

and transported to the interstitium was enhanced in diabetics compared to controls. The overexpression of CAV-1 and eNOS was also documented in diabetic groups suggesting enhanced transendothelial transport and hyperpermeability of these capillaries. In some cases immediate insulin replacement prevented the development of diabetes-related region-specific alterations.

These results indicate a close relationship between the segment-specific diabetic nitroergic neuropathy and vascular dysfunction of mesenteric capillaries running in the vicinity of myenteric plexus in the gut. Our data provide morphological, functional and molecular evidence that the endothelial cells of these vessels are direct targets of diabetic damage. We suggest therefore that these endothelial cells are potential therapeutic targets to prevent the development of the nitroergic neuropathy and the gut motility disorders in diabetic patients.

Supervisors: Éva Fekete, Mária Bagyánszki  
E-mail: bodiniki@freemail.hu

## **Molecular characterization of the computationally predicted *miR-282* microRNA gene of *Drosophila melanogaster***

Ágnes Bujna

Developmental Genetics Unit, Institute of Genetics, Biological Research Centre, Hungarian Academy of Sciences, Szeged, Hungary

MicroRNAs have been discovered as a new type of regulatory genes whose transcripts are marked by a representative intermediate form, the hairpin structure. Due to this typical secondary structure and the advanced bioinformatic methods, hundreds of new miRNA genes have been identified in animals, plants and even viruses. Hundreds of target genes for every single miRNA also have been predicted. In this way, a huge amount of data has been generated, which is waiting for interpretation and experimental confirmation.

MicroRNAs (miRNAs) are ~22 nucleotide long, single-stranded regulatory RNAs that bind to complementary sequences in the three prime untranslated regions of target mRNAs thereby, negatively regulating (by transcript degradation and translational suppression) the target genes. Although a significant group of miRNA genes is found in the introns or sometimes in exons of protein and non-protein coding genes, most microRNA genes lie in intergenic regions and contain their own promoter and regulatory components. MicroRNA primary transcripts (pri-miRNAs) are synthesized by RNA polymerase II. In this way, pri-miRNAs which range couple thousands of nucleotides in length have 5' m7G cap structure and usually subjected to polyadenylation in their 3' end. However the functional analyses are still in their infancy because they are hampered primarily by redundancy among miRNA genes occurring when different miRNAs share the same 5' seed sequence or their target(s) and if they are coexpressed. Moreover, most miRNA mutants show subtle or low-penetrance defects that may be difficult to identify. As a consequence, in only few cases can lead the lack of miRNA function to robust phenotypes. Despite of these findings, it has become clear today that miRNAs are required for the fine tuning of the regulation of sometimes very complex mechanisms and participate in the regulation of almost every biological processes investigated so far.

While in the fruit fly (*Drosophila melanogaster*) 176 miRNAs has been computationally predicted to date (miRBase release 16), the real target mRNAs and biological function have been assigned to only a dozen of them. We characterized a miRNA gene, *mir-282* of *Drosophila melanogaster* which is evolutionary conserved among insects. The *mir-282* gene is located on the third chromosome within a 13.9 kb genomic region devoid of any protein coding genes and our data strongly suggest an independent *mir-282* gene whose primary transcript has a distinct 5' start with a CAP and a few alternative 3' ends with polyA tail. We have determined the correct size of the pre- and mature *mir-282*. We found that the *mir-282* locus encodes a functional transcript which influences viability, longevity and egg production in *Drosophila*, most likely through the regulation of cAMP level at pupal stage.

Supervisor: Miklós Erdélyi  
E-mail: vargaagi@brc.hu

## **Neuroprotection with novel KYNA-amide**

Levente Gellért

Department of Physiology, Anatomy and Neuroscience, University of Szeged, Szeged, Hungary

Acute protection and the recovery of neurons from cerebral ischemic insults of whatever nature give rise to the main drive in the development of neuroprotective strategies.

The most widely accepted concept relating to ischemic brain damage is the concept of excitotoxicity.

Treatment with N-methyl-D-aspartate receptor antagonists is a widely accepted method with which to stop the advance of excitotoxic processes and concomitant neuronal death. From a clinical aspect, competitive glycine- and polyamine-site antagonists with relatively low affinity and moderate side-effects are taken into account. Endogenous kynurenic acid (KYNA) acts as an antagonist on the obligatory co-