

SIROCCO

Silencing RNAs: organizers and coordinators of complexity in eukaryotic organisms

AUG 2008 Newsletter 19

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Mouse miRNA library to open



Biologists working with knockout mice that have been genetically engineered to inactivate certain genes are creating a library of knockouts of all microRNAs known in mice. The collection, an initiative of the Sanger Institute in Cambridge UK is the first to tackle the nearly 500 miRNAs that scientists have identified in the mouse genome. The re-

source will eventually be available to all researchers studying the diverse systems affected by these short strands of nucleotides that regulate gene expression. Scientists speculate that mice may have more than a thousand miRNAs.

The Sanger project, named μ KOMP because it's a micro counterpart to KOMP, the Knockout Mouse Project for protein-coding genes run by the US National Institutes of Health, should help those who are making knockout mice. It will offer the genetic tools and, ultimately, embryonic stem-cell lines for knockout mice.

"This will actually cut out a part of the process," says Allan Bradley, director of the Sanger Institute. Making a knockout mouse can soak up a year or so of a researcher's time, and cost thousands of pounds with no guarantee of success.

"I wish they had it already," says Ying-Hui Fu, a neuroscientist at the University of California, San Francisco.

"More and more, people are realizing almost every biological pathway has miRNA involvement."

miRNAs regulate protein production in several biological systems and have been implicated in cancer and heart disease. The Sanger team will make all the knockouts using one method, and in the same strain of mice, so scientists will be able to directly compare different mutations. "That is so important," Fu says. "Different strain backgrounds sometimes give you totally different results." Source: www.nature.com

SIROCCO INTEGRATION ACTIVITIES

Funding is available to support seminar speakers within the SIROCCO consortium.

One of the goals of the SIROCCO project is to promote integration between the partner laboratories. With such a wealth of knowledge within the consortium SIROCCO hopes to facilitate the exchange of ideas between members.

Funding is also available for lab exchanges within the consortium.

Travel and accommodation can be arranged by the management office.

Please email Aileen
fah37@cam.ac.uk

Detailed Implementation Plan Months 25-42

- The draft report containing the detailed implementation plan for months 25-42 is currently being drawn up
- We will be asking for specific deliverables and milestones to be included in the workplan



RESEARCH SPOTLIGHT



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Cacchiarelli D, Santoni D, Bozzoni I. microRNAs as prime players in a combinatorial view of evolution. *RNA Biol.* 2008 Jul 8;5(3). [Epub ahead of print]

Lykke-Andersen K, Gilchrist MJ, Grabarek JB, Das P, Miska E, Zernicka-Goetz M. Maternal Argonaute 2 Is Essential for Early Mouse De-

velopment at the Maternal-Zygotic Transition. *Mol Biol Cell.* 2008 Aug 13. [Epub ahead of print]

Moxon S, Schwach F, Maclean D, Dalmay T, Studholme DJ, Moulton V. A toolkit for analysing large-scale plant small RNA datasets. *Bioinformatics.* 2008 Aug 19. [Epub ahead of print]

Rabionet R, Espinosa-Parrilla Y, Estivill X. Human genetics branches out in Barcelona. *Genome Biol.* 2008 Aug 13;9(8):318. [Epub ahead of print]



SIROCCO 2008 will be held 10-12 December 2008 at the Wellcome Trust Conference Centre which is in the WT Genome Campus—host to the Sanger Institute and the European Bioinformatics Institute

For SIROCCO bioinformaticians: a special one-day bioinformatics meeting in the IT suite at the Wellcome Trust Conference Centre on the day before
Tuesday 9th December

REGISTRATION

Please register for the meeting by Friday 10th October 2008
Email Aileen fah37@cam.ac.uk
<http://www.wtconference.org/>

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