THE DOSSIER

The Digest on CCR Staff Scientists and Staff Clinicians: Information, Employment and Research

June 2016 Issue 24

From the Editor

Welcome to the June issue of The Dossier, a newsletter dedicated to the Staff Scientists and Staff Clinicians (SSSC) of the CCR!

This issue contains important messages from the Director's Office and a special article by Eric O. Freed, Ph.D. A summary of the 2016 SSSC Retreat is provided by our Retreat Co-Chairs, Christina Stuelten, M.D., Ph.D., and Gabriella Andreotti, M.P.H., Ph.D. The published work of Jianbo Chen Ph.D., is highlighted in our Author's Corner, while we feature Jonathan M. Weiss, Ph.D., in the SSSC Corner. The collaborative efforts of Devaiah N. Ballachanda, Ph.D., and Daoud Meerzaman, Ph.D., at the Computational Genomics and Bioinformatics Group of CBIIT are described in our Core Corner.

We hope to continue to provide pertinent information to aid in the success of SSSCs. Please send your contributions, suggestions, and comments to budhua@mail.nih.gov.

Anuradha Budhu, Ph.D. (SS)
Editor-in-Chief
Laboratory of Human Carcinogenesis

In This Issue

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From the Office of the Director

The CCR is a special place in many ways! Our institution boasts one of the broadest research portfolios of any cancer institute in the nation and our ability to freely pursue the most pressing problems in cancer, be it basic discovery, translation, or patient care, is unprecedented.

One of CCR's most important distinguishing features is its strong presence and reliance on you, the Staff Scientist and Staff Clinician, as the drivers of some of the most impactful work done in our laboratories and the Clinical Center. While many institutions across the country are gradually beginning to embrace the concept of long-term, high-level research staff in their laboratories and clinics, the value of staff scientists and clinicians has long been a cornerstone of CCR's success.

I am often asked by my colleagues in academia and industry: What actually is a Staff Scientist or Staff Clinician? And what exactly do they do? It would seem easier to list the things they do not do. Depending on the setting, a Staff Scientist or Staff Clinician may perform a very specific set of tasks in a laboratory or clinical setting, or may broadly support a research or clinical program, or be in charge of a core facility. In many cases, a Staff Scientist or Staff Clinician is the lifeline of a laboratory and clinic. The diversity of activities reflects the value of your community to CCR.

Staff Scientist and Staff Clinician level positions are increasingly sought after. This is in all likelihood a function of an academic job market, which is ever more competitive and fueled by the often heard concern by many trainees to not be able to balance home life with a demanding academic career. The creation of staff scientist positions in institutions across the country was one of the recommendations in the white paper published by Tilghman, Alberts, Kirschner, and Varmus in 2014 on "Rescuing US biomedical research from its systemic flaws" to address some of the challenges of the national research enterprise. It was gratifying to see that the report highlighted the pioneering role of the NIH Intramural Program, which developed a strong staff scientist and staff clinician program decades ago.

An important aspect of the Staff Scientist and Staff Clinician position is career development. Many Staff Scientists and Staff Clinicians assume their positions with many years of their careers ahead of them. Long-term planning to ensure opportunities for career advances and professional growth are essential to ensure a fulfilling long-term career path. In an effort to create a rewarding career track for Staff Scientists and Staff Clinicians, about a decade ago Associate and Senior Scientist and Clinician positions were introduced, providing advancement opportunities. We will continue to be proactive in ensuring career opportunities and satisfaction of Staff Scientists and Staff Clinicians, and I am looking forward to hearing your thoughts on how to make these valuable positions even better.

The strong, dedicated community of SSSCs is one of the distinguishing features of CCR—and one that we will rely on greatly as we pursue new discoveries across CCR in the years to come. You are a big part of why we at CCR can do cancer research like nobody else!

Tom Misteli, Ph.D.
CCR Director

The 12th Annual SSSC Retreat

The 12th annual Staff Scientists and Staff Clinicians (SSSC) Retreat was held on April 29, 2016, at NCI Shady Grove. This year's retreat was themed, "The Microbiome: From the Front to the Back End," and was attended by over 130 SSSCs from CCR, DCEG and Leidos. The planning committee was co-chaired by Gabriella Andreotti, M.P.H., Ph.D. (DCEG) and Christina Stuelten, M.D., Ph.D. (CCR), and also included Siddhartha Datta, Ph.D., Chi-Ping Day, Ph.D., Sigrid Dubois, Ph.D., Balamurugan Kuppusamy, Ph.D., Gwen Murphy, Ph.D., Anu Puri, Ph.D., Shree Ram Singh, Ph.D., Sergey Tarasov, Ph.D., and Hannah Yang, M.P.H.

The morning session, which was opened with greetings from Stephen Chanock, M.D., Director of DCEG, and was moderated by Romina Goldszmid, Ph.D. (CCR), included keynote talks from Giorgio Trinchieri, M.D. (CCR), Christian Jobin, Ph.D. (University of Florida), and Curtis Huttenhower, Ph.D. (Harvard T.H. Chan School of Public Health). This was followed by a panel discussion with the invited speakers as well as Rashmi Sinha, Ph.D. (DCEG), and Jonathan Badger, Ph.D. (CCR). The afternoon session was moderated by Balamurugan Kuppusamy, Ph.D. (CCR), and included talks from Heidi Kong, M.D. (CCR), and Rashmi Sinha, Ph.D. (DCEG). The lectures and discussions covered a breadth of research on the microbiome and cancer, including laboratory animal studies, population-based human studies, methodologic issues and clinical considerations.

This year's retreat also featured brown bag lunch sessions with the participants, invited speakers and NCI leadership, Montserrat Garcia-Closas, M.D., Dr.P.H. (DCEG), and Glenn Merlino, Ph.D. (CCR). The poster presentations provided an opportunity for SSSCs to present and discuss their research. Over 60 posters were presented and were judged by expert scientists. This year's travel award recipients were: Cristina Bergamaschi, Ph.D. (CCR), Maki Inoue Choi, Ph.D. (DCEG), Michael Kruhlak, Ph.D. (CCR), and Cynthia Pise-Masison, Ph.D. (CCR).

Many thanks to the attendees, judges and the 2016 retreat planning committee for making this year's retreat a success! We appreciate the support of Jonathan Wiest, Ph.D. (Director, Center for Cancer Training and Associate Director, Office of Training and Education, CCR) and Jackie Lavigne, Ph.D., M.P.H. (Chief, Office of Education, DCEG), as well the assistance from Keyonna Earle, Angela Jones, and Doug Nichols.

Until next year!

Christina Stuelten, M.D., Ph.D., & Gabriella Andreotti, M.P.H., Ph.D.
2016 SSSC Retreat Co-Chairs

The Quadrennial Review Corner

Understanding the Staff Scientist Quadrennial Review Process

Staff Scientist Quadrennial (Quad) Reviews are required by the NIH and are an important tool used by CCR leadership. The process begins in September, when I contact all staff scientists, their PIs and their Administrative Officers (AOs) to inform them that they will need to submit a Quadrennial Review Package in December. In the email I also provide the link to the CCR Checklist and related materials. (https://home.ccr.cancer.gov/intra/arc/_FTE/StaffScientist.asp).

The Review package consists of three parts. The first component is the recommending memo from the PI. The first page of the memo includes a checklist designed to identify the major duties of the staff scientist (SS) in their Lab/Branch. The second portion of the memo is a review of the SS's performance in the evaluation categories: **SS's role; scientific productivity; presentations; participation in special interest groups-community involvement; mentoring/ teaching; tech transfer, involvement in GMP production, regulatory approval, CRADAs, INDs etc.; collaborations; continuing education; awards; significant achievements; and core activity and list of users/collaborators**. While there is no set format for the memo, the majority of PIs use the given headings to be sure they have covered the relevant information. The information provided should focus on the achievements in the past four years. The PI can use this opportunity to explain any difficulties that may have occurred during the review period that may have had an impact on any of the areas of evaluation. The PI should provide specific details about the SS's involvement in the lab and the greater scientific community.

The second part of the Review Package is the SS's CV. A standard CV template can be found at the above link. Like the recommending memo, the CV should provide detailed information of the SS's career, particularly over the review period. The reviewers only have the information provided in the package to rate the SS, so details such as the SS's role in collaborations and current positions held by their mentees will strengthen the package.

The final component of the Quad Review Package is a collection of at least two letters of recommendation from collaborators or scientists that know your work. When possible, the SS should solicit letters of support from individuals outside the Lab/Branch and the NCI to indicate recognition by the broader scientific community.

Once completed, the package is submitted to the CCR ARC through the Lab/Branch AO. The package then comes to my office in the Office of Scientific Programs. The packages are distributed to the Quadrennial Review Panel that is comprised of the Promotion Review Panel and available CCR Deputies. Each package is assigned three independent reviewers that are responsible for rating the SS and discussing the package at the Quad Review Meeting. The Quad Review Meeting is held in March to discuss the packages and finalize the SSs' ratings. The SS and their PI should receive their Quad Review Report from me in early April. Any SS and/or PI wishing to comment on the report can submit a response directly to me. This response will be included in their package that is submitted back to the CCR ARC and Senior Staff. The complete package is then reviewed by Senior Staff for pay adjustments (funds permitting) and renewal purposes. The rating system is similar to that used for Site Visit reviews: Outstanding, Outstanding-Excellent, Excellent-Outstanding, Excellent, Excellent -Good, Good, Borderline/Unsatisfactory. If the SS has additional information not included in the original package or comments about the rating, they have 10 days to submit a response to me. The response will be included in their final package. The Quad Review Panel will not make changes to the original rating, however, but the response will be considered by CCR Leadership when making decisions on renewals and pay adjustments. It is important to note that following a rating of "Excellent" or below, the CCR Scientific Director requires written communication of performance goals to ensure each SS understands the specific improvements and results required for future appointment renewals.

Please share this newsletter with your colleagues and visit the SSSC website at sssc.nci.nih.gov.

The Quadrennial Review Corner Con't

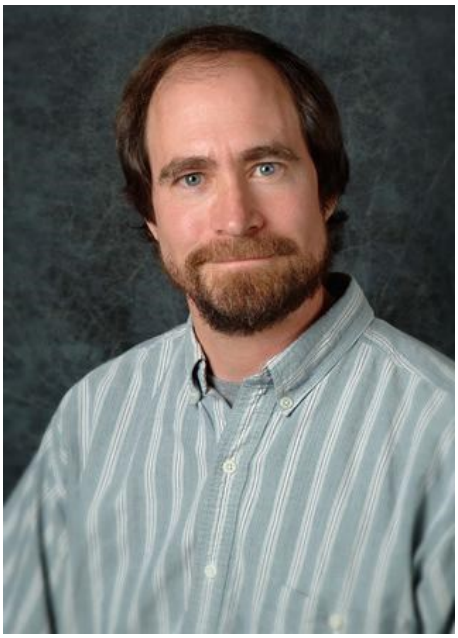
This year 38 SSs underwent Quad Review and 89% of them received an outstanding in their descriptor. Although the responsibilities and duties of each SS were as varied as the individuals, the information provided to the committee for those receiving top ratings all clearly conveyed the role and positive impact they had to the Laboratory/Branch and to the CCR.

Cynthia Pise-Masison, Ph.D.
Scientific Program Analyst, Office of the Director

The PI Corner

Section Editor: Lakshmi Balagopalan, Ph.D. (*SS*)

In my position as Director of the HIV Dynamics and Replication Program (HIV DRP), CCR, I have had the opportunity to interact with an extremely talented group of Staff Scientists who contribute to the mission of the Program in many ways. They provide scientific and technical expertise, continuity, and leadership within their labs and throughout the Program, and invaluable training and mentoring to postdoctoral fellows and students. Paul Boyer, Ph.D. is an expert at purifying HIV-1 reverse transcriptase and has been a key contributor to the elucidation of the structure and function of this important enzyme and in understanding how it becomes resistant to antiviral drugs. Abdul Waheed, Ph.D., is the go-to guy for a large number of techniques used in HIV research, and for the past eight years has been a devoted and effective mentor for our Werner H. Kirsten high school students. Jianbo Chen, Ph.D., has been instrumental in developing advanced microscopy techniques that have been applied to address key questions related to HIV-1 RNA trafficking. Siddhartha Datta, Ph.D., has developed many in vitro assays used to study the role of the HIV-1 Gag protein in virus assembly. Krista Delviks-Frankenberry, Ph.D., played a central role in ending the debate over whether XMRV was involved in chronic fatigue syndrome or prostate cancer. Together with her colleagues, she analyzed the ancestral origin of XMRV and determined that reported links between XMRV and disease were likely due to contamination. Finally, Mary Kearney, Ph.D., directs the Translation Research Unit (TRU) of the HIV DRP; in that capacity, she has directed research that has led to transformational discoveries about the nature of HIV-1 persistence in patients on antiretroviral therapy. I congratulate this stellar group of Staff Scientists on their many accomplishments and look forward to witnessing many more.



Eric O. Freed, Ph.D.
Senior Investigator, HIV Dynamics and Replication Program

The Core Corner

Section Editor: Anne Gegonne, Ph.D. (*SS*)

Discovery of BRD4 as a Novel Histone Acetyltransferase that Evicts Nucleosomes from the Chromatin Genome-Wide

One of the ongoing projects in the laboratory of Dinah Singer, Ph.D., at the Experimental Immunology Branch, NCI, has been the molecular characterization of the BRD4 protein. Bromodomain protein 4 (BRD4) is a master transcriptional and epigenetic regulator which plays a pivotal role in cancer development and immune diseases. Inhibiting its interaction with chromatin has been recently shown to be a successful therapeutic strategy against a variety of cancers that include acute myeloid leukemia, Burkitt's lymphoma, breast, colon and lung cancer. Current dogma suggests that BRD4 is an epigenetic 'reader' protein functioning as a passive mitotic bookmark and scaffolding protein for various transcription factors that activates transcription of key proto-oncogenes. However, BRD4 is responsible for significant changes in histone acetylation, chromatin architecture and transcription, leading us to investigate if it had a more direct role in epigenetic regulation.

Our studies showed that BRD4 has a previously undiscovered intrinsic histone acetyltransferase (HAT) activity through which it acetylates histones H3 and H4 in nucleosomes. BRD4 HAT activity was mapped to two consensus acetyl CoA binding sites and a 40 amino acid catalytic site on BRD4 through point and deletion mutants. BRD4 HAT activity is distinct from all other known HAT's with a unique lysine acetylation 'fingerprint' that includes acetylation of all histone H4 tail lysines and H3 tail lysines at K4, K9, K18 and K27 positions but not at K14. Most importantly, BRD4 acetylates H3K122, a key lysine residue critical for nucleosome stability located on the dyad axis of the nucleosome. Indeed, we showed that BRD4 HAT activity and H3K122 acetylation is responsible for nucleosome eviction and opening of the chromatin, as evidenced by the ability of BRD4, but not BRD4 HAT mutants, to evict nucleosomes both *in vitro* and *in vivo*.

In order to further characterize the role of BRD4 HAT activity genome-wide, we established a collaboration with the Computational Genomic Research (CGR) group headed by Daoud Meerzaman, Ph.D., at the Center for Biomedical Informatics and Information Technology (CBIIT), NCI. Through meta-gene analysis of data mined from the GEO database, Dr. Meerzaman and his group helped in demonstrating that BRD4 co-localized with H3K122ac marks genome-wide in a unique pattern. They further analyzed our Mnase-seq data to show that BRD4 HAT activity was responsible for decreased nucleosome occupancy genome-wide. Consistent with its role in localized chromatin de-compaction, BRD4 HAT activity regulates transcription at these gene loci as well. Analysis of data from RNA-seq of BRD4 WT and HAT mutant expressing cells showed a strong correlation between decreased nucleosome occupancy caused by BRD4 HAT activity and increased transcription genome-wide. Nucleosome clearance by BRD4 is selective and localized to the gene loci it is known to regulate such as *MYC*, *FOS* and *AURKB* (*Aurora B* kinase). Our collaboration with this NCI core was thus highly productive and effective.

Our successful collaboration with Dr. Meerzaman and his group at CBIIT helped us demonstrate that, contrary to dogma suggesting that BRD4 is a passive factor, BRD4 plays an active role in chromatin remodeling and transcription through its HAT activity. Based on our findings, we propose a new model where BRD4 is recruited to specific gene loci of M/G1 genes such as *MYC* and *FOS*, where it clears nucleosomes through its HAT activity to allow access to the transcriptional machinery. This work was published online on May 9, 2016 in Nature Structural and Molecular Biology; http://dx.doi.org/10.1038/nsmb.3228).

Please share this newsletter with your colleagues and visit the SSSC website at sssc.nci.nih.gov.

The Core Corner Con't

Section Editor: Anne Gegonne, Ph.D. (*SS*)

The Computational Genomics and Bioinformatics Group (CGBG) within CBIIT

The CGBG staff provide advanced computational genomics analysis, scientific consultation, and training to support the NCI scientific community. The CBIIT-CGBG team incorporates novel approaches utilizing in-house advanced analysis tools as well as open source tools to analyze, integrate, display, and interpret the diverse, systems-wide, large Next Generation Sequencing (NGS) data sets. The CBIIT-CGBG team provides sophisticated algorithms and expert bioinformatics support and assistance in the following areas:

Next Generation Sequence (NGS) data analysis:

Genomics: Whole genome and whole exome sequencing, Single nucleotides variations and mutations, Structural Variation Discovery e.g. Amplification and Deletion

Transcriptomics: RNA-Seq, Expression level, Novel transcripts, Fusion transcripts and Splice variants.

Epigenomics: ChIP-Seq, Methyl-Seq, Global mapping of DNA-protein interactions, DNA methylation and histone modification

Meta- genomics: Microbial genome Sequence, Microbial ID, Microbiome Sequencing

Microarray analysis: A variety of platforms such as Affymetrix, Illumina and custom arrays, SNP arrays, mRNA arrays, miRNA arrays and Proteomic arrays

Pathway and biological network interaction

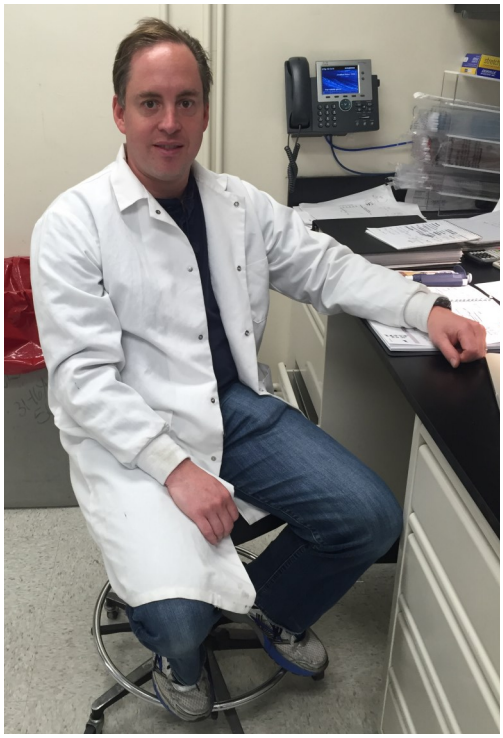
Multi-platforms and multi-experiment data integration and correlation.

Devaiah N. Ballachanda, Ph.D. (SS)
Experimental Immunology Branch

Daoud Meerzaman, Ph.D.
Section Head, Computational Genomics Research Group, Center for Biomedical Informatics & Information Technology

The SSSC Corner

Section Editor: Takashi Furusawa, Ph.D. (*SS*)



My first real foray into science was a summer job as a laboratory technician for a pharmaceutical company during college. Later I became completely hooked on the study of immunology when I took a graduate-level course in the subject during my undergraduate years at the University of Rochester. That course revealed to me the body contains specialized immune cells for fighting disease and left me with a passion for scientific research. During my graduate and postdoctoral years, I studied the migration and cytoskeletal reorganization of cells in response to inflammatory stimuli. My first "real" job was working at a local biotechnology firm where I worked for several years as a Research Scientist studying ways to improve dendritic cell-based anti-tumor vaccines.

I was very excited when a Staff Scientist position opened in the laboratory of Robert Wiltrout, Ph.D., at NCI at Frederick 11 years ago. Dr. Wiltrout is a world renowned expert in the field of mouse cancer models and immunotherapeutic strategies for cancer treatment and had a history of translating those advances to the clinic. My work was focused on the immunologic changes within the tumor microenvironment in response to immunotherapy and highlighted several mechanisms and putative biomarkers of anti-tumor responses. My research would not have been possible without the degree of freedom and responsibility that Dr. Wiltrout afforded me through my Staff Scientist position. Throughout my years at the NCI, I have been fortunate in being able to initiate multiple collaborations within the NCI community and with outside academic and/or biotech partners. I truly believe my success as a Staff Scientist has depended in large part upon these collaborations, which have opened up new avenues for research and training for me. In that way the Staff Scientist position has allowed me to network and to participate in "team science" which draws on the immense talents and unique expertise of many diverse scientists across Laboratories and Programs within the NIH and abroad.

With Dr. Wiltrout's retirement in 2015, I have joined a neighboring lab under the guidance of Daniel McVicar, Ph.D. In my new role, I am studying tumor-dependent alterations in immune cell metabolism and dissecting how various immune therapies may interact with these processes. As with my previous position, I am fortunate to again be surrounded by an immensely dedicated team of scientists, collaborators and technologic resources I'm not sure would be accessible to me in the private sector. Although my change in lab affiliation brings a certain degree of uncertainty, as I delve into new scientific topics and adjust to new laboratory dynamics, I am supported by incredible technical staff and confident that exciting new areas of cancer research will reveal themselves in the near future.

Please share this newsletter with your colleagues and visit the SSSC website at sssc.nci.nih.gov.

The SSSC Corner Con't

Section Editor: Takashi Furusawa, Ph.D. (*SS*)

Jonathan is pictured above while on vacation in Mexico with his son, Samuel, and daughter, Helena.

When I am not working in the lab, I enjoy spending as much time as possible traveling with my family and watching my two kids play team sports. My children remind me on a daily basis of the need to remain persistent in the face of adversity and to maintain a passion for discovery. The lab experiments may fail more often than succeed, but working at the NCI has truly been overwhelmingly rewarding to me!

Jonathan M. Weiss, Ph.D. *(SS)*
Cancer and Inflammation Program

The Author's Corner

Section Editor: Cristina Bergamaschi, Ph.D. (*SS*)

HIV-1 RNA genome dimerizes on the plasma membrane in the presence of Gag protein

Jianbo Chen, Sheikh Abdul Rahman, Olga A. Nikolaitchik, David Grunwald, Luca Sardo, Ryan C. Burdick, Sergey Plisov, Edward Liang, Sheldon Tai, Vinay K. Pathak, and Wei-Shau Hu. Proc Natl Acad Sci. 113(2): E201-8, 2016.

HIV-1, like all retroviruses, packages two copies of RNA in the form of a noncovalent-linked dimer as genome. Although each RNA contains all the genetic information necessary for viral replication, only one provirus is generated upon infecting a new target cell; thus, HIV-1 is pseudodiploid. This replication strategy allows the recovery of genetic information from damaged RNA genomes during DNA synthesis as reverse transcriptase can switch between the two RNA templates. In addition, the frequent template-switching process generates recombinant progeny, increases diversity in the viral population and helps the emergence of new variants that can evade the host immune response or resist antiviral treatments. Therefore, the strategy of packaging dimeric RNA affects both viral replication and viral evolution. Although its biological importance is appreciated, many aspects of the RNA dimerization process are unknown, including the location at which dimerization occurs and the factors involved.

The Viral Recombination Section directed by Wei-Shau Hu, Ph.D., within the HIV Dynamics and Replication Program, has recently developed a system that can efficiently label and detect HIV-1 RNA in viral particles and in living cells with single-RNA sensitivity. In the system, HIV-1 genomes were engineered to contain RNA stem-loops that are recognized by either the *Escherichia coli* BglG protein or the bacteriophage MS2 coat protein. Because these sequences are located in the *pol* gene, they are only present in full-length, unspliced HIV-1 RNAs. When introduced

into human cells, these constructs express full-length RNAs that can serve as templates for the translation of Gag proteins and as genomes in the viral particles. HIV-1 constructs were co-expressed with fluorescent proteins fused to BglG or MS2 coat protein, allowing the detection of the RNA genome by the signals from the fluorescent proteins. The results from these studies showed that most (>90%) of the particles contain RNA genomes, indicating that the full-length viral RNAs derived from these constructs are efficiently packaged. Furthermore, RNAs derived from different constructs can dimerize and copackage at a rate close to random distribution (1). This methodology allows one to detect HIV-1 RNA with single-RNA-molecule sensitivity (1) and to track HIV-1 RNA movement in the cytoplasm by using live-cell imaging (2).

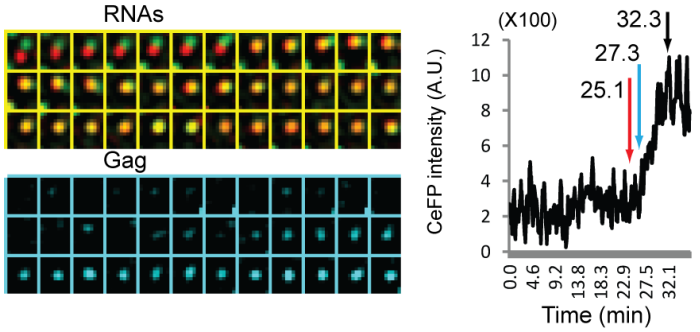


Figure 1. HIV-1 RNA-RNA interactions and Gag accumulation on the plasma membrane. One representative event showing RNA-merging (Red and Green) and detection and quantitation of GagCeFP.

To address the question of the location at which HIV-1 RNA dimerize and whether the Gag protein is required for RNA dimerization, Jianbo Chen, Ph.D., Staff Scientist in the Viral Recombination Section, tagged two HIV-1 RNAs and Gag, each with a different fluorescent protein, and studied their behavior at the plasma membrane by using total internal reflection fluorescence microscopy and live-cell imaging. This approach allowed him to simultaneously follow the particle assembly, RNA interaction, and RNA encapsidation in real time. It is often hypothesized that HIV-1 RNAs dimerize in the cytoplasm and the RNA-Gag complex is transported to the plasma membrane for virus assembly. Contrary to this hypothesis, Dr. Chen and co-authors found that HIV-1 RNAs dimerize not in the cytoplasm but on the plasma membrane. These results also shed light on the time frame in which RNA dimerization occurs during virus assembly. The authors observed dynamic interactions among HIV-1 RNA and merging of two RNA signals when neither, one or both were associated with detectable Gag signals. However, most of the RNA dimerization events were observed when both viral RNAs lack Gag signals (Figure 1), and Gag signal intensity increases after the observed dimerization event, indicating that the most RNA dimerize early in the assembly process. It was also found that HIV-1 RNA does not form a stable dimer in the absence of Gag, thus Gag protein is required for the formation or stabilization of RNA dimer. Taken together, these results suggest that the RNA dimerization process is probably mediated by the interactions of two RNA-Gag complexes, rather than two RNAs. These findings advance the current understanding of HIV-1 assembly and reveal important insights to viral replication mechanisms. The method Dr. Chen established provides a useful tool to further decipher the mechanisms regulating RNA packaging and dimerization.

Jianbo Chen, Ph.D. (SS)
Retroviral Replication Laboratory
HIV Dynamics and Replication Program

References:

1. Chen, J. Nikolaitchik, O., Wright, A., Bencsics, C., Coffin, JM. Na, N., Lockett, S., Pathak, V., Hu, W.-S. (2009). Simultaneous detection of two different RNAs in HIV-1 particles at single-RNA-molecule level by a novel labeling system. Proc. Natl. Acad. Sci. 106: 13535-13540.
2. Chen, J., Grunwald, D., Sardo, L., Galli, A., Plisov, S., Nikolaitchik ,O.A., Chen, D., Lockett, S., Larson, D.R., Pathak, V.K., Hu, W.S. (2014). Cytoplasmic HIV-1 RNA is mainly transported by diffusion in the presence or absence of Gag protein. Proc. Natl. Acad. Sci. 111: E5205-5213.

The Author's Corner Con't

Section Editor: Cristina Bergamaschi, Ph.D. (*SS*)

Dr. Jianbo Chen is a staff scientist in the Viral Recombination Section of the HIV Dynamics and Replication Program, NCI. As a staff scientist, Dr. Chen assists the Senior Investigator, designs and performs research projects, interacts with collaborators, and mentors students and postdoctoral fellows. Dr. Chen's research focuses on employing various fluorescent microscopy techniques to gain a better understanding in HIV-1 biology including the mechanisms of RNA genome encapsidation, RNA movement and RNA genome dimerization in living cells. He has collaborated extensively with intramural and extramural investigators to develop state-of-the-art microcopy techniques to study HIV-1 replication; these techniques have been used to complete several projects and are also used in ongoing research in the Section. His studies have made major contributions to our current understanding of HIV-1 RNA trafficking and packaging mechanism and is expected to continue to make important findings in HIV-1 biology.

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Announcements

Congratulations SSSCs!

2016 SSSC Retreat Travel Award Winners

Cristina Bergamaschi, Ph.D., (SS) Vaccine Branch (CCR)

Maki Inoue Choi, Ph.D., (SS) Metabolic Epidemiology Branch (DCEG)

Michael Kruhlak, Ph.D., (SS) Digital Imaging and Microscopy Facility (CCR)

Cynthia Pise-Masison, Ph.D., (SS) Office of The Director (CCR)

Looking for Editorial Experience?

The Dossier is looking for SSs or SCs to participate as Section Editors. If interested, please contact Anuradha Budhu at budhua@mail.nih.gov

A Call for Content

We need your input! Send your articles or suggestions with subject title "The Dossier" to budhua@mail.nih.gov.

This newsletter is an avenue for you to express your ideas and thoughts on being a Staff Scientist or Staff Clinician at CCR and to make pertinent announcements.

Your contribution is very important to the success of The Dossier. Please send us your commentary, announcements, and suggestions for topics/subject matter and we will do our utmost to include your material in upcoming issues.

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