Ronald Gstir

A microarray for the identification of regulatory ncRNAs in CNS disorders.

I was presenting our achievements in developing a neuro-specific ncRNA microarray platform employing a DNA oligo probe set that enables differential expression analysis of complex RNA samples in a single experiment. With this approach we aim to identify ncRNAs that are regulated in CNS disorders. To date, we have completed expression analysis of different brain regions in mouse models for Alzheimer's disease (Triple-transgenic mouse: $PS1_{M146V}$, APP_{Swe}, and tau_{P301L}) and Multiple System Atrophy (Trangenic mouse: $\alpha-$Synuclein overexpression), whereby cortex samples of the Alzheimer's disease model showed changes in the abundance of five ncRNA candidates. Their possible role in the etiology of Alzheimer's disease needs to be further investigated. We have discussed the difficulties in performing qRT-PCR from small uncharacterized RNA's for the confirmation of the results obtained from the microarray. In addition the issue of single nucleotide polymorphisms between the different mouse strains was raised and will be considered for the next probe set generation that is currently under development. In addition I informed the community that we established everything to perform the EXIQON LNA-miRNA chips, which can be used by the SFB members.
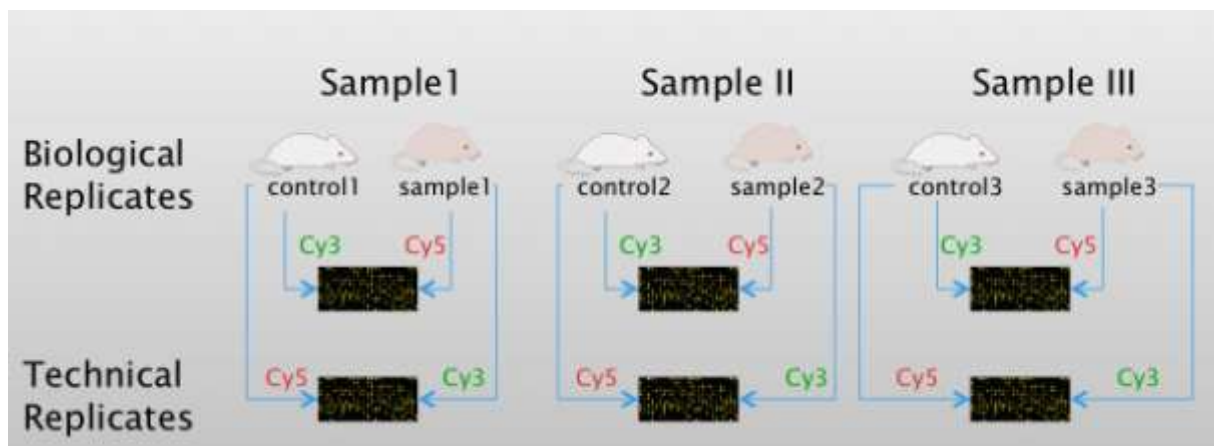

Abbildung 1: non-protein-coding RNAs in chronic CNS disorders