

Joan Martí - Carreras



Personalia

Date of birth 06 September 1993

Place of birth Llers, Spain

Contact Rega Institute for Medical Research - KU Leuven
Department of Microbiology, Immunology and Transplantation
Laboratory of Clinical and Epidemiological Virology
Herestraat 49 bus 1043 - 3000 Leuven, Belgium
Tel. (work): 0032 16379284
Tel. (mobile): 0034 653614415
E-mail: joan.marti.carreras@gmail.com or joan.marti@kuleuven.be
Web-page: www.joanmarticarreras.com

Languages **Catalan & Spanish:** Native, **English:** C1, **Dutch:** A2.

Expertise **Sequencing, Genomics, Molecular Biology, Infectious Diseases and Virology.**

Education/Employment

2020 – Present **Panel Expert** (Virology/Immunology/Oncology)
BioExpert Network, Capital Cell
Oficina 2D2, Plaça de Pau Vila, 1
08039 Barcelona, Spain

2017 - Present **Doctoral training in Biomedical Sciences**
Laboratory of Clinical and Epidemiological Virology
Rega Institute for Medical Research, KU Leuven, Leuven, Belgium

Towards complete large dsDNA virus genomes: Third-generation sequencing and herpesvirus genome diversity
Promotors: Prof. Dr. Piet Maes and Prof. Dr. Marc Van Ranst.

2015 - 2017 **Master's in Bioinformatics for Health Sciences**
Facultat de Ciències Experimentals i de la Salut, Universitat Pompeu Fabra – Universitat de Barcelona, Barcelona, Spain

[Research Associate] Biogeography of genes related to methyl-mercury degradation by comparative analyses of deep ocean metagenomes and metatranscriptomes
Promotors: Prof. Silvia G Acinas and Pablo Sánchez.
Institut de Ciències del Mar (ICM-CSIC), Barcelona, Spain

2011 - 2015 **Bachelor in Genetics**
Facultat de Biociències, Universitat Autònoma de Barcelona, Barcelona, Spain.

Molecular characterization of piRNA pathway genes in *Drosophila buzzatti* and *Drosophila koepferae* species
Promotor: Prof. Maria Pilar Garcia Guerreiro
Departament de Genètica, Grup de Biologia Evolutiva, Universitat Autònoma de Barcelona (UAB), Barcelona, Spain

[Freelance Biologist] Phylogeographic reconstruction of *Rhynchophorus ferrugineus* COI sequences

Promotor: Prof. Victor Sarto i Monteys

Institut de Ciència i Tecnologia Ambientals (ICTA), Conselleria d'Agricultura, Ramaderia i Pesca, Generalitat de Catalunya, Barcelona, Spain

Skills

Sequencing

Sanger, Illumina (NexteraXT, Westburg, Agilent SureSelect hybrid-capture), Nanopore (rapid, ligation, ultra-long read libraries). Some experience with IonTorrent.

Molecular biology

Cloning techniques (currently learning TAR cloning), PCR, RT-qPCR, FACS.

Cell culture

E. coli DH5a and DH10B, primary and immortalized lines (HFF, MRC-5, VeroE, Huh-7, THP-1, ...), transduction, production and titration of viral strains (herpes and SARS-CoV-2).

Biosafety

Expertise at BSL-1 to BSL-2, currently under **BSL-3 training** at the Rega Institute, KU Leuven.

Office

Experience in **Windows** (Microsoft Office) and **Ubuntu**. Basic graphic design (**Inkscape**). Project managing (**Scinote**).

Binary

Data-analysis and data visualization through **R** (Rstudio, tidyverse, Vegan, etc). Fluent in **Bash** and **Python** and some Perl. Project managing and accounting (**git**, <https://github.com/joanmarticarreras/>), pipeline managers (**Nextflow** and Snakemake) and virtualization of resources (Docker and **Singularity**).

Publications

Joan Martí-Carreras*#, Alejandro Rafael Gener*, Sierra D. Miller, Anderson F. Brito, Christiam E. Camacho, Ryan Connor, Ward Deboutte, Cody Glickman, David M. Kristensen, Wynn K. Meyer, Sejal Modha, Alexis L. Norris, Surya Saha, Anna K. Belford, Evan Biederstedt, J. Rodney Brister, Jan P. Buchmann, Nicholas P. Cooley, Robert A. Edwards, Kiran Javkar, Michael Muchow, Harihara Subrahmaniam Muralidharan, Charles Pepe-Ranney, Nidhi Shah, Migun Shakya, Michael J. Tisza, Benjamin J. Tully, Bert Vanmechelen, Valerie C. Virta, Jake L. Weissman, Vadim Zalunin, Alexandre Efremov, and Ben Busby. NCBI's Virus Discovery Codeathon: Building "FIVE" - the Federated Index of Viral Experiments API index. **Viruses – MDPI** [10.3390/v12121424](https://doi.org/10.3390/v12121424)

Jérémy S.P. Froidevaux#, Charlotte Roemer, Clément Lemarchand, **Joan Martí-Carreras**, Piet Maes, Vincent Rufay, Quentin Uriot, Sylvain Uriot, Adrià López-Baucells. Second capture of *Promops centralis* (Chiroptera) in French Guiana after 28 years of mist-netting and description of its echolocation and distress calls. **Acta Amazonica** **2020**. [10.1590/1809-4392202001451](https://doi.org/10.1590/1809-4392202001451)

Robbert Boudewijns, Hendrik Jan Thibaut, Suzanne Kaptein, Rong Li, Valentijn Vergote, Laura Seldeslachts, Johan Van Weyenbergh, Carolien De Keyzer, Lindsey Bervoets, Sapna Sharma, Laurens Liesenborghs, Ji Ma, Sander Jansen, Dominique Van Looveren, Thomas Vercruysse, Xinyu Wang, Dirk Jochmans, Erik Martens, Kenny Roose, Dorien De Vlioger, Bert Schepens, Tina Van Buyten, Sofie Jacobs, Yanan Liu, **Joan Martí-Carreras**, Bert Vanmechelen, Tony

Wawina-Bokalanga, Leen Delang, Joana Rocha-Pereira, Lotte Coelmont, Winston Chiu, Pieter Leyssen, Elisabeth Heylen, Dominique Schols, Lanjiao Wang, Lila Close, Jelle Matthijssens, Marc Van Ranst, Veerle Compennolle, Georg Schramm, Koen Van Laere, Xavier Saelens, Nico Callewaert, Ghislain Opdenakker, Piet Maes, Birgit Weynand, Christopher Cawthorne, Greetje Vande Velde, Zhongde Wang, Johan Neyts, and Kai Dallmeier. STAT2 signaling as double-edged sword restricting viral dissemination but driving severe pneumonia in SARS-CoV-2 infected hamsters. **Nature Communication** 2020. [10.1038/s41467-020-19684-y](https://doi.org/10.1038/s41467-020-19684-y)

Simon Dellicour#, Keith Durkin, Samuel L Hong, Bert Vanmechelen, **Joan Martí-Carreras**, Mandev S Gill, Cécile Meex, Sébastien Bontems, Emmanuel André, Marius Gilbert, Conor Walker, Nicola De Maio, Nuno R Faria, James Hadfield, Marie-Pierre Hayette, Vincent Bours, Tony Wawina-Bokalanga, Maria Artesi, Guy Baele, Piet Maes. A phylodynamic workflow to rapidly gain insights into the dispersal history and dynamics of SARS-CoV-2 lineages. **Molecular Biology and Evolution** 2020. [10.1093/molbev/msaa284](https://doi.org/10.1093/molbev/msaa284)

Tony Wawina-Bokalanga, Bert Vanmechelen, Valentine Lhermitte, **Joan Martí-Carreras**, Valentijn Vergote, Fara Raymond Koundouno, Joseph Akoi-Boré, Ruth Thom, Tom Tipton, Kimberley Steeds, Kéita Balla Moussa, Ablam Amento, Lies Laenen, Sophie Duraffour, Martin Gabriel, Paula Ruibal, Yper Hall, Mandy Kader-Kondé, Stephan Günther, Guy Baele, Cesar Muñoz-Fontela, Johan Van Weyenberg, Miles W. Carroll, Piet Maes#. Human diversity of Killer cell Immunoglobulin-like Receptors (KIRs) and HLA class I alleles, and their impact on Ebola virus disease outcome. **Accepted Emerging Infectious Diseases** 2020.

Cormac M Kinsella*#, Pauline Dianne Santos*, Ignacio Postigo-Hidalgo*, Alba Folgueiras-González*, Tim Casper Passchier*, Kevin P Szilatt*, Joyce Odeke Akello*, Beatriz Álvarez-Rodríguez*, **Joan Martí-Carreras***. Preparedness needs research: How fundamental science and international collaboration accelerated the response to COVID-19. **PLoS Pathogens** 2020. [10.1371/journal.ppat.1008902](https://doi.org/10.1371/journal.ppat.1008902)

Erik Alm, Eeva K Broberg, Thomas Connor, Emma B Hodcroft, Andrey B Komissarov, Sebastian Maurer-Stroh, Angeliki Melidou, Richard A Neher, Áine O'Toole, Dmitriy Pereyaslov, The WHO European Region sequencing laboratories and **GISAID EpiCoV group**. Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region, January to June 2020. **Eurosurveillance** 2020. [10.2807/1560-7917.ES.2020.25.32.2001410](https://doi.org/10.2807/1560-7917.ES.2020.25.32.2001410)

Joan Martí-Carreras, Olga Mineeva-Sangwo, Dimitrios Topalis, Robert Snoeck, Graciela Andrei and Piet Maes#. BKTyper: Free Online Tool for Polyoma BK Virus VP1 and NCCR Typing. **Viruses – MDPI** 2020. [10.3390/v12080837](https://doi.org/10.3390/v12080837)

Víctor Gámez-Visairas, Valèria Romero-Soriano, **Joan Martí-Carreras**, Eila Segarra-Carrillo and Maria Pilar García Guerreiro#. Drosophila Interspecific Hybridization Causes a Dereglulation of the piRNA Pathway Genes. **Genes – MDPI** 2020. [10.3390/genes11020215](https://doi.org/10.3390/genes11020215)

Ryan Connor, Rodney Brister, Jan P. Buchmann, Ward Deboutte, Rob Edwards, **Joan Martí-Carreras**, Mike Tisza, Vadim Zalunin, Juan Andrade-Martínez, Adrian Cantu, Michael D'Amour, Alexandre Efremov, Lydia Fleischmann, Laura Forero-Junco, Sanzhima Garmaeva, Melissa Giluso, Cody Glickman, Margaret Henderson, Benjamin Kellman, David Kristensen, Carl Leubsdorf, Kyle Levi, Shane Levi, Suman Pakala, Vikas Peddu, Alise Ponsoero, Eldred Ribeiro, Farrah Roy, Lindsay Rutter, Surya Saha, Migun Shakya, Ryan Shean, Matthew Miller, Benjamin Tully, Christopher Turkington, Ken Youens-Clark, Bert Vanmechelen and Ben Busby#. NCBI's Virus Discovery Hackathon: Engaging Research Communities to Identify Cloud Infrastructure Requirements. **Genes – MDPI** 2019. [10.3390/genes10090714](https://doi.org/10.3390/genes10090714)

Bram Vrancken*, Tony Wawina-Bokalanga*, Bert Vanmechelen, **Joan Martí-Carreras**, Miles W. Carroll, Justus Nsio, Jimmy Kapetshi, Sheila Makiala-Mandanda, Jean-Jacques Muyembe-

Tamfum, Guy Baele, Kurt Vermeire, Valentijn Vergote, Steve Ahuka-Mundeke, Piet Maes#. Accounting for population structure reveals ambiguity in the Zaire Ebolavirus reservoir dynamics. **PLoS NTD** 2019. [10.1371/journal.pntd.0008117](https://doi.org/10.1371/journal.pntd.0008117)

Tony Wawina-Bokalanga, Bert Vanmechelen, **Joan Martí-Carreras**, Valentijn Vergote, Kurt Vermeire, Jean-Jacques Muyembe-Tamfum, Steve Ahuka-Mundeke, Piet Maes#. Complete genome sequence of a new Ebola virus strain isolated during the 2017 Likati outbreak in the Democratic Republic of Congo. **MRA** 2019. [10.1128/MRA.00360-19](https://doi.org/10.1128/MRA.00360-19)

Joan Martí-Carreras, Piet Maes. Human cytomegalovirus genomics and transcriptomics through the lens of next-generation sequencing: revision and future challenges. **Virus Genes** 2019. [10.1007/s11262-018-1627-3](https://doi.org/10.1007/s11262-018-1627-3)

*Co-first authorship. #Corresponding author.

Presentations

Posters

- **Joan Martí-Carreras**, Piet Maes. **VANIR—NextFlow Pipeline for Viral Variant Calling and de Novo Assembly of Nanopore and Illumina Reads for High-Quality dsDNA Viral Genomes.** *Novel Concepts in Virology 2020.* 05-07/02/2020, Barcelona, **Spain.**
- **Joan Martí-Carreras**, Piet Maes. **BKTyper: Free Online Tool for Polyoma BK Virus VP1 and NCCR Typing.** *Novel Concepts in Virology 2020.* 05-07/02/2020, Barcelona, **Spain.**
- **Joan Martí-Carreras**, Piet Maes. **Detection of novel genome arrangements in human cytomegalovirus by long-read real-time sequencing.** *International Herpesvirus Workshop.* 23/07/2019, Knoxville, Tennessee, **USA.**

Orals

- **Joan Martí-Carreras**, Piet Maes. **Full-length genomic NGS assembly of viral pathogen with large (>100 kb) genomes.** *2nd HONOURS Annual Meeting.* 08-10/05/2019. Insel Riems, **Germany.**
- **Joan Martí-Carreras**, Piet Maes. **Detection of novel long genomic re-arrangements in human cytomegalovirus by HMW viral dsDNA enrichment.** *Nanopore Day Belgium.* 27/03/2019, Antwerpen, **Belgium.**
- **Joan Martí-Carreras**, Piet Maes. **Single-host and population analysis of Human Cytomegalovirus.** *1st HONOURS Annual Meeting.* 12-14/03/2018. Kandersteg, **Switzerland.**
- **Joan Martí-Carreras**, Guillem Salazar, Francisco M. Cornejo-Castillo, Isabel Sanz-Sáez, Josep M. Gasol, Pablo Sánchez, Silvia G. Acinas. **Biogeography of genes related to methyl-mercury degradation by comparative analyses of deep ocean metagenomes and metatranscriptomes.** *4th OOB-ICM meeting Biogeochemistry & Ecology.* 22–23/06/2017, Banyuls-sur-mer, **France.**

Awards/Grants

Marie-Sklodowska-Curie ITN (Host switching pathogens, infectious outbreaks and zoonosis, HONOURS, nr 721367) 2017 – 2020: Full-length genomic next-generation sequencing assembly of viral pathogens with large (> 100 kbp genomes).

Beca de Colaboración en Departamentos 2014-2015 at the Departament de Genètica i Microbiologia, Universitat Autònoma de Barcelona (UAB).

Beca Botet i Sisó 2011 at Universitat de Girona.

Educational activities

Invited lecturer at Computational Genomics Course (CGC) at Charles University, Prague, Czech Republic.

- Ed. 12-14/02/2020 'Next-generation sequencing theory and analysis' and 'Genomic analysis and epidemiology and diagnosis of unknown diseases'
- Ed. 11-13/02/2019 'Next-generation sequencing theory and analysis' and 'Genomic analysis and epidemiology and diagnosis of unknown diseases'
- Ed. 04-07/02/2018 'Basics of next-generation sequencing analysis' and 'Metagenomic analysis of environmental samples'

Organizer and lecturer at Nanopore sequencing workshop at Laboratory of Clinical and Epidemiological Virology, Rega Institute for Medical Research, KU Leuven, Leuven, Belgium.

- Basic Ed. 23-24/04/2019 'Amplicon sequencing', 'Long-read library preparations' and 'Bioinformatic analysis of nanopore reads'
- Advanced Ed. 05-07/12/2018 'Amplicon sequencing', 'Long-read library preparations', 'Assembly and annotation of nanopore reads' and 'NextFlow and Singularity pipeline building'

Courses

HONOURS-ITN

- **Vaccine design and commercialization**, 18-22/12/2019, MSD Animal Health, Boxmeer, The Netherlands.
- **Protein production**, 08-11/10/2019, Ingenasa, Madrid, Spain
- **Microarrays for virus detection**, 06-08/05/2019, FLI, Greifswald, Germany.
- **Novel diagnostics**, 21-23/01/2019, University of Leeds, Leeds, United Kingdom.
- **Optimization of next-generation protocols: VIDISCA**, 26-02/11/2018, AMC, Amsterdam, The Netherlands.
- **Primate non-human animal models**, 22-25/10/2018, BPRC, Rijswijk, The Netherlands.
- **Advanced diagnosis through RT-qPCR and oligo degeneration**, 25-29/11/2018, Charité Institute, Berlin, Germany.
- **Unbiased Next-generation sequencing with IonTorrent after shearing**, 18-22/11/2018, FLI, Greifswald, Germany.
- **Flavivirus serology and routine diagnostics**, 07-09/12/2017, IFIK, Bern, Switzerland.
- **Infectious Diseases**, 18-22/11/2017, AMC, Amsterdam, The Netherlands.
- **Outbreak Antenna Setting and Media training**, 13-15/11/2017, KU Leuven, Leuven, Belgium.

KU Leuven PhD training

- **BSL3/BSL3+ training**, Sep 2020 – Present, KU Leuven, Leuven, Belgium
- **Scientific Integrity I**, Nov 2018, KU Leuven, Leuven, Belgium

Hackathons

- **EUvsVirus Hack**, 24-26/04/2020, Remote.
- **NCBI Virus Discovery hackathon**, 08-13/11/2019, University of San Diego, San Diego, California, USA.
- **NCBI codeathon: Virus hunting in the cloud**, 04-06/01/2019, University of Maryland, College Park, Maryland, USA.

Other

- **A metagenomics hands-on training workshop using KAUST DMAP resource**, 28-30/03/2017, KAUST, Thurwal, Jeddah, Saudi Arabia.

Global Initiative on Sharing All Influenza Data (GISAID) submissions

- **> 1,000 Belgian SARS-CoV-2 complete genome sequences**