1P198 蛍光相関分光法を用いた生細胞におけるアルファシヌクレインの凝集の解析
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Analysis of aggregation of alpha-synuclein in live cell using fluorescence correlation spectroscopy
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Aggregation of α -synuclein, an abundant and conserved pre-synaptic brain protein, is implicated as a critical factor in several neurodegenerative diseases. These diseases known as synucleinopathies, include Parkinson's disease, dementia with Lewy bodies (LBs), diffuse LB disease, the LB variant of Alzheimer's disease, multiple system atrophy, and neurodegeneration with brain iron accumulation type I. However the precise nature of *in vivo* α -synuclein function remains elusive and the mechanism of aggregation of *in vivo* α -synuclein is still unknown. In this report, we will demonstrate the dynamics of *in vivo* α -synuclein as changing of diffusion constant and brightness per particle obtained by Fluorescence Correlation Spectroscopy (FCS). HeLa cells were transfected by the plasmids which codes wild type or A30P mutant of α -synuclein tagged GFP fused protein, or only EGFP as a control. In order to know the difference between the wild type α -synuclein tagged GFP, A30P α -synuclein tagged GFP and EGFP, we measure the changing of diffusion constant and brightness per particle using FCS at 12, 24, 48 and 96 hours after transfection.

1P200 モノアラガイの味覚嫌悪学習における遺伝子発現解析
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Altered Gene Activity Correlated with Long-Term Memory Formation of Conditioned Taste Aversion in *Lymnaea*
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The pond snail *Lymnaea stagnalis* is capable of learning conditioned taste aversion (CTA) and then consolidating that learning into long-term memory (LTM) that persists for at least 1 month. LTM requires *de novo* protein synthesis and altered gene activity. Changes in gene activity in *Lymnaea* that are correlated with, much less causative, memory formation have not yet been identified. As a first step toward rectifying this situation, we constructed a cDNA microarray with mRNAs extracted from the central nervous system (CNS) of *Lymnaea*. We then, using this microarray assay, identified genes whose activity either increased or decreased following CTA memory consolidation. We also identified genes whose expression levels were altered after inhibition of the cyclic AMP response element-binding protein (CREB) that is hypothesized to be a key transcription factor for CTA memory. We found that the molluscan insulin-related peptide II (MIP II) was upregulated during CTA-LTM, whereas the gene encoding pedal peptide prohormone (Pep) was downregulated by CREB2 RNA interference. We next examined mRNAs of MIP II and Pep using real-time RT-PCR with SYBR Green. The MIP II mRNA level in the CNS of snails exhibiting good memory for CTA was confirmed to be significantly higher than that from the CNS of snails exhibiting poor memory. These data suggest that in *Lymnaea* MIP II may play a role in the consolidation process that forms LTM following CTA training.

1P199 神経 RNA granule タンパク質 RNG105 ノックアウトによる興奮性-抑制性シナプス形成とバランスの異常
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A deficiency of the RNA granule protein RNG105 impairs the formation and the balance of excitatory/inhibitory synapses
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A balance between excitatory and inhibitory synapses is important to keep neuronal networks functional, and changes in the balance underlie some forms of neurobehavioral syndromes. In this study, we show that a deficiency of RNA granule protein 105 (RNG105), a component of RNA granules which control local translation at postsynaptic sites, impairs the formation of excitatory and inhibitory synapses in fetal brains. Cortical neurons from RNG105-knockout mice formed poor neuronal networks *in vitro*. There were less excitatory synapses and considerably fewer AMPA receptors but more inhibitory synapses containing GABA receptors in RNG105-knockout brains. In addition, an excess of inhibitory synapses are colocalized with excitatory synapses in the knockout brains. Cultured neurons from the RNG105-knockout brains exhibited a decrease in AMPA-dependent but increase in GABA-dependent neuronal activity. Our results demonstrate that the balance between excitatory (glutamatergic) and inhibitory (GABAergic) synapses in terms of composition and function is altered in RNG105-deficient mice, providing insights into the involvement of local translation in the formation of synapses through tuning of the synaptic balance.

1P201 ホヤの機械刺激受容システムに関わる遺伝子ファミリーの探索
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Molecular genetic characterization of mechanosensory systems in the simple chordate *Ciona intestinalis*
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In the brain vesicle of the larva of the ascidian *Ciona intestinalis*, two types of sensory organs, the otolith and hydrostatic pressure organ, have been proposed to be mechanosensory organs. The adhesive organ and epidermal sensory neurons of the ascidian larva have also been thought to be involved in mechanosensation. Among these candidate mechanoreceptors, only the gravity sensing function of the otolith has been demonstrated, and function of other sensory organs (cells) remains unknown. In order to investigate molecular bases of mechanosensing in the ascidian larva, we have identified and characterized *Ciona* homologues of genes that are known to be involved in mechanotransduction systems of other organisms. The gene families analyzed include the transient receptor potential (TRP) channel superfamily (TRPV, TRPN, TRPA, and TRPV), the myosin superfamily (myosin VI, myosin VII, and myosin XV), and the cadherin superfamily (cadherin 23). Spatial gene expression patterns visualized by whole-mount *in situ* hybridization revealed that *Ciona* homologues of *TRPN*, *TRPA*, and *cadherin 23* are expressed in distinct sites of the larva that are presumed to have sensory function. Full-length cDNAs of *Ciona* TRP channels were cloned into an expression vector for functional evaluation of mechanically gated property of the channels in mammalian cells. Based on the molecular phylogeny and gene expression patterns, the evolutionary pathway of chordate mechanosensory systems will be discussed.