CONFÉRENCE UNIVERSITAIRE DE SUISSE OCCIDENTALE

CUSO Doctoral Program in Microbial Sciences

INVITED SEMINAR

June 30, 2011

UNIL, Biophore, BIO 2817.2

Regulatory small RNAs in bacteria: biological roles, mechanistic aspects, and protein involvement

Prof. Gerhart Wagner,
Dept. of Cell and Molecular Biology, Uppsala University, 75124 Uppsala, Sweden; http://www.ucg.uu.se/GWagner.html

Hosts: Prof. Dieter Haas & Prof. Karine Lapouge, University of Lausanne

SUMMARY
Regulatory RNAs were first identified in bacteria, as key control elements in plasmid replication. Many years later, genome-wide searches for chromosomal genes encoding small RNAs (sRNAs) with putative regulatory functions were conducted around yr 2000. By now we know of hundreds of such RNAs in many different bacteria, and some archaea, and biological roles and mechanisms of action are beginning to be understood.
Post-transcriptional regulation of gene expression in bacteria involves numerous sRNAs, a heterogeneous class of RNAs that predominantly, but not exclusively, acts by an antisense mechanism, i.e. involving base-pairing between an antisense and a target RNA. This mode of action can result in up- or down-regulation of gene expression. Regulation can be achieved directly or indirectly by affecting the process of translation initiation, but alternative effects can be exerted through sRNA-mediated destabilization (targeted degradation) of mRNAs.
In general terms, sRNAs appear to be mostly involved in regulating stress responses and, in cases where such a life-style is an option, control of virulence traits. An interesting aspect of sRNA-mediated control is reminiscent of miRNAs in eukaryotes: they often have multiple targets, and this permits simultaneous control of many, functionally related target genes (target gene families). Conversely, several sRNAs occasionally converge on the same target for control. What we learned so far has led to a reassessment of how biological control

circuits are set up. More often than not, regulatory pathways are webs of control in which both traditional transcriptional (transcription factor-based) and post-transcriptional (sRNA-based) control levels are present.
Furthermore, in many bacteria, the homohexameric Hfq protein (a bacterial homolog of eukaryotic Sm proteins) is a key player required for sRNA-mediated control. E.g., the majority of enterobacterial sRNAs requires Hfq for regulatory efficiency, and mutations/ deletions in Hfq have strong pleiotropic phenotypes. These are often associated with compromised stress responses and loss of virulence in pathogens. The Hfq requirement may be explained by several established effects: RNA-RNA binding rate enhancement, RNA chaperone activity, protection of sRNAs from degradation - or any combination thereof. How this works is an area of vivid scientific activity.

AFTERNOON ROUND-TABLE DISCUSSION

Location: Biophore, Bio 2917.2, 14:00-15:30
Organizer: Prof. Gerhart Wagner

1) **Two papers for reading**

Darfeuille, F., Unoson, C., Vogel, J. & Wagner, E.G.H. (2007) An antisense RNA inhibits translation by competing with "standby" ribosomes. *Mol. Cell* 26, 381-392.
Fender, A., Elf, J, Hampel, K., Zimmermann, B., & Wagner, E.G.H. (2010) RNAs actively cycle on Hfq. *Genes & Dev.* 24, 2621-2626.

2) **Presentation and discussion of students' projects**

3) **General discussion**

To discuss projects in general, science as such, how to choose subjects to work at and by which criteria, how to distinguish good from bad science, problems with publishing policies (for instance, why do high profile journals like Science and Nature appear to frequently publish bad or flawed papers), etc.

PhD students interested in meeting the speaker, please register using the link: http://biologie.cuso.ch/microbiologie/activities/