



Society News

The latest congress of the DGNG was held in Lübeck and hosted by Christine Klein and Christine Zülcke from the Departments of Neurology and Human Genetics, respectively. Traditionally the main topics of the DGNG annual meetings reflect the research interests of the hosting institutions. Accordingly, the main topics in 2008 included genetics of movement disorders, abnormal brain development and psychiatric diseases. The event was outstanding, with excellent speakers who provided insight into cutting edge neurogenetic research at an international level. The excellent organisation and the charming surroundings of the ancient hanseatic city made this congress one of the highlights of the history of the DGNG.

The upcoming, 15th annual meeting of the DGNG is scheduled for October 8 - 10 in Homburg/Saar and will be hosted by Prof. Mathias Riemenschneider. Please mark this date in your calendars; we expect another excellent meeting with internationally renowned speakers.

As last year the DGNG will again provide a limited number of travel stipends as well as poster prizes and a DGNG junior research award.

The **Annual Junior Research Award** of € 2000,- will be awarded for a paper published or submitted within one year of the deadline of submission, which will be August 15, 2009.

Submissions should be sent as a single PDF-file including a cover letter, the full paper and a brief CV of the applicant and should be sent to the secretariat of the DGNG (elvira.biesinger@med.uni-tuebingen.de).

Thomas Gasser
President of the DGNG

Peter Bauer
Vice-President of the DGNG

Mathias Riemenschneider
Secretary of the DGNG

Daniela Berg
Treasurer of the DGNG

DGNG Mitgliederversammlung 2009

Liebe Kolleginnen und Kollegen,

ich möchte Sie ganz herzlich zur Mitgliederversammlung der Deutschen Gesellschaft für Neurogenetik am 09.10.2009 während der Jahrestagung in Homburg/Saar einladen.

Neben der Wahl des Vorstandes sind zukünftige DGNG-Tagungen und der Übergang der Nutzungsrechte der GeNeMove Biomaterialbank auf die Gesellschaft zu besprechen.

Der amtierende Vorstand wird sich erneut zur Wahl stellen. Weitere Vorschläge können eingereicht werden.

Mit freundlichen Grüßen

Ihr Thomas Gasser

Vorläufige Tagesordnung

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Science News

miRNAs and Neurodegeneration

The human genome sequencing project has shown us, that only a small number of genes are necessary to build a human being. The enormous complexity of this system is due to the fact that the different components of the genetic program are finely tuned in space and time during cell and tissue differentiation. Only recently it became apparent that a major part of this regulation is performed by microRNAs (miRNAs), small RNA molecules encoded by the genome that are not translated into proteins; rather, they control the expression of genes. The discovery of small noncoding miRNAs has revealed an unexpected and intriguing additional level of fine tuning of the genome activity. The transcriptome is utilized continuously in different combinations, for instance to generate the complex cellular networks of the brain. Since the initial studies performed 15 years ago [1], it has now become clear that miRNA pathways alter and modulate the expression of thousands of genes and contribute to a wide variety of physiological processes. The implications of dysregulation of miRNA networks for human disease are potentially

enormous. This is already well demonstrated in the field of cancer research [2] and the diagnostic and potentially also the therapeutic value of miRNAs are increasingly acknowledged in this field. Changes in miRNA expression profiles in schizophrenia [3] and Down syndrome patients [4] are examples of miRNAs potentially involved in neurological disease. Understanding the fundamental aspects of miRNA neurobiology and the possible clinical implications related to miRNA (dys)function are clearly important for all of neuroscience.

The biogenesis and function of miRNAs are increasingly well understood. Similar to classical protein-coding genes, miRNA genes are integrated in the genome [5] and are transcribed mostly by RNA polymerase II [6]. The human genome contains at least 695 miRNAs

(<http://microrna.sanger.ac.uk>). The genomic location of miRNAs varies and can be found in both, intergenic and intragenic and/or intronic regions of protein-coding transcripts. Additionally, some miRNAs can be co-transcribed as clusters. In the nucleus, the so-called "pri-miRNA" is processed by the Drosha enzyme complex to generate a ~70

nucleotide stem loop precursor miRNA (pre-miRNA) [7]. The pre-miRNA is transported to the cytoplasm via exportin 5 where it is cleaved by the type III RNase Dicer to generate mature (functional) 19–23 nucleotide double-stranded RNAs [8]. The mature miRNA is then loaded into the RNA-induced silencing complex (RISC), which is composed of argonaute and associated proteins [9]. RISC controls gene expression by binding via imperfect complementarity to the 3'-UTR of target mRNAs leading to translational repression of protein expression or even degradation of the mRNA.

A functional role for miRNAs in more specific neurological processes is also emerging, and their dysfunction could have direct relevance for our understanding of neurodegenerative disorders. For example, miR-134 is involved in dendritic spine formation [10] and miR-124 [11] in addition to miR-132 [12] are implicated in neurite outgrowth. Both gain- and loss-of-function experiments, for example introducing artificial miRNAs mimicking upregulation or antisense oligonucleotides inducing loss of function into primary neurons in culture, support those conclusions. Dystrophic neurites and synaptic

defects are early events in Alzheimer's disease (AD) [13]. Thus changes in these miRNAs either as a primary (e.g. as a consequence of ageing) or as a secondary effect (e.g. by amyloid or Tau toxicity) might contribute to these phenotypes. Interestingly, miR-132 is involved in a regulatory feedback loop as its expression can be induced by synaptic activity [14]. Abnormal synaptic activity and remodeling may play a role in the etiology of AD [15]. Another miRNA, miR-133b, implicated in the differentiation and/or maintenance of dopaminergic neurons and also operating in a negative feedback loop together with the Pitx3 transcription factor, is downregulated in Parkinson's disease (PD) mouse models and the sporadic PD brain [16]. miRNAs clearly have a role in cell-cycle control and apoptosis [17,18], both of which are processes that have been implicated in AD and PD [19,20].

In summary, it is clear that miRNAs, and also other non coding RNAs, provide a novel and exciting layer of complexity to molecular neuronal biology. In addition, it can be surely predicted that we will see a strong increase in publications in the next years, which will offers novel insights into this interesting field of research.

Literature

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