



2013 RiboClub Program
Deducing RNA functions from high-throughput data
September 22-25
**In partnership with the non-coding RNAs grant in aid and
the RNA Society of Japan**
Hotel et Villégiature Chéribourg
2603 Chemin du Parc
Orford (Magog) Québec

Sunday, September 22nd, 2013

15:00 – 18:00 Registration for early arrivals

Monday, September 23rd

08:00 – 09:00 Registration

09:00 – 09:10 Welcoming notes (Sherif Abou Elela)

09:10 – 09:15 Presentation of Keynote speaker

09:15 – 10:15 **Keynote presentation:**
The hidden layer of regulatory RNA in human development
John Mattick, University of Queensland, Brisbane

10:15 – 10:40 Coffee break

Session 1:
Translation and ribosome

Chair: Christian Spahn (*session host Martin Bisailon*)

10:40 – 10:45 Introduction

10:45 – 11:10 Structure and structural dynamics of mammalian ribosomal complexes during translation elongation
Christian Spahn, Humboldt Universität, Berlin

11:10 – 11:35 Reorganization of an intersubunit bridge induced by disparate 16S ribosomal ambiguity mutations mimics an EF-Tu-bound state
Kurt Fredrick, The Ohio State University, Columbia



- 11:35 – 11:50 Translational control and miRNA-mediated deadenylation via RNA-binding proteins that interact with PAIP2A at the 3' end of mRNA
Akiko Yanagiya, McGill University, Quebec
- 11:50 – 12:05 Cancer cells hijack eIF4E2-directed translation initiation for tumorigenesis and adaptation to hypoxia
James Uniacke, University of Guelph, Ontario
- 12:05 – 12:20 Sequence-specific Modulation of RNA G-Quadruplexes
Jean-Pierre Perreault, Université de Sherbrooke, Québec
- 12:20 – 12:35 An Arginine-Aspartate network in the active site of E.coli TruB is critical for catalyzing pseudouridine formation
Ute Kothe, University of Lethbridge, Lethbridge
- 12:35 – 13:45 Lunch

Session 2:

RNA technology and applications

Chair: Feng Zhang (*session host Jean-Pierre Perreault*)

- 13:45 – 13:50 Introduction
- 13:50 – 14:15 Genome Engineering: Technologies and Applications
Feng Zhang, Broad Institute of MIT, Boston
- 14:15 – 14:40 Genetic code reprogramming for the expression of de novo macrocycles
Hiroaki Suga, University of Tokyo, Tokyo
- 14:40 – 14:55 Regulation of gene expression by HIV TAR miRNAs
Dominique Ouellet, Université de Laval, Québec
- 14:55 – 15:20 Aptamer-targeted antigen delivery
Matthew Levy, Albert Einstein College of Medicine, New York
- 15:20 – 15:35 RNA Tracking in Living Cells with Fluorescence-Activating RNA Aptamers
E. Dolgosheina, Simon Fraser University, Vancouver
- 15:35 – 16:20 Coffee Break



Session 3:

Gene silencing by small RNAs

Chair: Danesh Moazed (*session host Raymund Wellinger*)

- 16:20 – 16:25 Introduction
- 16:25 – 16:50 Biogenesis of PIWI-interacting RNAs
Mikiko Siomi, University of Tokyo, Tokyo
- 16:50 – 17:15 RNAi-mediated heterochromatin formation
Danesh Moazed, Harvard Medical School, Boston
- 17:15 – 17:30 Roles of the intron in the dg ncRNA in the formation of centromeric heterochromatin
Masatoshi Muttazono, Kumamoto University, Kumamoto
- 17:30 – 17:45 A developmental switch that activates miRNA-mediated mRNA decay during zebrafish embryogenesis
Yuichiro Mishima, University of Tokyo, Tokyo
- 17:45 – 18:00 Molecular mechanism for the inhibition of let-7 biogenesis by the pluripotency factor Lin28
Pascale Legault, Université de Montréal, Montréal
- 18:00 – 18:15 Defining fundamental steps in the assembly of Drosophila RNAi enzyme complex
Yukihide Tomari, University of Tokyo
- 18:15 – 19:15 Poster competition IA: (Odd numbers)
- 19:15 – 20:15 Poster competition IB: (Even numbers)
- 20:15 – 21:15 Dinner
- 21:15 – 21:20 Presentations of the travel awards
Eric Massé, Université de Sherbrooke, Sherbrooke
- 21:20 – 21:25 Presentation of the after dinner speaker
Benoit Chabot, Université de Sherbrooke, Sherbrooke
- 21:25 – 22:25 **After-dinner general presentation**
My life as an RNA molecule
Alan Bernstein, Canadian Institute for Advanced Research



Tuesday, September 24th

7:00 – 8:40 Breakfast

Session 4:

The life cycle of messenger RNA

Chair: Roy Parker (*session host Eric Massé*)

08:40 – 08:45 Introduction

08:45 – 09:10 The eukaryotic mRNA cycle: Movement of yeast mRNAs between polysomes, stress granules, and P-bodies and its role in the control of translation and degradation
Roy Parker, University of Colorado, Boulder

09:10 – 09:35 Novel E3 ubiquitin ligase is required for an endonucleolytic cleavage of mRNA by translation arrest
Toshifumi Inada, Tohoku University, Sendai

09:35 – 09:50 Coordinated assembly of localization and translational control factors on mRNA during transcription
Pascal Chartrand, Université de Montréal, Montréal

09:50 – 10:05 Developmentally-Regulated Elimination of Damaged Nuclei via a Chk2-Dependent Mechanism of mRNA Nuclear Retention
Éric Lécuyer, IRCM, Montréal

10:05 – 10:50 Coffee break

Session 5:

RNA-mediated genome maintenance

Chair: Fabrizio d'Adda di Fagagna (*session host Brendan Bell*)

10:50 – 10:55 Introduction

10:55 – 11:20 The direct role of nuclear non coding RNAs at sites of DNA damage in the control of genome integrity
Fabrizio d'Adda di Fagagna, IFOM Foundation, Milan



- 11:20 – 11:45 RNA-mediated epigenetic silencing in fission yeast
André Verdel, Université Joseph Fourier, Grenoble
- 11:45 – 12:00 Mouse Tudor domain containing 12 (Tdrd12) is essential for biogenesis of piRNAs entering nuclear Piwi protein Miwi2
Ramesh S. Pillai, EMBL, Grenoble
- 12:00 – 12:15 Nol12: ribosome biogenesis meets DNA damage and senescence
Pierre J Zindy, IRCM, Montréal
- 12:15 – 12:30 2013 Group Photo
- 12:30 – 15:05 Lunch and social time
- 15:05 – 15:30 Students **Best Seminar Award**
Introduced by Samuel Rouleau and Julie-Anna Benjamin

Session 6:

Diverse functions of non-coding RNAs

Chair: Shinichi Nakagawa (*session host Michelle Scott*)

- 15:30 – 15:35 Introduction
- 15:35 – 16:00 Functional analyses of abundant nuclear long noncoding RNAs
Shinichi Nakagawa, RIKEN, Hirosawa
- 16:00 – 16:25 Structural basis for specific, high-affinity tRNA binding by the T-box riboswitch Stem I domain
Adrian R. Ferré-D'Amaré, National Heart Lung and Blood Institute, Bethesda
- 16:25 – 16:40 Towards a prebiotically plausible mechanism for the emergence of RNA, ribozymes and the RNA World
Lyssa Martin, Simon Fraser University, Burnaby
- 16:40 – 16:55 *Drosophila* Lobe-less RNA is essential for axon guidance in development of mushroom body neurons
Yuji Kageyama, Kobe University, Kobe
- 16:55 – 18:10 Social time (complimentary cocktail)
- 18:10 – 19:10 Poster competition IIA (Odd numbers)
- 19:10 – 20:10 Poster competition IIB: (Even numbers)



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| 20:10 – 22:40 | Banquet |
| 21:40 – 22:00 | Musical Interlude (Part 1) |
| 22:00 – 22:10 | Poster prizes Michelle Scott , Université de Sherbrooke |
| 22:10 – 22:15 | RNA Group and Blue jacket award Benoit Chabot , Université de Sherbrooke |
| 22:40 – 23:00 | Musical Interlude (Part 2) |
| 23:00 – | Dance |

Wednesday, September 25th

Session 7A:

Deducing RNA functions from high-throughput data

Chair: Stefan Stamm (*session host Benoit Chabot*)

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| 09:00 – 09:05 | Introduction |
| 09:05 – 09:30 | The complexity of mammalian transcription Piero Carninci , RIKEN Center for Life Science Technologies, Kobe |
| 09:30 – 09:45 | Conserved features of an RNA promoter for RNA Polymerase II determined from high-throughput sequencing of a population of hepatitis delta virus Martin Pelchat , University of Ottawa, Ottawa |
| 09:45 – 10:10 | Splicing kinetics and transcript release from the chromatin compartment limit the rate of Lipid-A induced gene expression Doug Black , UCLA, Los Angeles |
| 10:10 – 10:25 | Analysis of Natural Compounds that Affect formation of nuclear speckles and Alternative Pre-mRNA Splicing in Mammalian Cells Kurogi Yutaro , Kumamoto University, Kumamoto |
| 10:25 – 10:50 | Coffee Break |



Session 7B:

Deducing RNA functions from high-throughput data

Chair: Stefan Stamm (*session host Benoit Chabot*)

- 10:50 – 11:15 Regulation of gene expression by processed snoRNAs
Stefan Stamm, University of Kentucky, Lexington
- 11:15 – 11:30 Exploring the roles of the RNA-binding protein FXR1P during myogenesis: evidences for regulation of myoblasts cell-cycle and terminal differentiation by modulating p21/Cdkn1a mRNA stability
Laetitia Davidovic, CNRS, Nice
- 11:30 – 11:45 Genomic view of eukaryotic RNase III reactivity and degradation signals
Mathieu Lavoie, Université de Sherbrooke, Sherbrooke
- 11:45 – 12:00 InteRRact: A scalable method for predicting conserved RNA-RNA interactions
Daniel Lai, University of British Columbia, Vancouver
- 12:00 – 13:30 Lunch
- 13:30 – 13:45 Integrative AUF1 PAR-CLIP analysis uncovers AUF1 role in translation and genome integrity
Je-Hyun Yoon, National Institutes of Health, Baltimore
- 13:45 – 14:00 A comprehensive analysis of RNA secondary structure with deletion, insertion and mutation
Risa Kawaguchi, University of Tokyo, Tokyo
- 14:00 – 14:25 RNA modifications as naturally-selected chemical diversity involved in various biological processes
Tsutomu Suzuki, University of Tokyo, Tokyo
- 14:25 – 15:25 Harry Noller, University of California, Santa Cruz
Student Choice Seminar
Introduction by the student's representatives

Departure