The Protein-Protein Interaction Networks of Dendritic Spines in the Early Phase of Long-Term Potentiation

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Abstract

The neuron is a basic element of brain networks. Changes of nerve cell excitability, the conduction of excitation, synaptic memory-forming in the case of the temporal coincidence of synaptic events are the obvious functions of the neuron - element of brain networks. The implementation of the neuron function depends on actions of its numerous molecular systems. The generalization of the complex processes of emergence of synaptic memory, that occur even in separate neuronal compartments, without special tools is a difficult, if at all possible, task. A technology that combines the creation of databases (elements and their relationships) with a visual representation in the form of networks facilitates this process. The developed protein-protein interaction network in dendritic spines of hippocampal pyramidal neurons facilitates the synthesis of numerous experimental data in conceptual knowledge about the principles and molecular mechanisms of neurons functioning.

Keywords: Early-phase long-term potentiation; CA1 pyramidal neurons of the hippocampus; Dendritic spines; Glutamate receptors; Small gtpases; Actin-binding proteins; Protein-protein interaction networks

Introduction

In course of evolution the development of a brain correlates with complication of a molecular nerve cell organization [1-3]. The activity of a neuron entails changes in its connections with other neurons as well as in its molecular networks. Over the last decade notion about the synapse as a relatively simple structure has transformed. Synapses are highly dynamic structures. Their molecular composition is altered in an activity-dependent manner, which modulates the efficacy of subsequent synaptic transmission events. The synapse is a zone of the contacts between cells, transmitting the information and processing it by detecting specific patterns of neural activity and converting this electrical activity into intracellular biochemical events that change the properties of the neuron [4]. Dendritic spines are the postsynaptic component of glutamatergic synapses that originates from an axial dendrite [5]. Dendritic spines are the structure of the excitatory synapse majority of a mammal brain. The flux of ions into postsynaptic terminal of excitatory synapse is regulated by tuning the distribution of receptors and their subunit composition (synaptic plasticity) [5-7] as well as tuning the morphology of dendritic spines (structural plasticity) [8]. Learning and memory are associated with changes of synaptic modifications that take place in the postsynaptic dendritic part of synapse [9]. The hippocampus is a brain structure involved in short-term memory and the phenomenon of long-term potentiation (LTP) (increases the efficacy of synaptic transmission after an intense and short-term release of neurotransmitter) is the dominant cellular model of learning and memory [10]. Proteomic studies have identified hundreds of postsynaptic proteins organized through physical interactions into multiprotein complexes and networks [11].

The implementation of the neuron function depends on actions of its numerous molecular systems. The generalization of the complex processes of emergence synaptic memory, that occur even in separate neuronal compartments, without special tools designed for formalized description and automated visualization of molecular networks is a difficult, if at all possible, task.

The main purpose of this review is a reconstruction of molecular network of the dendritic spine of pyramidal neurons of the CA1 hippocampal region of rodent, and the action sequence of functional (executive) systems of the neuron involved in synaptic modulations in the early phase of long-term potentiation.

The Functional Systems of the Neuron Involved in Synaptic Modulations in the Early Phase of LTP

Dendritic spines are the postsynaptic component of glutamatergic synapses that originates from an axial dendrite (button less than 1 µm³). Dendritic spines are the structure of the majority excitatory synapse of a mammal brain. Molecular networks of the dendritic spine of pyramidal neurons of the CA1 hippocampal region of rodent in the early phase of LTP have been reconstructed using GenNet computer system [12-15]. The protein-protein interaction (PPI) network of dendritic spines is presented on the site (http://wwwmgs.bionet.nsc.ru/mgs/gnw/genenet/viewer/Early_long-term_potentiation.html (PPI1)) Datasets of elementary units of the protein-protein interaction networks were made according to the expression of genes encoding proteins (mRNA) of pyramidal neurons of the CA1 hippocampal region of the adult rodent (mouse predominantly). We have used the experimental information which has been manually extracted from the published articles (PubMed) or databases (Swiss-Prot, EMBL, MGI, GeneCard, and TRRD). Journal publications which contain data about the behavior of molecules of dendritic spines of pyramidal neurons of the CA1 hippocampal region in the early phase of long-term potentiation have been mainly used.

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In this scheme reflected the interactions between network objects (green arrows) and various influence reactions (red arrows – on influence; dark arrows – off influence; pink arrows – increase influence; blue arrows – decrease influence) (Figure 1). PPII network contain the descriptions for 58 proteins (Mus musculus) in GeneNet database format. In this reflects the organization of dendritic spine in one of the possible states. In constructing PPII network, we have taken into account the ordered structure of spine with a specific horizontal and vertical compartmental organization at all levels: the membrane (synaptic, perisynaptic, extrasynaptic membrane (EM)); the submembrane (submembrane proteins and postsynaptic density (PSD)); the cytoplasm (the network objects interactions, the receptor intracellular store vesicles (recycling endosome), the receptor transporting vesicles (endocytic vesicle) (Figure 1). Each compartment contains the specific protein set, their functionality defined of synaptic activity.

Proteins that anchor the receptors and bind them to the cytoskeleton (scaffold proteins), protein kinases, proteases, and GTPases form the postsynaptic density (PSD) located under the synaptic membrane [16]. Scaffold proteins control the size and stability of the PSD. These proteins have one or several short conserved sequences of amino acids, called PDZ microdomains. PDZ-microdomains perform high affinity interactions between proteins (not enzymatic). Scaffold proteins form an orthogonal framework of vertical (mostly protein PSD95, SAP97, and S-SCAM) and horizontal (primarily proteins Shank and GKAP) filaments [17]. PSD anchors glutamate receptors in the active area of a dendritic spine.

Glutamate receptors are receptor-channel complexes. The classification of these receptors is based on their sensitivity to N-methyl-D-aspartate and (NMDA) and α-amino-3-hydroxyl-5-methyl-4-isoaxazole-propionate (AMPA). In mature hippocampal neurons, AMPA receptors (AMPAR) comprise two of three subunits (Glur1-3), such as AMPAR type 1/2 (Glur1/GluR2) and AMPAR type 2/3 (Glur2/GluR3) [18]. AMPARs are permeable to Na⁺. NMDARs are permeable to Ca²⁺, have chemo- and potential-sensitivity. Mg²⁺ blocks the ability of NMDAR to bind glutamate at the resting potential (this block is removed by depolarization) [19].

NMDARs are directly anchored at the center of the PSD and AMPAR are anchored through a family of stargazin proteins at the periphery [20,21]. In PSDs there are the physical interactions between molecules and positioning the partner molecules in complexes (micro microdomains). AMPARs and NMDARs form a connection with a specific set of proteins in PSD [10].

The dendritic spine cytoskeleton comprises a polymeric (F-actin) and monomeric (G-actin) actin, and F-actin is dominant. A family of small GTPase proteins and actin-binding proteins regulate spinal morphology and synaptic function by modulating reorganization and F-actin turnover. Actin-binding proteins regulate the disassembling of actin microfilaments, the formation of growth complexes, branching and stabilizing of filaments. Dimers of myosin II support the actomyosin

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**Figure 1:** Fragment of network (Early long-term potentiation) (screenshot). Fragment of network reflecting the basic mechanisms which provide the translating of the neurotransmission to the dendritic spine cytoarchitecture change. Main processes (blue rectangles): inductions (High Frequency Stimulation, membrane depolarization) and expression (breaking of the submembrane actin network - form actomyosin complexes, cross-linking and contractile of actin filaments; form of new the submembrane actin network – elongation and branching of actin filaments).
The spatiotemporal dynamics of Rho GTPases differ. Activation of RhoA and Cdc42 reaches a maximum in about 30 s and then activity is reduced and stably maintained for more than 30 min [35]. Activation of Cdc42 is limited by the activated spine. The high spatial gradient of Cdc42 between the stimulated spine and dendrite is maintained for more than 30 min, Cdc42 must be continuously activated in spines during plasticity, and is inactivated immediately after exiting from the spine [34]. Ras activation increases to a maximum within 1 min after stimulation and returns to a baseline within 15 min [34]. Active RhoA and Ras require about 1 s to relocate from the spine to the dendrite. Active RhoA and Ras are propagated about 10 μm by diffusion along of the parent dendrite and invade about 10 to 20 neighboring spines [35], active RhoAs are propagated about 5 μm [34]. A propagation mechanism of Rho GTPases along the parent dendrite might underlie the association of signals coming out of the neural network to the neighboring spines.

Cascade NMDAR-CaMKII-Cdc42-Pak is specific for spine signal transduction; it cover the time from 1 s to 30 min. Minor proteins of the actin cytoskeleton are targets of RhoA-ROCK and Rac1/Cdc42-Pak. Key proteins involved in spine cytoskeletal reorganization are presented in PPI1 network of dendritic spines. Ca²⁺/calmodulin complexes are key regulators of Ca-sensitive kinases and phosphatases [36]. In the first 2 min after potentiation, activation of the calcineurin-Cofilin, RhoA-ROCK-myosin II cascades leads to the breakdown of existing F-actin, appearance of the open ends of F-actin, and a pool of G-actin, which is necessary for the nucleation of new filaments, their branching, and elongation. Activation cascades of Rac1/Cdc42-Pak controls nucleation and branching of the actin network through activation of cortactin-Arp2/3/WAVE/N-WASP functional protein.
complex. Activation of the cascades is also important for stabilizing the new actin network that lasts up to 10 min. Cascades Rac1/Cdc42-PAK, RhoA-ROCK through the activation of LIM-kinase and phosphorylation of cofilin stabilize new bundles and individual filaments of actin [37], PAK inactivates MLC-kinase, which reduces the activity of myosin II and F-actin tension [38].

PPI1 network of dendritic spines and the description of the processes that are initiated by activation of glutamate receptor reflect the ability of nanosized compartments of the neuron to self-development (the transition to a new level of efficient synaptic transmission) using the own resources. However, for maintaining the new state of spine resources from other compartments of the neuron are needed.

The synthesis of new proteins, occurring in the soma of the neuron, including AMPA receptors [39] is necessary to maintain long-term LTP. LTP in hippocampus is maintained for a long time, but not longer than 30-60 minutes if the synthesis of proteins is blockaded. To maintain the LTP in this initial period a post-translational modification of proteins and the formation of protein-lipid vesicles in the vacuolar system [40,41] are required to a greater extent than protein synthesis. Maintaining the new level of transfer is accompanied by replacement of AMPAR1/2 on AMPAR2/3 subtype [42]. The molecular network (PPI2), mediating these processes is available at: http://wwwmgs.bionet.nsc.ru/mgs/gmw/genenet/viewer/AMPA.html.

The basal stocks of AMPARs2/3 are in the vacuolar system, where they are included in the vesicles and are delivered to the spines. The movement of proteins between compartments of vacuolar system (endoplasmic reticulum, Golgi apparatus, trans-Golgi network, endosomes) and their delivery to the spine are mediated by small transport vesicles, branching off from a donor compartment and then fuse with an acceptor compartment [43]. The accuracy of vesicle assembly is controlled by its coating proteins. The initiation of the vesicle coating formation and also its branching off from a donor compartment is regulated by small GTPas protein family – ARF (ADP-ribosylation factor). The transport vesicles with AMPA receptors are delivered to the dendrite where they can be incorporated in the plasmatic membrane of spine dendrite or in the dendritic depot of receptors. Experimental data suggest that the violation of vesicle assembly does not prevent a transition of spines to new level of the synaptic transmission efficiency but leads to a significant reduce of the synaptic transmission efficiency in the first 20 min after potentiating [44].

Conclusion

Simulation of complex systems is necessary, because multicomponent molecular system of nerve cell cannot be perceived as a whole without it. We integrated the proteins of pyramidal neurons of the CA1 hippocampal region of the early phase of LTP into a conceptual model. PPI1, PPI2 networks represent a basic set of the molecules and its functional interactions, required for translation of conceptual model. PPI1, PPI2 networks represent a basic set of the CA1 hippocampal region of the early phase of LTP into a conceptual model. PPI1, PPI2 networks represent a basic set of the molecules and its functional interactions, required for translation of conceptual model. PPI1, PPI2 networks represent a basic set of the CA1 hippocampal region of the early phase of LTP into a conceptual model. PPI1, PPI2 networks represent a basic set of the molecules and its functional interactions, required for translation of conceptual model. PPI1, PPI2 networks represent a basic set of the CA1 hippocampal region of the early phase of LTP into a conceptual model. PPI1, PPI2 networks represent a basic set of the molecules and its functional interactions, required for translation of conceptual model.

References


41. Brown TC, Tran IC, Backos DS, Esteban JA (2005) NMDA receptor-dependent activation of the small GTPase Rab5 drives the removal of synaptic AMPA receptors during hippocampal LTD. Neuron 45: 81-94.

