HENG-CHANG CHEN   *Update Feb 1st, 2021*

Current Position Postdoctoral Fellow
Institut de Génétique Humaine (IGH)
UMR 9002 CNRS - Université de Montpellier
Laboratory of Molecular Virology
Dr. Benkirane Lab
141 rue de la Cardonille
Montpellier - FRANCE

E-Mail: chen.heng-chang@igh.cnrs.fr
Personal website: http://chenhcinaki.wix.com/silence

ORCiD

I am molecular virologist and data scientist with over seven years of experience; I attempt to understand the interaction between human genomics and the regulation of HIV expression by using my skills involved in biotechnology and bioinformatics.

1. Education
2008 - 2012	Dr. rer. nat. (Ph.D.)	Institute of Biology, Humboldt-Universität zu Berlin	Berlin, Germany
2004 - 2006	M.Sc.	College of Medicine, National Taiwan University	Taipei, Taiwan
2000 - 2004	B.Sc.	College of Life Science, Tzu Chi University	Hualien, Taiwan

2. Positions
09/2018-Current	Postdoctoral scientist	Institut de Génétique Humaine (IGH)	Montpellier, France
2014-08/2018	Postdoctoral scientist	Centre de Regulació Genòmica (CRG)	Barcelona, Spain
2011-2013	Lab Manager	Centre de Regulació Genòmica (CRG)	Barcelona, Spain

3. Language
English | German | French | Spanish | Mandarin

I am fluent in spoken English and German (B2) and French (B1) and Mandarin (native speaker), full professional proficiency in reading and writing. I have a working knowledge of Spanish.

4. Research Experience
09/2018-Current	Postdoctoral scientist, Institut de Génétique Humaine (IGH)	Montpellier, France
2014-7/2018	Postdoctoral fellow, Centre de Regulació Genòmica (CRG)	Barcelona, Spain
1/2017-2/2017	Visiting scientist, CNRS UMR7216, Université Paris 7	Paris, France
2008-2011	Ph.D. fellow, Institute of Biology, Humboldt-Universität zu Berlin	Berlin, Germany

5. Computing expertise
R | Shiny: Advanced knowledge
HTML5 | CSS3 | awk | Linux | Markdown | Syntax | Python: Working knowledge

GitHub**:** https://github.com/HCAngelC

I use R and awk and Python for data mining; I have experience in analyzing different types of Big Data, including genome assembly (BWA-MEM & minimap2), RNA-seq data (kallisto, DESeq, DESeq2, edgeR), ChIP-seq data (Zerone), HiC data (Juicer & HiCcompare), Gene Ontology analysis and Gene Set Enrichment Analysis (GSEA) and developing the novel analysis pipeline for Oxford Nanopore long-read sequencing data. I also have experience in developing Big Data database by using HTML5, CSS3 and Shiny.

6. Research Awards and Grants
3/2018	Marie Sklodowska-Curie Actions Proposal Seal of Excellence 786552 - HIV-MAP
2/2017	EMBO Short-term Fellowship ASTF699-2016
2016	Awarded student talk in the 13th Horizons in Molecular Biology Symposium, Göttingen, Germany
2008-2011	Ph.D. fellowship funded by German Research Foundation (DFG)
2004	Student exchange program, Colorado College, Colorado, USA (refused)
2003	Bio-prize awarded by the Tzu Chi University, Taiwan (R.O.C.)

7. Publications
7.1. Peer Reviewed Publications
Please find peer reviewed publications in the list of the completed publications in the final page.

7.2. Monographs and Press
» **Chen, H.-C.** *2013*. Scientific Image - HIV Infection, ***El-lipse***, NÙM. 66.

I regularly post blog articles for public science. Please see my personal website: http://chenhcinaki.wix.com/silence for details.

7.3. Cover Images & Image Credits
» Natural Product Reports (ISSN: 0265-0568), Vol. 32, No. 1, January, *2015*
» Molecular Cell (ISSN: 1097-2765), Vol. 52, Issue 5, 12 December, *2013*
» iCLIP: Genomic views of protein-RNA interactions, EMBO Practical Course, *2013*

8. Competitively Invited Talks and Oral Presentations
8.1. Selected Invited Talks
6/2018   Fluctuations in HIV expression and the host genome (Hosted by DEBYSER, Z. & Francqui Foundation)
      Workshop on "Nuclear architecture and retroviral integration"   Leuven, Flanders, Belgium
9/2017   HIV expression, PEV and 3D genome (Hosted by PARISSI, V. & EMILIANI, S.)
      6th International Conference on Retroviral Integration   Bordeaux, France
3/2017   HIV latency, chromatin and genome architecture (Hosted by LEE, C.-K.)
      College of Medicine, National Taiwan University   Taipei, Taiwan
2/2017   HIV latency and genome evolution in reservoirs
      METU Evolutionary Biology Conference, Middle East Technical University   Ankara, Turkey

8.2. Selected Oral Presentations
06/2017   Faculty-selected talks: The invisible world of HIV latency in the human genome
      8th CRG Postdoctoral Symposium   Barcelona, Spain
2016   Visualisation of HIV latency by the new technology Barcoded HIV Ensembles
      13th Horizons in Molecular Biology Symposium   Göttingen, Germany
2014   Lighting talk: Visualisation of HIV-1 latency
      The 2nd EMBO Conference Visualizing Biological Data (*VIZBI*)   Heidelberg, Germany

9. Professional Organizations and Activities
2016   Organization committee of the CRG postdoctoral Retreat   Barcelona, Spain
2014   Organization committee of the V CRG postdoctoral Symposium   Barcelona, Spain

10. Teaching and Mentoring
10.1. Mentoring
SP 2017   *Gerlinde VANSANT* (FWO grant), CRG   Barcelona, Spain
SS 2014   *Oguzhan BEGIK* (Erasmus programme), CRG   Barcelona, Spain
SP 2012   Fundació Catalunya E^{2}C^3-Centre Recerca practical course, CRG   Barcelona, Spain
SP 2010   3rd-year master student, Free University   Berlin, Germany
SP 2009   2nd-year bachelor student, Free University   Berlin, Germany

Methods and skills used in Molecular Biology and library preparation for high-throughput sequencing were taught dependent on scientific levels of the students.

10.2. Workshop
SP 2015   Art, Science and Data Visualization, CRG PhD retreat   Castellar de n'Hug, Spain

I illustrate the principle for scientific data visualization with the point of view of fine art.

10.3. Informal Teaching and talks
2016   CRG summer school   Barcelona, Spain
2013   Lab Workshop assistant, CRG Teaching Day   Barcelona, Spain
2012   Lab introducer, CRG Open Day   Barcelona, Spain

Description of research accomplishments

2020 - Current
» Understanding the possible mechanism of elite controller patients to restrict HIV infection
(Supervisor: M. Benkirane, Institut de Génétique Humaine, Montpellier, France)
We attempt to understand whether HIV displays the distinct transcriptional phenotype in CD4+ T cells isolated from elite controller patients in vitro.

2019 - Current
» Genetically defective HIV proviruses are prone to be present in host genomic repeat regions
(Supervisor: M. Benkirane, Institut de Génétique Humaine, Montpellier, France)
*We developed a new technology LAMP-seq to associate the nearly full-length HIV genomic sequences with host genomic sequences surrounding integration sites. We show that the genetic integrity of the proviruses present in host genomic repeat regions is less intact than those outside the host genomic repeat regions (**Chen et al., manuscript under preparation**).*

» The impact of immunity stimuli on the selection of HIV integration sites and reactivation
(Supervisor: M. Benkirane, Institut de Génétique Humaine, Montpellier, France)
*We proof that HIV displays different transcriptional profiles in primary CD4+ T cells activated by different immunity stimuli. HIV proviruses are prone to integrate and be reactivated by the same stimuli used for primary CD4+ T cells activation upon infection (**Chen et al., manuscript under preparation**).*

2017-2019
» The chromatin landscape at the HIV-1 provirus integration site determines viral expression
(Personal Research Collaboration with the lab of Z. Debyser, KU Leuven, Leuven, Flanders, Belgium)
We proof that LEDGINs, which are small molecule inhibitors of HIV integrase-LEDGF/p75 interaction enable to retarget HIV out of gene-dense and actively transcribed regions and consequently reduce viral RNA expression and increase the proportion of silent provirus (Vansant, G., **H.-C. Chen* et al., 2020; *Shared first authors**).*

2015-2018
» The selection of HIV integration sites in the 3D genome
(Supervisor: G. Filion, Centre de Regulació Genòmica, Barcelona, Spain)
We show the bias of HIV integration in the 3D genomic architecture: viruses tend to integrate in spatial proximity of super-enhancers in primary CD4+ T cells and in T cell cultures in vitro (Lucic, B., **H.-C. Chen* et al., 2019, *Shared first authors**).*

2013-2016
» Position effects influence HIV latency reversal
(Supervisor: G. Filion, Centre de Regulació Genòmica, Barcelona, Spain)
*We successfully proof that HIV transcription is influenced by the local genomic context: viruses which integrate close to endogenous enhancers display the higher transcriptional level than those integrating far from enhancers (**Chen et al., 2017** & **Chen et al., 2018**).*

2008-2011
» Identification and characterization of a novel *Salmonella* gene product STM0029
(Supervisor: L.H. Wieler & K. Tedin, Humboldt-Universität zu Berlin, Berlin, Germany)
*We reveal the importance of a novel Salmonella gene product STM0029 which contributes to the resistance to host antimicrobial peptide killing (**DOI: 10.18452/16658**).*

2004-2006
» Characterization of a putative function of the two-component system ScnRK in *Streptococcus mutans*
(Supervisor: J.S. Chia, National Taiwan University, Taipei, Taiwan)
*We identify the function of S. mutans two-component system ScnRK involved in the resistance of hydrogen peroxide and murine macrophage killing (**Chen et al., 2008**).*

Completed list of Publications

I. Peer-Reviewed Research Publications
2020
» Vansant*, G., **H.-C. Chen***, E. Zorita, Trejbalová, K., Miklík, D., G. Filion, and Z. Debyser. 2020. The chromatin landscape at the HIV-1 provirus integration site determines viral expression. ***Nucleic Acids Research.*** doi.org/10.1093/nar/gkaa536 (***Shared first authors**) (**Q1**; IF: **11.147**)
» Machida, S., D. Depierre, **H.-C. Chen**, S. Houssier, G. Petitjean, C. Doyen, M. Takaku, O. Cuvier and M. Benkirane. 2020. Exploring histone loading on HIV DNA reveals a dynamic nucleosome positioning between unintegrated and integrated viral genome. ***PNAS***. doi: 10.1073/pnas.1913754117 (**Q1**; IF: **9.58**)
2019
» Lucic, B.*, **H.-C. Chen***, M. Kuzman*, E. Zorita*, J. Wegner, V. Minneker, W. Wang, R. Fronza, M. Schmidt, and R. Stadhouders, V. Roukos, K. Vlahovicek, G. Filion and M. Lusic. 2019. Spatially clustered loci with multiple enhancers are frequent targets of HIV-1. ***Nat. Communications.*** doi: 10.1038/s41467-019-12046-3 (***Shared first authors**) (**Q1**; IF: **11.878**; citation: **3**)
2018
» Abner, E., M. Stoszko, L. Zeng, **H.-C. Chen**, A. Izquierdo-Bouldstridge, T. Konuma, E. Zorita, E. Fanunza, Q. Zhang, T. Mahmoudi, M.-M. Zhou, G. Filion, and A. Jordan. 2018. A new quinoline BRD4 inhibitor targets a distinct latent HIV-1 reservoir for re-activation from other 'shock' drugs. ***J Virol***. doi: 10.1128/JVI.02056-17. (**Q1**; IF: **4.324**; citation: **10**)

» **Chen, H.-C.***, E. Zorita, and G. Filion*. 2018. Using Barcoded HIV Ensembles (B-HIVE) for single provirus transcriptomics. ***Curr Protoc Mol Biol.*** doi: 10.1002/cpmb.56 (***Corresponding authorship**) (**Q1**; citation: **3**)

» Lucic, B.*, **H.-C. Chen***, M. Kuzman*, E. Zorita*, J. Wegner, V. Minneker, V. Roukos, W. Wang, R. Fronza, M. Schmidt, M. Benkirane, R. Stadhouders, K. Vlahovicek, G. Filion and M. Lusic. 2018. Spatially clustered loci with multiple enhancers are frequent targets of HIV-1. 2018. Spatially clustered loci with multiple enhancers are frequent targets of HIV-1. ***BioRxiv.*** doi: https://doi.org/10.1101/287896. (***Shared first authors**)
2017
» **Chen, H.-C.**, J.P. Martinez, E. Zorita, A. Meyerhans, and G. Filion. 2017. Position effects influence HIV latency reversal. ***Nat Struct Mol Biol.*** doi: 10.1038/nsmb.3328. (**Q1**; IF: **12.109**; citation: **56**)

2015
» Corrales, M., P. Cusco, D.R. Usmanova, **H.-C. Chen**, N.S. Bogatyreva, G.J. Filion, and D.N. Ivankov. 2015. Machine learning: how much does it tell about protein folding rates? ***PLoS One.*** doi:10:e0143166. (**Q1**; IF: **2.776**; citation: **12**)

2008
» Chen, P.M., **H.-C. Chen**, C.T. Ho, C.J. Jung, H.T. Lien, J.Y. Chen, and J.S. Chia. 2008. The two-component system ScnRK of *Streptococcus mutans* affects hydrogen peroxide resistance and murine macrophage killing. ***Microbes and Infection***. doi:10:293-301. (**Q2**; IF: **2.669**; citation: **32**)

II. Peer-Reviewed Monographs
2020
» **Chen, H.-C.** *2020. Translated title:* Position matters: discussions about position effect variegation and HIV gene expression (article written in Chinese). ***Science Monthly*** (ISSN: 0250-331X). *article accepted*
Due to the issue of intellectual property, I refused to public this article in the journal Science Monthly.

III. Press
2013
» **Chen, H.-C.** *2013*. Scientific Image - HIV Infection, ***El-lipse***, NÙM. 66.

IV. Conference publications
2019
» Vansant, G., **H.-C. Chen**, E. Zorita, G. Filion, and Z. Debyser. 2019. HIV integration site selection affects transcription. **CSHL retroviruses**. Cold Spring Harbor, New York.

V. Cover Images & Image Credits
» Natural Product Reports (ISSN: 0265-0568), Vol. 32, No. 1, January, *2015*
» Molecular Cell (ISSN: 1097-2765), Vol. 52, Issue 5, 12 December, *2013*
» **i**CLIP: Genomic views of protein-RNA interactions, EMBO Practical Course, *2013*