SFB 1286 Quantitative Synaptology

UNIVERSITÄTSMEDIZIN GÖTTINGEN UMG

Online – Seminar

"Dynamics of receptors and scaffold proteins at inhibitory synapses: insights from modeling and experiments"

Speaker

Dr. **Jonas Ranft**
Neuronal Algorithms Group
Institut de Biologie de l'ENS (IBENS)
Ecole Normale Supérieure & CNRS
Paris, France

Date and time

Thursday, 12th May 2022
5 PM

Location

via Zoom
https://gwdg.zoom.us/j/88974926448?pwd=cmdIZC9Tbm84L1NsM0pLUExuRTR0UT09
Meeting ID: 889 7492 6448
Passcode: 768991

Abstract

Postsynaptic scaffold proteins immobilise neurotransmitter receptors in the synaptic membrane opposite to presynaptic vesicle release sites, thus ensuring efficient synaptic transmission. At inhibitory synapses in the spinal cord, the main scaffold protein gephyrin assembles in dense molecule clusters that provide binding sites for glycine receptors (GlyRs). Gephyrin and GlyRs can also interact outside of synapses where they form receptor-scaffold complexes. While several models for the formation of postsynaptic scaffold domains in the presence of receptor-scaffold interactions have been advanced, a clear picture of the coupled dynamics of receptors and scaffold proteins at synapses is lacking.

In this talk, I will first present experimental data of the GlyR and gephyrin dynamics at inhibitory synapses, where we performed fluorescence time-lapse imaging after photoconversion in order to directly visualise the exchange kinetics of recombinant Dendra2-gephyrin in cultured spinal cord neurons. Notably, the immuno-immobilisation of GlyRs significantly reduced the exchange of Dendra2-gephyrin compared to control conditions, suggesting that the kinetics of the synaptic gephyrin pool is strongly dependent on GlyR-gephyrin interactions.

I will then show that our experimental data can be quantitatively accounted for by a model of receptor-scaffold dynamics that includes a tightly interacting receptor-scaffold domain, as well as more loosely bound receptor and scaffold populations that exchange with extrasynaptic pools. The model makes predictions for single molecule data such as typical dwell times of synaptic proteins. Taken together, our data demonstrate the reciprocal stabilisation of GlyRs and gephyrin at inhibitory synapses and provide a quantitative understanding of their dynamic organisation.

Hosted by Prof. Silvio O Rizzoli