was observed with the KK series of mutants where the silencing construct is inserted into a standard „landing site" in the 2nd chromosome ensuring an uniform strong expression. The same constructs inserted at accidental places (GD series) had no lethal effect, probably due to lower expression.

By P transposon remobilization, we isolated 8 intragenic deletion mutants in the *DMS-R1* gene which abolished the gene function. However, in contradiction to the RNAi results above, the homozygous mutant flies proved to be fully viable and fertile. The contradiction could be explained with the „off-target" effect: if the RNAi construct contains a ≥20-mer sequence motif shared by a non-target gene, both genes will be silenced, and the lethality can come from the non-specific off-target effect. Another possibility is that the lethality is caused by the Act-Gal4 driver activating the gene expression at tissues or organs in which the gene is not normally expressed. These possibilities are investigated now by using more specific drivers, e.g. elav-Gal4 which is restricted to the CNS neurons.

It is known that the 5' upstream DNA sequence regulates the expression pattern of the *FMRFa* gene in the *Drosophila* CNS (Benveniste and Taghert, J. Neurobiol. 38, 507-520), and certain parts of this sequence can reproduce specific parts of the pattern.We amplified by PCR these DNA sequences, cloned them into the pBPGUw vector upstream to the Gal4 coding sequence, and made transgenic stocks carrying these constructs. These new drivers can be used in future experiments to target UAS-dependent expression to the FMRFa-expressing neurons.

In cooperation with Dr.Michal Žurovec (Inst. of Entomology, Czech Acad. Sci., České-Budejovice) we test the above mutant combinations for their basic metabolism (CO_2 production) and moving activity. In CO_2 production there was no difference between the mutant and the wild type adults. However, the mutants showed significantly less moving activity than the wild type. Experiments to test the possible mutant effect on heartbeat frequency are also in progress.

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Biogas production from protein rich substrates

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In the European Union currently there are approximately 6000-7000 biogas plants, none of them processes protein-rich waste. However, in the course of food production and processing many protein-rich by-products and waste are made. These are serious pollutants, their disposal is a costly and energy-consuming task. In the world millions of tons of protein-rich hazardous waste are produced continuously. Biogas is a renewable energy carrier and the production of biogas is associated with double benefits: elimination of environmental pollution problems is coupled with the generation of renewable energy carrier. The digestion effluent is used as fertilizer for agricultural nutrient recovery and eliminates the need for artificial fertilizers, the production of which is a highly energy demanding process. Anaerobic digestion of slaughterhouse waste presents a specific task because this waste stream is rich in proteins. Blood, casein and meat powder have a very low C/N ratio therefore they are not favorable substrates for biogas production. Several earlier attempts corroborated the inhibitory effects of elevated NH_3 – NH_4^+ concentrations on anaerobic digestion.

Anaerobic digestion of animal waste was investigated in batch and continuously stirred tank reactor experiments at 37°C. In all experiments efficient degradation of blood, casein and meat-powder containing samples were observed using a specially adapted microbiological consortium. Contrary to the findings published earlier ammonia did not inhibit the biogas process at concentrations up to 10 g N/dm^3.

As pH raises the free ammonia concentration increases significantly. The experiments were designed to compare the protein hydrolysis potential of substrates that were acclimated and non-acclimated to protein rich media.

Proteinase activities of the consortia were monitored regularly. The changes in acetate and ammonium-nitrogen concentrations were followed during the fermentations. Volatile fatty acid compositions (acetic, propionic, isobutyric, butyric, isovaleric, valeric, caproic acids) were determined using HPLC to monitor the microbiological activity in the reactors. Total carbon and total organic carbon contents have been measured to determine the C/N ratio of the biomass. Volumetric biogas yields gave information about the efficacy of the anaerobic digestion process. The composition of the evolved gas was determined by gas chromatography.

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