

SIROCCO

Silencing RNAs: organizers and coordinators of complexity in eukaryotic organisms

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SIROCCO Partner Gyorgy Hutvagner and his colleagues have published a paper in RNA showing that highly abundant small RNA fragments derived from mature tRNAs are likely produced by specific processing rather than from random degradation. Moreover, the processing of small RNAs derived from tRNA^{Gln} is dependent on Dicer in vivo and Dicer cleaves the tRNA in vitro. The authors speculate that there may be a connection between the accumulation of the Dicer dependent small tRNAs and the aberrantly elevated tRNA expression in transformed cells and that the transformation is caused by the competition between tRNAs and pre-miRNAs for Dicer accessibility, resulting in impaired miRNA homeostasis, particularly as only certain tRNA anticodon types are expressed at high levels and processed. Alternatively, the cytoplasmic miRNA processing machinery may be actively processing misfolded inactive tRNAs as a defense response to tRNA overexpression.

Detlef Weigel awarded Otto Bayer Award 2010



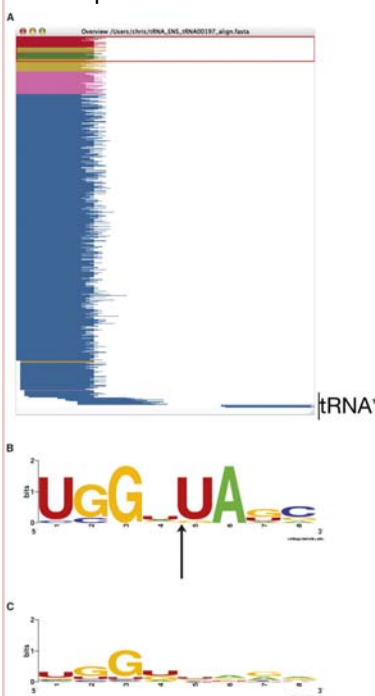
SIROCCO Partner Detlef Weigel will receive the Otto Bayer Award 2010 - one of the most prestigious scientific prizes in the German speaking countries. Detlef Weigel, Director of the Max Planck Institute for Developmental Biology in Tübingen, has contributed to our understanding of the molecular basis of plant variability and has allowed predictions on how wild as well as agricultural plants will adapt to climate change.

The prize also recognizes Detlef's work on microRNAs in plant development and his development of technologies for artificial microRNA production.

The Otto Bayer Prize was initiated in 1984 and is awarded every two years by the Bayer Science and Education Foundation.

The award will be presented by the CEO of Bayer, Werner Wenning, in Berlin on 12 February 2010.

<http://www.bayer.de/de/News-Detail.aspx?id=12579>



Sequence reads aligning to a known tRNA sequence as determined by Vmatch. Sequence reads are color coded by abundance with red >500 reads and blue <10 reads. The majority of the reads align to the 5' end of the tRNA. A small number of complementary sequences can be seen aligning to the 3' end: tRNA*. (B) Sequence motif logo for tRNA 8mer sequence around the 19–20 position of selective cleavage. Nonredundant set of tRNAs with matching read abundances of at least 2000 (B), and a nonredundant set of all human tRNAs (C). Arrow indicates the tRNA cleavage site.

Filtering of deep sequencing data reveals the existence of abundant Dicer-dependent small RNAs derived from tRNAs. Cole C, Sobala A, Lu C, Thatcher SR, Bowman A, Brown JW, Green PJ, Barton GJ, Hutvagner G. RNA. 2009 Dec;15(12):2147-60.



RESEARCH SPOTLIGHT



Repertoire and evolution of miRNA genes in four divergent nematode species.

de Wit E, Linsen SE, Cuppen E, Berezikov E.
Genome Res. 2009 Nov;19(11):2064-74. Epub 2009 Sep 15.

Transient assays for the analysis of miRNA processing and function. de Felippes FF, Weigel D.

Methods Mol Biol. 2010;592:255-64.

Analyzing mRNA expression identifies Smad3 as a microRNA-140 target regulated only at protein level.

Pais H, Nicolas FE, Soond SM, Swingler TE, Clark IM, Chantry A, Moulton V, Dalmay T.
RNA. 2010 Jan 13. [Epub ahead of print]

Structure Determinants for Accurate Processing of miR172a in Arabidopsis thaliana.

Werner S, Wollmann H, Schneeberger K, Weigel D.
Curr Biol. 2009 Dec 14. [Epub ahead of print]

Abundant and dynamically expressed miRNAs, piRNAs, and other small RNAs in the vertebrate Xenopus tropicalis.

Armisen J, Gilchrist MJ, Wilczynska A, Standart N, Miska EA.
Genome Res. 2009 Oct;19(10):1766-75. Epub 2009 Jul 23.

SeqBuster, a bioinformatic tool for the processing and analysis of small RNAs datasets, reveals ubiquitous miRNA modifications in human embryonic cells. Pantano L, Estivill X, Martí E. Nucleic Acids Res. [Epub ahead of print]

Small RNAs in flower development.

Wollmann H, Weigel D.
Eur J Cell Biol. 2009 Dec 21. [Epub ahead of print]

Filtering of deep sequencing data reveals the existence of abundant Dicer-dependent small RNAs derived from tRNAs.

Cole C, Sobala A, Lu C, Thatcher SR, Bowman A, Brown JW, Green PJ, Barton GJ, Hutvagner G.
RNA. 2009 Dec;15(12):2147-60. Epub 2009 Oct 22.

REPORTS NOW DUE

Financial reports for the third period (2009) are now due

Full Annual Report must be received at the European Commission by 14 February 2010

Reports should include:

- Form C financial statement
- Audit Certificate if necessary
- Major costs tables
- Justification of Major Costs table

Please email financial reports to fah37@cam.ac.uk
And courier signed documents to:

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