


Curriculum Vitae

A. Basic Information

NAME, SURNAME (EMAIL)	CURRENT POSITION	BIRTH INFORMATION	
Chung-Chau, HON chungchau.hon@riken.jp	Research Scientist, Genome Information Analysis Team, Division of Genomic Technology, RIKEN Center for Life Science Technologies, Yokohama, Japan	22/04/1979 Male, Age: 35 , Hong Kong	
		HOMEPAGE	
		http://genomebytes.wordpress.com/	

EDUCATION and TRAINING

Institution (Location)	Degree / Position	Year	Subject
The University of Hong Kong (Hong Kong)	Bachelor of Science	1998-2001	Molecular Biotechnology, General Bioinformatics Supervisor: Prof. Frederick Chi-Ching Leung fcleung@hkucc.hku.hk
The University of Hong Kong (Hong Kong)	Master of Philosophy	2001-2003	Molecular Virology Supervisor: Prof. Frederick Chi-Ching Leung fcleung@hkucc.hku.hk
IBM Computational Biology Center (New York, USA)	Computational biologist (Intern)	2005	Massively parallel molecular dynamics simulations Supervisor: Dr. Ruhong Zhou ruhongz@us.ibm.com
The University of Hong Kong (Hong Kong)	Doctor of Philosophy	2003-2008	Population Genetics of Viruses Supervisor: Prof. Frederick Chi-Ching Leung fcleung@hkucc.hku.hk

EXPERTISE by TOPICS (Duration)

- Genomics and transcriptomics of protozoan parasites (**3 years**);
- Designing and analyzing RNA-Seq experiments (**3 years**);
- Gene regulation by small RNA and long non-coding RNA in protozoan parasites (**2 years**);
- Comparative genomics of closely related species (**3 years**);
- Gene expression analyses using microarray and RNA-Seq (**5 years**);
- Phylogenetics and population genetics of viruses (**8 years**);
- Origins of emerging viral diseases (**8 years**);
- Massively parallel molecular dynamics simulations (**1 year**);

EXPERTISE by TECHNIQUES (Level)

- Development of custom scripts for analyses of next generation sequencing data (**proficient**);
- Genome-wide mapping of transcription start sites and polyadenylation sites of Pol II transcripts (**proficient**);
- Discovery of cis-regulatory motifs for transcription initiation and polyadenylation (**semi-proficient**);
- Revision of gene models and annotation of antisense transcripts using RNA-Seq (**proficient**);
- Annotation of alternative splicing transcript isoforms using RNA-Seq (**proficient**);
- Characterization of endogenous small RNA populations using RNA-Seq (**proficient**);
- Differential expression and functional enrichment analyses based on next generation sequencing data (**semi-proficient**);
- Weighted gene correlation network analyses using microarray expression data (**semi-proficient**);
- Identification of orthological and syntenic genes between closely related species (**proficient**);
- Application of Bayesian, parsimony and likelihood methods in population genetics (**semi-proficient**);
- Large scale genotyping of viruses (**proficient**);

B. Postdoctoral Employment

I. Research Scientist,

Genome Information Analysis Team, Division of Genomic Technology,
RIKEN Center for Life Science Technologies (Yokohama, Japan)

2014-Now

- **Topic:** long non-coding RNA
- **Supervisor:** Dr Alistair Forrest; email: forrest@gsc.riken.jp

II. Senior Postdoctoral Fellow,

Cellular Biology of Parasitism Unit & Transcriptome and Epigenome Platform of Genopole
Institute of Pasteur (Paris)

2011-2014

- **Topic:** Application of Next Generation Sequencing on Comparative genomics and Transcriptomics of *Entamoeba*;
- **Supervisor:** Dr Nancy Guillen; email: nguillen@pasteur.fr

III. Postdoctoral Fellow,

Cellular Biology of Parasitism Unit,
Institute of Pasteur (Paris)

2008-2011

- **Topic:** Genomics of *Entamoeba*;
- **Supervisor:** Dr Nancy Guillen; email: nguillen@pasteur.fr

C. Competitive External Funds

I. Agence Nationale Recherche Genomic Grant 2010

2010-2013

- **Title:** Understating the Pathogenicity of *Entamoeba* Using Comparative Transcriptomics and Phylogenomics
- **Amount:** €641,744 (US\$869,258), in total for 3 years;
- **Role:** Proposal writing, project management, corresponding author, high throughput sequencing data analysis

D. Skill Sets

I. Computational Skills (Level)

- Perl scripting (**proficient**);
- Unix command line, system maintenance and software compiling and installation (**proficient**);
- Shell scripting (**semi-proficient**);
- Python scripting (**amateur**);

II. Next Generation Sequencing Data Analysis Skills (Level)

- Basic read data mapping using **bowtie**, **tophat**, **eXpress**, **SOAP** etc (**proficient**);
- Basic read data format handling using **samtools**, **picard**, **bamtools**, **fastqc** etc (**proficient**);
- Discovery of transcription start sites and polyadenylation sites using **custom scripts** (**proficient**);
- Transcriptome assembly using **cufflinks** and **custom scripts** (**proficient**);
- Genome-wide discovery of cis-regulatory motifs using **MEME suite** and **custom scripts** (**proficient**);
- Annotation of long non-coding and antisense transcripts using **custom scripts** (**proficient**);

III. Gene Expression Data and System Biology Analysis Skills (Level)

- Differential expression analyses using **DESeq**, **Cuffdiff**, **EdgeR** etc (**proficient**);
- Functional enrichment analyses using **GSEA**, **GOSeq**, **FUNC_hyper**, etc (**proficient**);
- Gene co-expression network analyses using **WGCNA**, **Cytoscape** and **custom scripts** (**semi-proficient**);

IV. Comparative Genomic Analysis Skills (Level)

- Identification of orthological genes using **orthoMCL** and **inparanoid** (**proficient**);
- Identification of syntenic genes using **DAGChainer** etc (**semi-proficient**);
- Genome-wide protein family clustering and classification using spectral clustering (SCPS) (**proficient**);

V. Phylogenetic and Population Genetics Analysis Skills (Level)

- Bayesian based molecular clock and coalescent analyses using **BEAST** (**proficient**);
- Likelihood based selection pressure analyses using **PAML** and **HyPhy** (**semi-proficient**);
- Large scale phylogeny reconstruction using **PAML**, **PAUP***, **mrBayes**, **BEAST** etc (**proficient**);

D. Publications

(Abstracts can be found at <http://genomebytes.wordpress.com/publications/>)

I. Genomics and Transcriptomics

1. Zhang, Q., Siegel, T.N., Martins, R.M., Wang, F., Cao, J., Gao, Q., Cheng, X., Jiang, L., **Hon, C.-C.**, Scheidig-Benatar, C., Sakamoto H., Turner L., Jensen A. T. R., Claes A., Guizetti J, Malmquist N.A, and Scherf A. (2014) Exonuclease-mediated degradation of nascent RNA silences genes linked to severe malaria. Nature, 10.1038/nature13468.
2. Reynolds, D., Cliffe, L., Förstner, K., **Hon, C.-C.**, Siegel, T and Sabatini, R. Regulation of Transcription Termination by Glucosylated Hydroxymethyluracil, Base J, in *Leishmania major* and *Trypanosoma brucei*. (2014) Nucleic Acids Res in press.
3. **Hon,C.-C.**, Weber, C., Sismeiro, O., Proux, C., Koutero, M., Deloger, M., Das, S., Agrahari, M., Dillies, M.-A., Jagla, B., Coppee, J.Y., Bhattacharya, A. and Guillen, N. (2012) Quantification of stochastic noise of splicing and polyadenylation in *Entamoeba histolytica*. Nucleic Acids Res, 10.1093/nar/gks1271. (*Corresponding and first author*).
4. Vasquez,J.-J., **Hon,C.-C.**, Vanselow J.T., Schlosser A. and Siegel, T.N (2013). Comparative ribosome-profiling reveals extensive translational complexity in different *Trypanosoma brucei* life-cycle stages. Nucleic Acids Res 10.1093/nar/gkt1386
5. Thibeaux, R., Weber. C., **Hon,C.-C.**, Dillies, M.-A., Copee, J.Y., Labruye, E. and Guillen, N. (2013). Identification of the virulence landscape essential for *Entamoeba histolytica* invasion of the human colon. PLoS Pathogens, 9(12):e1003824.
6. Njoya, E.M., Weber. C., Hernandez-Cuevas. N.A., **Hon,C.-C.**, Janin, Y, Kamini, M.F.G, Moundipa, P.F and Guillén, N (2013). Bioassay-guided fractionation of *Codiaeum variegatum*'s aqueous extract killing *Entamoeba histolytica* target ceramide biosynthesis. PLoS Negl Trop Dis, 8(1): e2607.
7. **Hon,C.-C.**, Weber,C., Koutero,M., Coppée,J.-Y., Deloger,M and Guillen,N. Surveying *Entamoeba histolytica* transcriptome using massively parallel cDNA sequencing. In 'Amebiasis: Biology and Pathogenesis of Entamoeba' by SPRINGER **In Press**. (*Corresponding and first author*)
8. Janbon, G., Ormerod, K. L., Paulet , D., Byrnes, E., Chatterjee, G., Yadav, V., **Hon,C.-C.**, A., Cuomo, C. A., Dietrich, F. S., Billmyre, Brunel, F, Bahn Y.-S., Chen, W., Chen, Y., Chow E. W. L., Coppée, J.Y., Floyd-Averette, A., Gaillardin C., Gerik, K. J., Goebels, C., Goldberg, J., Gonzalez-Hilarion S., Gujja, S., Hamlin, J. L., Hsueh, Y.-P., Ianiri, G., Jones, S., Kodira, C. D., Lam, W., Marra, M., Mesner, L. D., Mieczkowski, P.A., Moyrand, F., Nielsen, K., Proux, C., Rossignol, T., Scheinl, J. E., Sun, S., Wood, I. A., Zeng, Q., Neuvéglise, C., Newlon, C. S., Perfect, J. R., Lodge, J. K., Idnurm. A., Stajich, J. E., Kronstad, J. W., Sanya, K. Heitman, J., Fraser, J., Cuomo C. A. and Dietrich F. (2013). The genome sequence of *Cryptococcus neoformans* var. *grubii* reveals complex mechanisms of RNA expression and virulence plasticity. PLoS Genetics 10.1371/journal.pgen.1004261
9. Siegel, N, **Hon,C.-C.**, Zhang,Q., Lopez-Rubio,J.J., Coppée,J.-Y., Sismeiro,O and Scherf,A. (2014) Strand-specific RNA-Seq reveals widespread and developmentally regulated transcription of natural antisense transcripts in *Plasmodium falciparum*. BMC Genomics 10.1186/1471-2164-15-150
10. Santi-Rocca,J., Smith,S., Weber,C., Pineda,E., **Hon,C.-C.**, Saavedra,E., Olivos-García,A., Rousseau,S., Dillies,M.-A., Coppée,J.-Y. and Guillén, N (2012) Endoplasmic reticulum stress-sensing mechanism is activated in *Entamoeba histolytica* upon treatment with nitric oxide. PLoS ONE, 7, e31777.
11. Marquay Markiewicz,J., Syan,S., **Hon,C.-C.**, Weber,C., Faust,D. and Guillen,N. (2011) A proteomic and cellular analysis of uropods in the pathogen *Entamoeba histolytica*. PLoS Negl Trop Dis, 5, e1002.
12. **Hon,C.-C.**, Nakada-Tsukui,K., Nozaki,T. and Guillen,N. (2009) Dissecting the actin cytoskeleton of *Entamoeba histolytica* from a genomic perspective. In Anaerobic Parasitic Protozoa: Genomics and Molecular Biology. Edited by G. C. Clark, P. J. Johnson & A. R.D. Tucson AZ, USA: Caister Academic Press. (*First author*)
13. Yeung,Y.S., Yip,C.W., **Hon,C.-C.**, Chow,K.Y.C., Ma,I.C.M., Zeng,F. and Leung,F.C.C. (2008) Transcriptional profiling of Vero E6 cells over-expressing SARS-CoV S2 subunit: insights on viral regulation of apoptosis and proliferation. Virology, 371, 32–43.

14. Wang, Y., Zeng, F., **Hon, C.-C.**, Zhang, Y. and Leung, F.C.C. (2008) The mitochondrial genome of the Basidiomycete fungus *Pleurotus ostreatus* (oyster mushroom). **FEMS Microbiol Lett**, 280, 34–41.
15. Wong, R.T.-Y., **Hon, C.-C.**, Zeng, F. and Leung, F.C.C. (2007) Screening of differentially expressed transcripts in infectious bursal disease virus-induced apoptotic chicken embryonic fibroblasts by using cDNA microarrays. **J Gen Virol**, 88, 1785–1796.
16. Zeng, F., **Hon, C.-C.**, Sit, W.-H., Chow, K.Y.-C., Hui, R.K.-H., Law, I.K.-M., Ng, V.W.-L., Yang, X.-T., Leung, F.C.C. and Wan, J.M.-F. (2005) Molecular characterization of *Coriolus versicolor* PSP-induced apoptosis in human promyelotic leukemic HL-60 cells using cDNA microarray. **Int J Oncol**, 27, 513–523.
17. Cheung, K.H., **Hon, C.-C.**, and Leung, F.C.C. (2003) Illustration of Enhanced Features of Visual Genome Explorer Beta 2.1 by Comparative Analysis of *Helicobacter pylori* Strains 26695 and J99 Genomes. **Biocomputing: Computer Tools for Biologists**.
18. **Hon, C.-C.**, Chow, Y.C., Zeng, F.Y. and Leung, F.C.C. (2003) Genetic authentication of ginseng and other traditional Chinese medicine. **Acta Pharmacol Sin**, 24, 841–846. (*First author*)

II. Phylogenetics and Population Genetics

19. Lam, T.T.-Y., Chong, Y.L., Shi, M., **Hon, C.-C.**, Li, J., Martin, D.P., Tang, J.W.-T., Mok, C.-K., Shih, S.-R., Yip, C.W., Jiang, J., Hui, R.K., Pybus, O.G., Holmes, E.C., and Leung, F.C.C. (2013) Systematic phylogenetic analysis of influenza A virus reveals many novel mosaic genome segments. **Infect Genet Evol**, 10.1016/j.meegid.2013.03.015.
20. Lam, T.T.-Y., **Hon, C.-C.**, Lemey, P., Pybus, O.G., Shi, M., Tun, H.M., Li, J., Jiang, J., Holmes, E.C. and Leung, F.C.C. (2012) Phylodynamics of H5N1 avian influenza virus in Indonesia. **Mol Ecol**, 21, 3062–3077.
21. Shi, M., Lam, T.T.-Y., **Hon, C.-C.**, Hui, R.K.-H., Faaberg, K.S., Wennblom, T., Murtaugh, M.P., Stadejek, T. and Leung, F.C.C. (2010) Molecular epidemiology of PRRSV: a phylogenetic perspective. **Virus Res**, 154, 7–17.
22. Li, Y., Ge, X., **Hon, C.-C.**, Zhang, H., Zhou, P., Zhang, Y., Wu, Y., Wang, L.-F. and Shi, Z. (2010) Prevalence and genetic diversity of adeno-associated viruses in bats from China. **J Gen Virol** 91, 2601–2609.
23. Shi, M., Lam, T.T.-Y., **Hon, C.-C.**, Murtaugh, M.P., Davies, P.R., Hui, R.K.-H., Li, J., Wong, L.T.-W., Yip, C.W., Jiang, J.-W., and Leung, F.C.C. (2010) Phylogeny-based evolutionary, demographical, and geographical dissection of North American type 2 porcine reproductive and respiratory syndrome viruses. **J Virol**, 84, 8700–8711.
24. Yuan, J., **Hon, C.-C.**, Li, Y., Wang, D., Xu, G., Zhang, H., Zhou, P., Poon, L.L.M., Lam, T.T.-Y., Leung, F.C.C., and Shi, Z. (2010) Intraspecies diversity of SARS-like coronaviruses in *Rhinolophus sinicus* and its implications for the origin of SARS coronaviruses in humans. **J Gen Virol**, 91, 1058–1062. (*Equally contributed first author*)
25. Lam, T.T.-Y., **Hon, C.-C.**, and Tang, J.W. (2010) Use of phylogenetics in the molecular epidemiology and evolutionary studies of viral infections. **Critical Reviews in Clinical Laboratory Sciences**, 47, 5–49.
26. Yip, C.W., **Hon, C.-C.**, Shi, M., Lam, T.T.-Y., Chow, K.Y.-C., Zeng, F. and Leung, F.C.C. (2009) Phylogenetic perspectives on the epidemiology and origins of SARS and SARS-like coronaviruses. **Infect Genet Evol**, 9, 1185–1196.
27. **Hon, C.-C.**, Lam, T.T.-Y., Yip, C.W., Wong, R.T.-Y., Shi, M., Jiang, J., Zeng, F. and Leung, F.C.C. (2008) Phylogenetic evidence for homologous recombination within the family Birnaviridae. **J Gen Virol**, 89, 3156–3164. (*First author*)
28. **Hon, C.-C.**, Lam, T.-Y., Shi, Z.-L., Drummond, A.J., Yip, C.W., Zeng, F., Lam, P.-Y. and Leung, F.C.C. (2008) Evidence of the recombinant origin of a bat severe acute respiratory syndrome (SARS)-like coronavirus and its implications on the direct ancestor of SARS coronavirus. **J Virol**, 82, 1819–1826. (*First author*)
29. Lam, T.-Y., **Hon, C.-C.**, Wang, Z., Hui, R.K.-H., Zeng, F. and Leung, F.C.C. (2008) Evolutionary analyses of European H1N2 swine influenza A virus by placing timestamps on the multiple reassortment events. **Virus Res**, 131, 271–278.
30. Lam, T.T.-Y., **Hon, C.-C.**, Lam, P.-Y., Yip, C.W., Zeng, F. and Leung, F.C.C. (2008) Comments to the predecessor of human SARS coronavirus in 2003-2004 epidemic. **Vet Microbiol**, 126, 390–393.
31. Lam, T.T.-Y., **Hon, C.-C.**, Pybus, O.G., Kosakovsky Pond, S.L., Wong, R.T.-Y., Yip, C.W., Zeng, F. and Leung, F.C.C. (2008) Evolutionary and transmission dynamics of reassortant H5N1 influenza virus in Indonesia. **PLoS Pathog**, 4, e1000130.

32. Ma,C.M., **Hon,C.-C.**, Lam,T.-Y., Li,V.Y.-Y., Wong,C.K.-W., de Oliveira,T. and Leung,F.C.C. (2007) Evidence for recombination in natural populations of porcine circovirus type 2 in Hong Kong and mainland China. **J Gen Virol**, 88, 1733–1737.
33. **Hon,C.-C.**, Lam,T.-Y., Drummond,A., Rambaut,A., Lee,Y.-F., Yip,C.W., Zeng,F., Lam,P.-Y., Ng,P.T.W. and Leung,F.C.C. (2006) Phylogenetic analysis reveals a correlation between the expansion of very virulent infectious bursal disease virus and reassortment of its genome segment B. **J Virol**, 80, 8503–8509. (**First author**)
34. Guan,Y., Peiris,J.S.M., Zheng,B., Poon,L.L.M., Chan,K.H., Zeng,F.Y., Chan,C.W.M., Chan,M.N., Chen,J.D., Chow,K.Y.C. **Hon,C.-C.**, Hui, K.H., Li, J., Li, V.Y.Y., Wang, Y., Leung, S.W., Yuen, K.Y. and Leung F.C. (2004) Molecular epidemiology of the novel coronavirus that causes severe acute respiratory syndrome. **Lancet**, 363, 99–104.
35. Chow,K.Y.-C., **Hon,C.-C.**, Hui,R.K.-H., Wong,R.T.-Y., Yip,C.W., Zeng,F. and Leung,F.C.C. (2003) Molecular advances in severe acute respiratory syndrome-associated coronavirus (SARS-CoV). **Genomics Proteomics Bioinformatics**, 1, 247–262.
36. Zeng,F.Y., Chan,C.W.M., Chan,M.N., Chen,J.D., Chow,K.Y.C., **Hon,C.-C.**, Hui,K.H., Li,J., Li,V.Y.Y., Wang, C.Y., Hui, K.H., Li, J., Li, V.Y.Y., Wang, C.Y., Wang, P.Y., Guan, Y., Zheng, B., Poon, L.L.M., Chan, K.H., Yuen, K.Y., Peiris, J.S.M., and Leung F.C. (2003) The complete genome sequence of severe acute respiratory syndrome coronavirus strain HKU-39849 (HK-39). **Exp. Biol. Med. (Maywood)**, 228, 866–873.

III. Molecular Virology and Immunology

37. Li,K.K.B., Yip,C.W., **Hon,C.-C.**, Lam,C.Y., Zeng,F. and Leung,F.C.C. (2012) Characterisation of animal angiotensin-converting enzyme 2 receptors and use of pseudotyped virus to correlate receptor binding with susceptibility of SARS-CoV infection. **Hong Kong Med J**, 18 Suppl 3, 35–38.
38. Yip,C.W., **Hon,C.-C.**, Zeng,F. and Leung,F.C.C. (2012) Cell culture-adapted IBVDV uses endocytosis for entry in DF-1 chicken embryonic fibroblasts. **Virus Res**, 165, 9–16.
39. Chow,K.Y., Yeung,Y.S., **Hon,C.-C.**, Zeng,F., Law,K.M. and Leung,F.C. (2008) SARS coronavirus and apoptosis. **Hong Kong Med J**, 14 Suppl 4, 8–13.
40. Yip,C.W., Yeung,Y.S., Ma,C.M., Lam,P.-Y., **Hon,C.-C.**, Zeng,F. and Leung,F.C.C. (2007) Demonstration of receptor binding properties of VP2 of very virulent strain infectious bursal disease virus on Vero cells. **Virus Res**, 123, 50–56.
41. Yip,C.W., **Hon,C.-C.**, Zeng,F., Chow,K.Y.C., Chan,K.H., Peiris,J.S.M. and Leung,F.C.C. (2007) Naturally occurring anti-Escherichia coli protein antibodies in the sera of healthy humans cause analytical interference in a recombinant nucleocapsid protein-based enzyme-linked immunosorbent assay for serodiagnosis of severe acute respiratory syndrome. **Clin. Vaccine Immunol.**, 14, 99–101.
42. Zeng,F., **Hon,C.-C.**, Yip,C.W., Law,K.M., Yeung,Y.S., Chan,K.H., Malik Peiris,J.S. and Leung,F.C.C. (2006) Quantitative comparison of the efficiency of antibodies against S1 and S2 subunit of SARS coronavirus spike protein in virus neutralization and blocking of receptor binding: implications for the functional roles of S2 subunit. **FEBS Lett**, 580, 5612–5620.
43. Chow,K.Y.C., Yeung,Y.S., **Hon,C.-C.**, Zeng,F., Law,K.M. and Leung,F.C.C. (2005) Adenovirus-mediated expression of the C-terminal domain of SARS-CoV spike protein is sufficient to induce apoptosis in Vero E6 cells. **FEBS Lett**, 579, 6699–6704.
44. Yip,C.W., **Hon,C.-C.**, Zeng,F., Chow,K.Y.C. and Leung,F.C.C. (2004) Prevalence of non-pneumonic infections with SARS-correlated virus. **Lancet**, 363, 1825–author reply 1826–7.
45. Zeng,F., Chow,K.Y.-C., **Hon,C.-C.**, Law,K.M., Yip,C.W., Chan,K.H., Peiris,J.S.M. and Leung,F.C.C. (2004) Characterization of humoral responses in mice immunized with plasmid DNAs encoding SARS-CoV spike gene fragments. **Biochem Biophys Res Commun**, 315, 1134–1139.

IV. Massively Parallel Molecular Dynamics Simulations

46. Zhou,R., Eleftheriou,M., **Hon,C.-C.**, Germain,R.S., Royyuru,A.K. and Berne,B.J. (2008) Massively parallel molecular dynamics simulations of lysozyme unfolding. **Ibm J Res Dev**, 52, 19–30.