africa <input checked="" type="checkbox"/> Americas <input type="checkbox"/> Asia and Pacific <input type="checkbox"/> Europe <input type="checkbox"/> Middle East	Studies of canine and equine influenza virus
University of Florida	United States of America	<input type="checkbox"/> Africa <input checked="" type="checkbox"/> Americas <input type="checkbox"/> Asia and Pacific <input type="checkbox"/> Europe <input type="checkbox"/> Middle East	United States of America
State Central Veterinary Laboratory	Mongolia	<input type="checkbox"/> Africa <input type="checkbox"/> Americas <input checked="" type="checkbox"/> Asia and Pacific <input type="checkbox"/> Europe <input type="checkbox"/> Middle East	Studies of equine and avian influenza
Universidad Peruana Cayetano-Heredia	Peru	<input type="checkbox"/> Africa <input checked="" type="checkbox"/> Americas <input type="checkbox"/> Asia and Pacific <input type="checkbox"/> Europe <input type="checkbox"/> Middle East	Studies on bat-transmitted rabies virus
OIE reference laboratory for avian influenza and Newcastle disease, Istituto Zooprofilattico Sperimentale delle Venezie	Italy	<input type="checkbox"/> Africa <input type="checkbox"/> Americas <input type="checkbox"/> Asia and Pacific <input checked="" type="checkbox"/> Europe <input type="checkbox"/> Middle East	Studies on viral population complexity of avian influenza virus during infection.

Dutch National Reference lab for Fish diseases, Utrecht University	Netherlands	<input type="checkbox"/> Africa <input type="checkbox"/> Americas <input type="checkbox"/> Asia and Pacific <input checked="" type="checkbox"/> Europe <input type="checkbox"/> Middle East	Sequencing and genome assembly of Ranaviruses
University of São Paulo	Brazil	<input type="checkbox"/> Africa <input checked="" type="checkbox"/> Americas <input type="checkbox"/> Asia and Pacific <input type="checkbox"/> Europe <input type="checkbox"/> Middle East	high-throughput sequencing (HTS) to investigate the diversity of parvoviruses infecting wild and domestic animals in Brazil

**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?**

Yes

Name of expert	Kind of consultancy	Subject
Prof Massimo Palmarini	Chair: Ad hoc group	High throughput sequencing, bioinformatics and computational genomics
Prof Massimo Palmarini	Collaboration on preparation of OIE genomic pathogen platform within WAHAS+	Genomic pathogen platform

**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?**

Yes

- a) Technical visits: 1
- b) Seminars: 0
- c) Hands-on training courses: 3
- 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

a	Bioinformatics analysis of African Swine Fever viral isolates	Uganda	1
c	<p>Overview of Next-generation sequencing technologies</p> <ul style="list-style-type: none"> <li>• Basic command line</li> <li>• Bash scripting</li> <li>• Reference assembly: aligning sequence reads to a known reference and visualizing the alignment (e.g., bowtie2, BWA, Tanoti, Tablet, UGENE)</li> <li>• Variant calling: consensus sequence generation, low frequency variant calling and error correction (e.g., LoFreq, Qure)</li> <li>• De-novo assembly (e.g., idba-ud, Spades)</li> <li>• Assembly quality assessment: merging contigs, filling gaps and correcting errors (QUAST, GARM, scaffold builder)</li> <li>• Genomics: improving the assembly, finishing the assembly, gene annotation (e.g., ICORN2, Artemis, Sequin)</li> <li>• Metagenomic analyses: sanitizing sequence datasets, assembling, annotating, visualizing (e.g., MetAMOS, Krona)</li> <li>• Phylogenetic analysis: Using publically available data, introduction to multiple sequence alignments and phylogenetic reconstruction (e.g. GenBank, MAFFT, RAxML).</li> </ul>	United Kingdom	7

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c	<p>Viral Bioinformatics and Genomics (Ho Chi Minh City, Vietnam)</p> <p><a href="https://coursesandconferences.wellcomegenomecampus.org/our-events/viral-bioinformatics-genomics-vietnam-2018/">https://coursesandconferences.wellcomegenomecampus.org/our-events/viral-bioinformatics-genomics-vietnam-2018/</a></p>	Vietnam	
c	<p>Genomics and Clinical Virology</p> <p><a href="https://coursesandconferences.wellcomegenomecampus.org/our-events/genomics-and-clinical-virology-2018/">https://coursesandconferences.wellcomegenomecampus.org/our-events/genomics-and-clinical-virology-2018/</a></p>	United Kingdom	

**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: 25

1. Cotmore SF, Agbandje-McKenna M, Canuti M, Chiorini JA, Eis-Hubinger AM, Hughes J, Mietzsch M, Modha S, Ogliastro M, Péntzes JJ, Pintel DJ, Qiu J, Soderlund-Venermo M, Tattersall P, Tijssen P, Ictv Report Consortium. 2019 Jan 23. ICTV Virus Taxonomy Profile: Parvoviridae. The Journal of general virology :
2. Rezelj VV, Mottram TJ, Hughes J, Elliott RM, Kohl A, Brennan B. 2018 Dec 19. M segment-based minigenomes and virus-like particle assays as an approach to assess the potential of tick-borne *Phlebovirus* genome reassortment. Journal of virology :
3. Singer JB, Thomson EC, McLauchlan J, Hughes J, Gifford RJ. 2018 Dec 18. GLUE: a flexible software system for virus sequence data. BMC bioinformatics 19:532
4. Mercuri L, Thomson EC, Hughes J, Karayiannis P. 2018. Quasispecies Changes with Distinctive Point Mutations in the Hepatitis C Virus Internal Ribosome Entry Site (IRES) Derived from PBMCs and Plasma. Advances in virology 2018:4835252
5. Babayan SA, Orton RJ, Streicker DG. 2018 Nov 2. Predicting reservoir hosts and arthropod vectors from evolutionary signatures in RNA virus genomes. Science (New York, N.Y.)362:577-580
6. Becker DJ, Bergner LM, Bentz AB, Orton RJ, Altizer S, Streicker DG. 2018 Sep. Genetic diversity, infection prevalence, and possible transmission routes of Bartonella spp. in vampire bats. PLoS neglected tropical diseases 12:e0006786
7. Davis C, Mgomella GS, da Silva Filipe A, Frost EH, Giroux G, Hughes J, Hogan C, Kaleebu P, Asiki G, McLauchlan J, Niebel M, Ocamo P, Pomila C, Pybus OG, Pépin J, Simmonds P, Singer JB, Sreenu VB, Wekesa C, Young EH, Murphy DG, Sandhu M, Thomson EC. 2018 Nov 2. New highly diverse hepatitis C strains detected in sub-Saharan Africa have unknown susceptibility to direct-acting antiviral treatments. Hepatology (Baltimore, Md.) :
8. Dunlop JI, Szemiel AM, Navarro A, Wilkie GS, Tong L, Modha S, Mair D, Sreenu VB, Da Silva Filipe A, Li P, Huang YS, Brennan B, Hughes J, Vanlandingham DL, Higgs S, Elliott RM, Kohl A. 2018 Oct. Development of reverse genetics systems and investigation of host response antagonism and reassortment potential for Cache Valley and Kairi viruses, two emerging orthobunyaviruses of the Americas. PLoS neglected tropical diseases 12:e0006884
9. Maia FGM, de Souza WM, Sabino-Santos G Jr, Fumagalli MJ, Modha S, Murcia PR, Figueiredo LTM. 2018 Oct. A novel polyomavirus in sigmodontine rodents from São Paulo State, Brazil. Archives of virology 163:2913-2915
10. de Souza WM, Romeiro MF, Sabino-Santos G Jr, Maia FGM, Fumagalli MJ, Modha S, Nunes MRT, Murcia PR, Figueiredo LTM. 2018 Jun. Novel orthohepeviruses in wild rodents from São Paulo State, Brazil. Virology 519:12-16
11. de Souza WM, Dennis T, Fumagalli MJ, Araujo J, Sabino-Santos G, Maia FGM, Acrani GO, Carrasco AOT, Romeiro MF, Modha S, Vieira LC, Ometto T, Queiroz LH, Durigon EL, Nunes MRT, Figueiredo LTM, Gifford RJ. 2018 Mar 22. Novel Parvoviruses from Wild and Domestic Animals in Brazil Provide New Insights into Parvovirus Distribution and Diversity. Viruses 10:
12. de Souza WM, Fumagalli MJ, de Araujo J, Sabino-Santos G Jr, Maia FGM, Romeiro MF, Modha S, Nardi MS, Queiroz LH, Durigon EL, Nunes MRT, Murcia PR, Figueiredo LTM. 2018 Jan 15. Discovery of novel anelloviruses in small mammals expands the host range and diversity of the Anelloviridae. Virology 514:9-17
13. Saucedo B, Hughes J, Spitzen-van der Sluijs A, Kruihof N, Schills M, Rijks JM, Jacinto-Maldonado M, Suarez N, Haenen OLM, Voorbergen-Laarman M, van den Broek J, Gilbert M, Gröne A, van Beurden SJ, Verheije MH. 2018 Apr 4. Ranavirus genotypes in the Netherlands and their potential association with virulence in water frogs (*Pelophylax* spp.). Emerging microbes & infections 7:56
14. Modha S, Thanki AS, Cotmore SF, Davison AJ, Hughes J. 2018 Jul 1. ViCTree: an automated framework for taxonomic classification from protein sequences. Bioinformatics (Oxford, England) 34:2195-2200
15. da Silva Filipe A, Sreenu V, Hughes J, Aranday-Cortes E, Irving WL, Foster GR, Agarwal K, Rosenberg W, Macdonald D, Richardson P, Aldersley MA, Wiselka M, Ustianowski A, McLauchlan J, Thomson EC. 2018 Jan 12. Reply to: "Reply to: 'Response to DAA therapy in the NHS England Early Access Programme for rare HCV subtypes from low and middle income countries'". Journal of hepatology :
16. McNaughton AL, Sreenu VB, Wilkie G, Gunson R, Templeton K, Leitch ECM. 2018 May. Prevalence of mixed genotype hepatitis C virus infections in the UK as determined by genotype-specific PCR and deep sequencing. Journal of viral hepatitis 25:524-534
17. Lourenço-de-Oliveira R, Marques JT, Sreenu VB, Atyame Nten C, Aguiar ERGR, Varjak M, Kohl A, Failloux AB. 2018 Feb. Culex quinquefasciatus mosquitoes do not support replication of Zika virus. The Journal of general virology 99:258-264
18. Chauché C, Nogales A, Zhu H, Goldfarb D, Ahmad Shanizza AI, Gu Q, Parrish CR, Martínez-Sobrido L, Marshall JF, Murcia PR. 2018 Mar 1. Mammalian Adaptation of an Avian Influenza A Virus Involves Stepwise Changes in

NS1. Journal of virology 92:

19. Lefkowitz EJ, Dempsey DM, Hendrickson RC, Orton RJ, Siddell SG, Smith DB. 2018 Jan 4. Virus taxonomy: the database of the International Committee on Taxonomy of Viruses (ICTV). *Nucleic acids research* 46:D708-D717

20. Masembe, C. , Sreenu, V. B., Da Silva Filipe, A., Wilkie, G. S., Ogweng, P., Mayega, F. J., Muwanika, V. B., Biek, R. , Palmarini, M. and Davison, A. J. (2018) Genome sequences of five African swine fever virus genotype IX isolates from domestic pigs in Uganda. *Microbiology Resource Announcements*, 7(13), e01018-18. (doi:10.1128/mra.01018-18)

21. Bryant, N.A. et al. (2018) Genetic diversity of equine herpesvirus 1 isolated from neurological, abortigenic and respiratory disease outbreaks. *Transboundary and Emerging Diseases*, 65(3), pp. 817-832. (doi:10.1111/tbed.12809) (PMID:29423949)

22. Henriquez, R. N., Polchana, J., Kanchanakhon, S., Davison, A. J. , Waltzek, T. B. and Subramaniam, K. (2018) Genome sequence of a novel alloherpesvirus isolated from glass catfish (*Kryptopterus bicirrhis*). *Genome Announcements*, 6(19), e00403-18. (doi:10.1128/genomeA.00403-18)(PMID:29748409)

23. Gao, Y., Suárez, N. M., Wilkie, G. S., Dong, C., Bergmann, S., Lee, P.-Y. A., Davison, A. J. , Vanderplasschen, A. F.C. and Boutier, M. (2018) Genomic and biologic comparisons of cyprinid herpesvirus 3 strains. *Veterinary Research*, 49, 40. (doi:10.1186/s13567-018-0532-z) (PMID:29716648)

24. Marshall, J., Davison, A. J. , Kopf, R. K., Boutier, M., Stevenson, P. and Vanderplasschen, A. (2018) Biocontrol of invasive carp: risks abound. *Science*, 359(6378), p. 877. (doi:10.1126/science.aar7827) (PMID:29472472)

25. Garvey, M., Suárez, N., Kerr, K., Hector, R. , Moloney-Quinn, L., Arkins, S. and Davison, A. J. (2018) Equid herpesvirus 8: complete genome sequence and association with abortion in mares. *PLoS ONE*, 13(2), e0192301. (doi:10.1371/journal.pone.0192301) (PMID:29414990) (PMCID:PMC5802896)

b) International conferences: 0

c) National conferences: 0

d) Other

(Provide website address or link to appropriate information): 2

<http://www.bioinformatics.cvr.ac.uk/>

<http://bioinformatics.cvr.ac.uk/blog/>