

Non-coding RNAs in development

The BioPark Hertfordshire, Welwyn Garden City, AL7 3AX: 1st October 2010

Eukaryotic gene expression is modulated at many layers of regulatory control. It is becoming apparent that differentiation and development involve the action of numerous regulatory non-protein coding RNAs (ncRNAs). This meeting will focus on the discovery and characterization of ncRNAs in the context of embryogenesis and organismal development, highlighting recent technological advances for high-throughput functional genomics. Meeting Chair: [Paul Bertone](#), European Bioinformatics Institute, Cambridge, UK

This event has CPD accreditation and a troubleshooting panel session.

On registration you will be able to submit your questions to the panel that will be asked by the chair on the day of the event

- 9:00 – 9:45 **Registration**
- 9:45 – 10:00 **Introduction by the Chair:** [Paul Bertone](#), European Bioinformatics Institute, Cambridge, UK
- 10:00 – 10:30 **Talk title to be confirmed**
[Dr Anna Git](#), Cancer Research UK Cambridge Research Institute (CRI), Li Ka Shing Centre, Robinson Way, Cambridge, UK
- 10:30 – 11:00 **Title to be confirmed**
[Dr Anton Enright](#), EMBL - European Bioinformatics Institute, Cambridge, UK
- 11:00 – 11:10 **Speakers photo**
- 11:10 – 11:30 **Mid-morning break**
- 11:30 – 12:00 **The complex life of small RNA**
[Dr Eric Miska](#), Gurdon Institute, Wellcome Trust/Cancer Research UK Gurdon Institute, The Henry Wellcome Building of Cancer and Developmental Biology, Cambridge, UK
icroRNAs (miRNAs) are 22 nucleotide small RNAs that act as endogenous regulators of gene expression by base-pairing with target mRNAs. Here we analyse the function of the six members of the *C. elegans* miR-51 family of miRNAs (miR-51, miR-52, miR-53, miR-54, miR-55, miR-56). miR-51 family miRNAs are broadly expressed from mid-embryogenesis onwards. The miR-51 family is redundantly required for embryonic development. miR-51 family mutants display a highly penetrant pharynx unattached (Pun) phenotype, where the pharyngeal muscle, the food pump of *C. elegans*, is not attached to the mouth. Unusually, the Pun phenotype in miR-51 family mutants is not due to a failure to attach, but a failure to maintain attachment during late embryogenesis. Expression of the miR-51 family in the mouth is sufficient to maintain attachment. The Fat cadherin ortholog CDH-3 is expressed in the mouth, and is a direct target of the miR-51 family miRNAs. Genetic analysis reveals that miR-51 family miRNAs act in part through CDH-3 to regulate pharynx attachment. This study is the first to assign a function to the miR-51/miR-100 miRNA family in any organism.
- 12:00 – 12:30 **Micro RNAs in disease and drug discovery**
[Dr Michael R. Barnes](#), GlaxoSmithKline Medicines Research Centre, Hertfordshire, UK
- 12:30 – 14:00 **Lunch and Poster Viewing**
- 14:00 – 15:00 **Question and Answer Session**
Delegates will be asked to submit questions to a panel of experts. Questions can be submitted before the event or on the day
- 15:00 – 15:30 To be confirmed
- 15:30 – 16:00 **Afternoon Tea/Coffee and Last Poster Viewing**
- 16:00 – 16:30 **Connectivity Mapping of small RNAs**
[Dr Gerome D Breen](#), Kings College, London, UK
- 16:30 – 17:00 **Chairman's summing up**

You can network with people from this event at

Nature network - <http://network.nature.com/groups/euroscicon/>

Linked In- <http://www.linkedin.com/groups?gid=1939569>

Facebook - <http://www.facebook.com/group.php?gid=70847076549>

Twitter - <http://twitter.com/Euroscicon/>

About the chair

Paul Bertone received the PhD from Yale University and is currently a Group Leader at the EMBL European Bioinformatics Institute in Cambridge. He also holds joint appointments in the Developmental Biology and Genome Biology Units at the EMBL in Heidelberg. His work to date has included the development of novel technologies for large-scale genome annotation, protein functional analysis and computational biology. His research group is applying state-of-the-art experimental platforms and computational methods to the characterisation of stem cell lineage commitment, differentiation and reprogramming. This includes the elucidation of transcription factor-mediated gene regulatory pathways, functional characterisation of non-coding RNAs, and comprehensive transcriptome analysis using next-generation sequencing technologies.

About the Speakers

Eric Miska received a BA in Biochemistry from Trinity College, Dublin, Ireland in 1996. He received his PhD in pathology from the University of Cambridge, Cambridge, UK in 2000. He was a postdoctoral fellow in the laboratory of Bob Horvitz at the Massachusetts Institute of Technology, Cambridge, MA, USA from 2000 to 2004.

Dont forget to sign up to Euroscicons e-newsletter at www.euroscicon.com/signup.htm to keep up to date with European Life Science news and events and to be notified of the follow up to this event