

**Structural/functional analysis of synaptotagmin 1 in
synaptic transmission using hippocampal autapses**

PhD Thesis

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Submitted by

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Affidavit

The PhD thesis presented here is written independently and the content in the thesis is contributed by my own work with no other sources and aids than quoted.

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Abstract

Synaptotagmin 1 is a presynaptic vesicular protein, which has been implicated as a putative Ca^{2+} sensor for fast neurotransmitter release in central nervous system. Structurally, it possesses two Ca^{2+} binding C_2 domains in its cytosolic C-terminal. The biochemical interaction of synaptotagmin 1 with other molecules has been extensively addressed in recent studies, while the exact physiological roles of the two C_2 domains and the mechanism of action of synaptotagmin 1 in exocytosis are still poorly understood.

To answer these questions better, a systematic study combining electrophysiological and molecular biological approaches was performed. The synaptic transmission of the cultured synaptotagmin 1 null murine hippocampal neurons transfected with the mutated synaptotagmin 1 was evaluated with standard whole-cell patch clamp electrophysiology. To take a closer look at how the structure of the C_2 domains is important for the function of synaptotagmin 1, we made a series of the C_2 domain mutations. Truncation of either C_2 domain, neutralization of the Ca^{2+} binding aspartate sites (namely, D_{172, 230, 232}A; D_{303, 363, 365}A) in either C_2 domain and replacement of either C_2 domains with the C_2 domain from other synaptotagmin isoform (i.e. synaptotagmin 7) all suggested that the two C_2 domains are non redundant in synaptic transmission. Specifically, the C_2A domain is related to readily releasable pool control and the regulation of fast release, whereas the C_2B domain is essential for fast release.

Synaptotagmin 1 has a set of hydrophobic residues (M₁₇₃, F_{231, 234}; V₃₀₄, Y₃₆₄, I₃₆₇) in the C_2 domains, which have been biochemically shown to interact with the phospholipid plasma membrane. We replaced these residues with Tryptophans with the idea of introducing greater hydrophobicity into the domains so as to correlate its physiological consequences on its phospholipid binding. These mutations result in enhancement in the release probability and apparent Ca^{2+} sensitivity. Furthermore, the polybasic residues in the C_2B domain of

synaptotagmin 1 have been shown to have multiple interactions (i. e. with another copy of synaptotagmin, PIP₂ in plasma membrane, AP-2 and Ca²⁺ channels, etc). These interactions can be abolished by neutralizing these residues (K_{326, 327}A). The physiological analysis of the phenotype of synaptotagmin 1 with K_{326, 327}A mutation shows that the neurotransmitter release does not get abolished, rather it is reduced, which correlates with a corresponding decrease in *in vitro* Ca²⁺ dependent synaptotagmin 1-phospholipid binding. Interestingly, this K_{326, 327}A phenotype bears striking similarity to the previously described synaptotagmin 1 C₂A domain R₂₃₃Q mutation. To further investigate this phenomenon, the corresponding site of the R₂₃₃Q mutation in the C₂B domain was mutated (K₃₆₆Q), however, the latter one showed a wild type like behavior both *in vitro* and *in vivo*. Taken together, the asymmetrical distribution of these basic residues for vesicle release control in the two C₂ domains indicates that the two C₂ domains interact with plasma membrane upon coming Ca²⁺ in different orientation.

Overall, these C₂ domain mutation studies suggest that the Ca²⁺ dependent synaptotagmin 1-phospholipid interaction is critical for the efficiency of synaptic transmission, which ultimately supports the general notion that synaptotagmin 1 must essentially interact with the plasma membrane so as to enable vesicle fusion.

1. Introduction

The human brain functioning as the information processing and storage center consists of more than a hundred billion basic units- neurons. A neuron is a specially polarized cell with three morphological parts: dendrites for receiving electric signals from other neurons; soma for information integration and axon for passing over regenerated signals to other recipients. The specialized terminal contacts for signal transmission from one neuron to another are termed as synapses by Sir Charles Sherrington (1897), which originally comes from the Greek "to fasten together". The high fidelity and fast speed of signal transmission through the synapses are mainly dependent on neurotransmitter release to transform the electrical signals to chemical signals. Especially the step of triggering of neurotransmitter release is the focus of this study.

This introduction will firstly address the structure and functions of synapses and then proceed on with the detail description of the vesicle cycle in the presynaptic terminals, emphasizing on the critical step of vesicular fusion culminating in release of neurotransmitters. The main focus of this thesis project being synaptotagmin, this section will include a brief insight into the family of synaptotagmins and the current overview of the mechanism of action of synaptotagmin in exocytosis.

1.1 The general structure and functions of synapses

Synapses are usually classified into two types, electrical or chemical synapses upon whether the transmission occurs in neuronal terminals via direct electrical pulses propagation or via chemical intermediates. Usually, the signal transmission in electrical synapses is bi-directional, while in chemical synapses it propagates in single direction (although retrograde signal transmissions generally

exist in these synapses). Here all descriptions are of chemical synapses unless mentioned.

Synapses under electron microscopy (EM) are easily recognized by their morphological characters and are distinguished from other organelle structures with two hallmarks: a cluster of small, round and electron-lucent vesicles with uniform size apposite or docking to a layer of plasma membrane/ protein matrix (named as active zone) and a thickened electron-dense scaffold/ membrane opposite to it (named as postsynaptic density, PSD)(Fig 1.1). A typical synapse comprises of three parts, presynaptic terminal accommodating numerous vesicles, postsynaptic terminal holding receptors to bind with neurotransmitters and synaptic cleft separating them. According to the synaptic functions, central nervous system (CNS) synapses have two major groups, excitatory (primarily glutamatergic) and inhibitory (primarily γ -aminobutyric acid (GABA) or glycinergic) synapses.

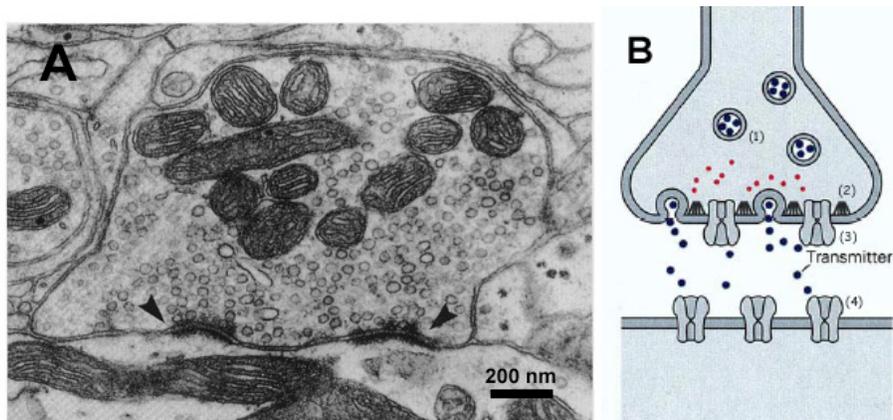


Figure 1.1 Structure of a synapse. A. Electron micrograph of a neuronal synapse, the arrows indicate the active zones in the presynaptic terminal (image from Prof. Kristen M. Harris's lab); B. a schematic illustration of the synapse. (1) synaptic vesicles, (2) active zone matrix, (3) voltage-gated Ca^{2+} channels; (4) postsynaptic receptors. Red dots represent the Ca^{2+} ions and black dots represent neurotransmitters (diagram adapted from "Principles of Neural Science", 4th edition, by Eric R. Kandel et al.).

Synapses can keep the synaptic transmission in high spatial precision and speed through neurotransmitters (chemical intermediates) released from presynaptic vesicles. The general scheme of synaptic transmission is as follows: In resting state, a neuron keeps a certain potential difference across the membrane, which is called the membrane potential (ranging from -60 to -90 mV, the intracellular potential lower than the extra cellular one). Depolarization of the neuronal membrane potential above a certain threshold leads to Na^+ ions influx and firing action potentials (APs), which propagate along the axon to presynaptic terminals. Coupled to the invasion of APs, the voltage-dependent calcium channels (mostly P/Q- and N- type) present on the presynaptic membrane open and external Ca^{2+} ions (millimolar range) flux into the presynaptic terminals where a low Ca^{2+} concentration is maintained in resting condition (about 100 nM, Zucker RS and Regehr WG, 2002). A transient elevation of presynaptic terminals Ca^{2+} concentration (tens of micromolar or higher, Bollmann JH, et al., 2000; Schneggenburger R and Neher E, 2000) facilitates Ca^{2+} binding to Ca^{2+} sensors, which activate a not completely defined molecular machinery. This can induce the fusion of the vesicular membrane with the plasma membrane to release vesicular neurotransmitters. After crossing the synaptic cleft by diffusion, neurotransmitters bind ionotropic receptors on postsynaptic membrane and open ligand-gated ion channels on postsynaptic neuron for ions influx/efflux (Na^+ , K^+ , Cl^- and Ca^{2+} , etc.). The change of the intra/extra cellular ion concentration ratio in the postsynaptic terminals will depolarize or hyperpolarize the neuron, thus the chemical signal converts back to an electric signal. If the signal recipient neuron is held in whole-cell voltage clamp mode, excitatory/ inhibitory postsynaptic currents (EPSCs/ IPSCs) can be recorded. In the absence of stimulations in presynaptic terminals, synaptic activities with small amplitudes (about 20 pA) can be observed, which is believed to be due to spontaneous vesicle fusion (called as miniature response). As the vesicles deplete their contents, their membrane is internalized and the vesicles are refilled with neurotransmitters for next round of release.

The important property of synapses is not only that they can convey information between neurons, but also that they can regulate the synaptic strength. The change in synaptic strength has a short-term effect (Short-term plasticity. for review, Zucker RS and Regehr WG, 2002), which lasts for at most a few minutes and a long-term effect (Long-term plasticity. for review, Malenka RC, 2003; Collingridge GL, et al., 2004) that can last more than a few hours, even to weeks. Both forms of synaptic plasticity can be an enhancement or attenuation of synaptic strength, but the origins of these two forms of synaptic plasticity are quite different.

Short-term synaptic enhancement, such as facilitation or augmentation, is proposed to be mainly due to the elevation of residual Ca^{2+} concentration in presynaptic terminals (Katz B and Miledi R, 1968; Delaney KR and Tank DW, 1994; Regehr WG, et al., 1994); and the short-term synaptic depression is originated from many aspects, such as depletion of vesicles ready for release, presynaptic terminals regulation by release of modulatory substances (Miller RJ, 1998; Wu LG and Saggau P, 1997) and desensitization of postsynaptic receptors (receptors become less sensitive to neurotransmitters, MacDermott AB, et al., 1999). As far as the long-term synaptic plasticity is concerned, besides the presynaptic mechanism, the membrane trafficking of postsynaptic ionotropic receptors, especially the glutamate receptors, such as NMDAR (N-methyl-D-aspartate receptor) and AMPAR (α -amino-3-hydroxy-5-methyl-4-isoxazole-propionic acid receptor), have been suggested to be pivotal for the initiation of long-term synaptic plasticity (for review, Collingridge GL, et al., 2004).

1.2 Synaptic vesicle recycling

The postulation that neurotransmitters are released in quantal mode (Del Castillo J and Katz B, 1954a-d) and the EM observation of small vesicular organelles (with the size ranging from 20 to 150 nm) in presynaptic terminals (Palay SL and Palade G, 1955) greatly absorbed people's interests in understanding their

correlation. Physiological study suggests that three different vesicle pools exist in the presynaptic terminal: the readily releasable pool which is immediately releasable upon stimulations; the recycling pool which maintains releasing vesicles under moderate stimulations and the reserve pool whose vesicles will not release unless intense stimulations occur (for review, Rizzoli SO and Betz WJ, 2005). Although there are distinct physiological properties of vesicles in the synaptic vesicle pool, under EM these vesicles do not have morphological differences and there is no convincing evidence to show that their distribution in presynaptic terminal is different.

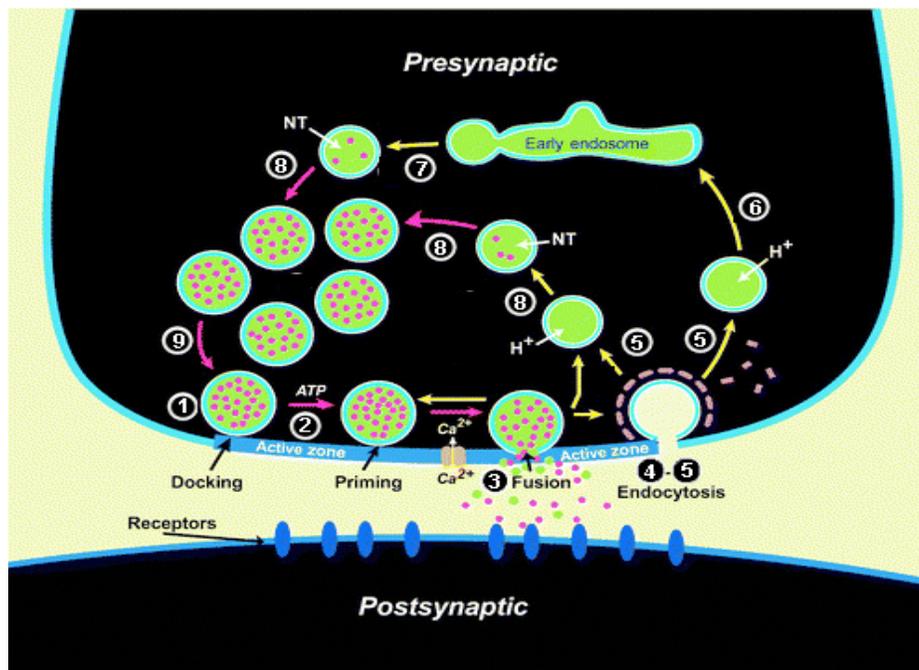


Figure 1.2 The schematic illustration of the synaptic vesicle recycle (Detailed description is in text. Figure is adapted from the review, Sudhof TC, 2004.)

To understand synaptic vesicles better, their activities in presynaptic terminals are worth investigating, especially their recycling pathway. The classical model of vesicle cycle conceptually contains nine steps, as described in the following: vesicles dock on the presynaptic active zone (step 1, docking); after that, an ATP-dependent pre-fusion occurs between vesicles and plasma membrane (step 2, priming); then presynaptic Ca^{2+} influx triggers a rapid reaction completing

membrane fusion and neurotransmitters are released (step 3, fusion); after exocytosis, the vesicles undergo clathrin-mediated retrieval (step 4, endocytosis); later on, these recovered vesicles leave the active zone and fuse with the endosome (step 5, 6); simultaneously, some new formed vesicles bud off the endosome (step 7) and are filled with neurotransmitters consuming the energy provided by the electrochemical gradient that vacuolar proton pumps build up (step 8); matured vesicles translocate and approach the active zone ready for a next round of release (step9) (Heuser JE and Reese TS, 1973; Sudhof TC, 1995). Although this model has been accepted generally, an alternative pathway of vesicle recycling, namely “kiss-and-run”, has been found both at neuromuscular junction (Ceccarelli B, et al., 1973) and in central synapses (Stevens CF and Williams JH, 2000; Gandhi SP and Stevens CF, 2003). The main difference between these two modes of vesicle recycling lies in whether vesicles keep their identities during recycling. ‘Kiss-and-run’ mode vesicles are retrieved from the membrane quickly and keep their identities for the next round fusion, while in classical mode, the vesicles after releasing the neurotransmitters will remix with the endosome before the next turn occurs.

Synaptic vesicle recycling is a complex process (for review, Sudhof TC, 2004), and even a single step involves many protein interactions. Taking the step most relevant to this study, vesicular exocytosis, as an example, numerous works have been done and quite a few proteins participating in this step have been identified. Essentially, there are two molecular level questions existing in vesicular exocytosis: how can the vesicular membrane fuse to the plasma membrane and how can vesicles sense the Ca^{2+} influx signal?

To fuse the vesicular membrane with the plasma membrane, firstly the membranes need to overcome their own electrostatic counteracting forces to be in close proximity; secondly the close membranes will be destabilized and a non-bilayer transition state is generated leading to later fusion pore forming (for review, Jahn R, et al., 2003). The vesicular soluble **N**-ethylmaleimide-sensitive

factor attachment protein receptor (SNARE) proteins present on both membranes have been suggested to form extraordinarily stable coiled coils (named as core complex or SNARE complex), which contribute the energy needed for membranes to overcome the counteracting force barrier (Fasshauer D, et al., 2002). There are three different SNARE proteins (one copy each) in the SNARE complex: synaptobrevin on vesicular membrane (also referred as v-SNARE), syntaxin and SNAP-25 (**synaptosomal-associated protein of 25 k Da**) on plasma membrane (referred as t-SNAREs). T- /v-SNAREs share a common motif consisting of about 60 amino acids, which form four parallel α helices in the SNARE complex (two helices from SNAP-25 and each of the others contributes one, Poirier MA, et al., 1998). Crystal structure of this α -helix bundle revealed several layers of interior hydrophobic residues and some polar residues (one/two glutamines from syntaxin/SNAP-25 and one arginine from synaptobrevin) in the centre of the complex (Sutton RB, et al., 1998).

Reconstitution experiments showed that synaptobrevin and SNAP-25/syntaxin incorporating into separate liposomes could cause membrane fusion, which strongly argues for the SNARE complex as the minimal machinery for fusion process (Weber T, et al., 1998). The slow Ca^{2+} dependent fusion rate observed in these experiments together with other in vitro studies (Hu K, et al., 2002) has been questioned of their physiological relevance. The possible explanations can be the instability of the SNARE complex and/or that the shortage of some protein(s) sensing Ca^{2+} slows down this fusion process.

Complexin, a cytoplasmic protein interacting with SNARE via its C-terminal α helix in high affinity (dissociation constant about 10nM, Pabst S, et al., 2002) is thought to tighten the interface between synaptobrevin and syntaxin so as to stabilize the SNARE complex (Chen X, et al., 2002; Rizo J and Sudhof TC, 2002). Knocking out complexin 1 and 2 can reduce the evoked synchronous release (reflecting those vesicles with full tightened SNARE complex) but no change in the asynchronous release (reflecting vesicles with incomplete

tightened SNARE complex) in hippocampal neuronal terminals (Reim K, et al., 2001). Parallely, it has been suggested that the degree of tightness of the SNARE complex can affect the vesicle release from the heterogeneous readily releasable pool in adrenal chromaffin cells (vesicles with fully zippered SNARE complex form rapidly releasable pool, while vesicles with insufficient assembling of the SNARE complex form slowly releasable pool, Rettig J and Neher E, 2002). Whether the hypothesis is applicable to synaptic terminals is not completely sure, since the unresolved issue is whether synchronous release and asynchronous release originates from rapid and slow readily releasable pool respectively, although the existence of heterogeneous readily releasable pool has been reported both in the calyx of Held (a giant synapse in the auditory pathway, Sakaba T and Neher E, 2001a-b; Trommershauser J, et al., 2003) and in hippocampal neurons (Murthy VN, et al., 1997; Rosenmund C, et al., 2002).

Besides complexin, there are other proteins that have been shown to interact with the SNARE complex. Synaptotagmin 1, a presynaptic protein, has been shown to regulate SNARE complex assembling *in vivo* (Littleton JT, et al., 2001) and the Ca^{2+} dependent binding of synaptotagmin 1 to the C-terminal SNAP-25 in the SNARE complex is essential for Ca^{2+} triggered exocytosis in PC12 cells (Gerona RR, et al., 2000; Zhang X, et al., 2002).

The function of synaptotagmin 1 is thought to be more than just interaction with the SNARE complex. That the murine neurons lack of synaptotagmin 1 only exhibited the asynchronous release (Geppert M, et al., 1994) led to a proposition of synaptotagmin 1 as the Ca^{2+} sensor for fast synaptic transmission. This notion was further supported by the observation that the addition of synaptotagmin 1 greatly accelerated the SNARE complex mediated membrane fusion *in vitro* (Tucker WC, et al. 2004). Additionally, the SNARE complex has been suggested to be directly involved in Ca^{2+} sensing, since if neutralizing two residues in SNAP25 (E₁₇₀, Q₁₇₇), which are postulated to be involved in Ca^{2+} cooperation for vesicle release, the fast Ca^{2+} triggered exocytosis was abolished (Sorensen JB,

et al., 2002). While a recent study showed different opinion by screening the surface of the SNARE complex for appropriate Ca^{2+} affinity binding sites (Chen X, et al., 2005). The results excluded the SNARE complex as the Ca^{2+} sensor due to its rather low Ca^{2+} affinity. Furthermore, the neutralization of those two residues (E₁₇₀, Q₁₇₇) in SNAP25 was found to have no effect on the SNAP-25/synaptotagmin 1 interaction but to destabilize the SNARE complex. These findings taken together suggest that the SNARE complex does not act directly as Ca^{2+} receptors but its assembly is tightly coupled to Ca^{2+} -sensing, and the lack of Ca^{2+} sensing molecule(s) (i.e. synaptotagmin 1) may lead to the slow fusion rate observed in the previous reconstitution experiments (Weber T, et al., 1998).

The dual role of synaptotagmin 1 (interaction with SNARE complex and Ca^{2+} sensor) makes the molecular level explanation of exocytosis very complicated, so it is necessary to understand the function of synaptotagmin 1 in exocytosis better.

1.3 The family of synaptotagmins

Since synaptotagmin 1 was found in an antibody screening for synaptic proteins (Matthew WD, et al., 1981), 16 different synaptotagmin isoforms have been subsequently identified (for review, Sudhof TC, 2002; Fukuda M, 2003a-b). Most of them are poorly characterized with the exception of synaptotagmin 1, 2, 3, 4 and 7. The family members are classified by a common structural building: an N-terminal transmembrane region (TMR), a central linker and two C-terminal C₂ domains.

Most synaptotagmin proteins mainly express in the brain, while in some tissues out of the central nerve system, some of these proteins have also been detected. For example, synaptotagmin 1 and 2 were found in adrenal chromaffin cells; synaptotagmin 7 was detected in heart, lung and spleen (Li C, et al., 1995) and synaptotagmin 13 has been found in sperm heads (Hutt DM, et al., 2002) and in

the kidney (Kishore BK, et al., 1998). These ubiquitously expressed synaptotagmins also show different localization in presynaptic terminals. Synaptotagmin 1, 2, 9 are vesicular proteins; while the localization of synaptotagmin 3 and 7 is controversial, since some studies suggested they are vesicular proteins (Ullrich B, et al., 1994; Martinez I, et al., 2000), and other studies defined them as plasma membrane proteins (Xu T and Bajjalieh SM, 2001; Sugita S, et al., 2001; Sugita S, et al., 2002).

Synaptotagmins contain two C_2 domains, referred as the C_{2A} and the C_{2B} domain, accounting for most functions of synaptotagmin. Each C_2 domain has a similar eight-strand β barrel tertiary structure with three top loops (Fig. 1.3). It has been reported that three and two Ca^{2+} ions can bind to the C_{2A} domain (Ubach J, et al., 1998) and C_{2B} domain (Fernandez I, et al., 2001) respectively in synaptotagmin 1 (a recent study showed that the third Ca^{2+} coordination site in C_{2B} domain can be generated by D₃₀₉ and N₃₃₃ in higher Ca^{2+} concentration (600mM $CaCl_2$), Cheng Y, et al., 2004). The Ca^{2+} binding sites in each domain specifically contain five aspartates that exist in the two out of three top loops (Loop 1 and 3, Shao X, et al., 1996). The number of bound Ca^{2+} ions in the C_2 domains is the same for synaptotagmin 1-3, 5-7 and 9-10. For synaptotagmin 8, 12, 13, they lack Ca^{2+} binding residues in two C_2 domains and for synaptotagmin 4 and 11, their C_{2A} domain can only bind one or two Ca^{2+} ions. The intrinsic Ca^{2+} affinity in each C_2 domain is low ($K_d > 1mM$ and $> 0.3mM$ for the C_{2A} domain and C_{2B} domain of synaptotagmin 1 respectively), but in the presence of phospholipid, it can be increased more than 100 folds (1-20 μM , Fernandez-Chacon R, et al., 2001; Fernandez I, et al., 2001). Since the Ca^{2+} affinity of the C_2 domains (in the presence of phospholipid) falls in the range of microscopic Ca^{2+} concentration upon Ca^{2+} influx in presynaptic terminal (10-25 μM , Bollman JH, et al., 2000; Schneggenburger R and Neher E, 2000), this leads to the speculation of synaptotagmins functioning as Ca^{2+} sensors for exocytosis. The structure and function of synaptotagmin 1 are by far the most well studied protein in this family and also it is the central molecule investigated in this thesis.

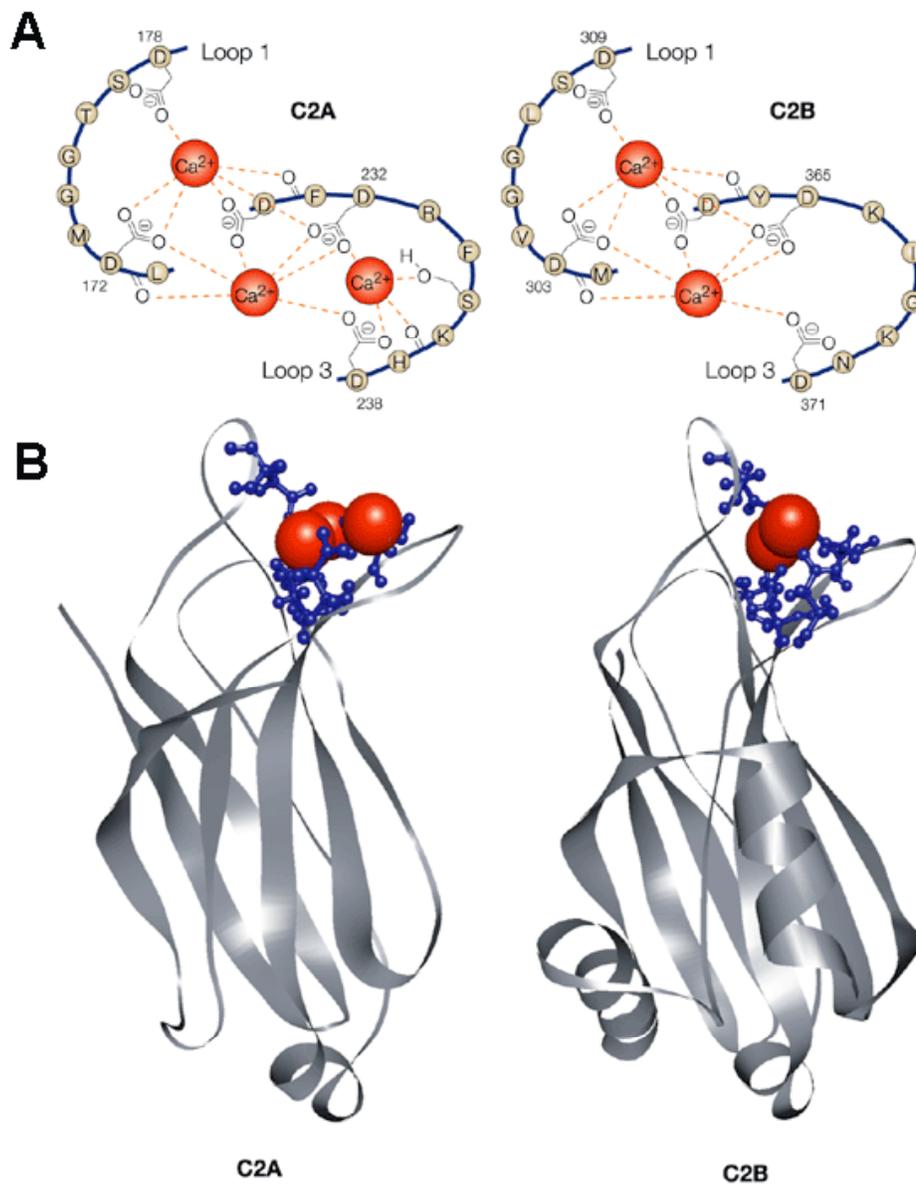


Figure 1.3 The structure of the C₂ domains of synaptotagmin 1. A. Schematic drawing shows the interaction between the Ca²⁺ ions and amino acids in the C₂A and C₂B domains. B. Three dimensional structure of the C₂A and C₂B domains in Ca²⁺ binding state. Red balls represent Ca²⁺ ions. (From the review, Chapman ER, 2002)

1.4 The mechanism of action of synaptotagmin for exocytosis

In respect to Ca^{2+} influx, evoked neurotransmitter release can be separated into a fast (synchronous) form and a slow (asynchronous) form. This biphasic release form leads to the speculation that it is differentially regulated by two distinct Ca^{2+} sensors (Goda Y and Stevens CF, 1994). A low affinity Ca^{2+} sensor can trigger a fast release and the higher affinity Ca^{2+} sensor mainly senses the tail of Ca^{2+} transient to induce a slow but long lasting vesicle fusion. This 'two Ca^{2+} sensor model' was supported by some genetic studies of synaptotagmin 1 knock out models (Nonet ML, et al., 1993; Littleton JT, et al., 1993; Geppert M, et al., 1994), where the total release decreased, or synchronous release was eliminated. Thus, synaptotagmin 1 appear to be as the most likely Ca^{2+} sensor candidate for synchronous release. (In the following part, without other mentioning, synaptotagmin refers to synaptotagmin 1)

1.4.1 Multiple functions of synaptotagmin in vesicle recycling

In addition to a role in Ca^{2+} sensing, synaptotagmin has been postulated to have multiple functions in vesicle recycling, such as vesicle docking, fusion pore regulation, and vesicle endocytosis.

The quantitative morphological finding that the number of docked synaptic vesicles in synaptotagmin null *Drosophila* larvae was significantly reduced led to the hypothesis that synaptotagmin facilitates vesicle docking (Reist NE, et al., 1998). While a long lasting (>1 hr) high K^+ induced vesicle fusion was observed in synaptotagmin null *Drosophila* (Yoshihara M and Littleton JT, 2002) and similar quanta release by hypertonic solution application was found between wild type and synaptotagmin null mutants (from review, Tucker WC and Chapman

ER, 2002), it strongly questioned the previous hypothesis that synaptotagmin affects the vesicle docking process.

After the close proximity of vesicle membrane and plasma membrane, a fusion pore forms to connect the vesicle lumen with the extra cellular environment. The amperometry study can directly monitor the fusion pore kinetics: the neurotransmitters (catecholamine, a class of hormone stored in large dense core vesicles of PC12 cells) dilation of the fusion pore result in a spike of amperometric current, which is preceded by a steady level of current (PSF, pre-spike foot) reflecting the limited flux of neurotransmitters through the fusion pore before its dilation. It has been observed that overexpression of synaptotagmin in PC12 cells increased the duration of PSF signals, indicating that synaptotagmin can stabilize the fusion pore to regulate the last step of membrane fusion (Wang CT, et al., 2001); a further study even suggested that the C₂A domain favors a full vesicle fusion while the C₂B domain regulates “kiss-and-run” mode fusion (Wang CT, et al., 2003). The fusion pore dynamics is not solely controlled by synaptotagmin, since disrupting the synaptotagmin/t-SNARE interaction has been showed graded reductions in the duration of PSF signals (Bai J, et al., 2004b).

Vesicle retrieval from plasma membrane is AP-2 dependent (a class of adaptor protein, binding to synaptic vesicle to trigger assembly of clathrin for endocytosis). The biochemical study revealed a high affinity interaction between AP-2 and synaptotagmin (Zhang JZ, et al., 1994), which in general agrees to the findings that a marked depletion of synaptic vesicles was seen at nerve terminals of synaptotagmin null *C. elegans* (Jorgensen EM et al., 1995) and a kinetic deficiency of endocytosis in synaptotagmin null mice hippocampal neurons (Nicholson-Tomishima K and Ryan TA, 2004). To determine the AP-2 binding sites in synaptotagmin, a screening study was performed and localized the position to the C₂B domain (K_{326, 327}, Chapman ER, et al., 1998), which was confirmed by the findings that the fly mutant with the deletion of the C₂B domain

had a dysfunctional vesicle recycling (Littleton JT, et al., 2001). Another study argued that this AP-2 binding site in synaptotagmin is a regulator of endocytosis instead of an internalization signal (Jarousse N, et al., 2001) and a new internalization site in synaptotagmin was reported to be a tryptophan residue in the last β strand of the C₂B domain (Jarousse N, et al., 2003). The polybasic site (K_{326, 327}) in the C₂B domain is very interesting, because it has been identified to bind multiple molecules besides AP-2, for example, inositol polyphosphates (Fukuda M, et al., 1994), another copy of synaptotagmin (oligomerization, Chapman ER, et al., 1996; Sugita S, et al., 1996; Desai RC, et al., 2000), Ca²⁺ channels (Sheng ZH, et al., 1997; Kim DK and Catterall WA, 1997), etc. So it is necessary to clarify the sequence of these interactions and their relationship with endocytosis (if it exists). A recent finding shed some light in this direction, which showed that the C₂B domain oligomerization is a prerequisite for AP-2 binding (Grass I, et al., 2004). Since synaptotagmin oligomerization is thought to be involved in the vesicular exocytosis process (Littleton JT, et al., 2001), then the oligomerization step preceding the AP-2 binding step depicts a regulatory transition of vesicles from exocytosis to endocytosis by synaptotagmin.

1.4.2 The mechanism of action of synaptotagmin for vesicle fusion

So far the multiple roles of synaptotagmin in vesicle recycling has been described except for exocytosis, which actually is by far the most well-studied and controversial topic about synaptotagmin (for review, Koh TW and Bellen HJ, 2003; Bai J and Chapman ER, 2004; Sudhof TC, 2004).

During vesicle exocytosis, several interactions of synaptotagmin are important for understanding the mechanism of action of synaptotagmin: 1) Phospholipid interaction; 2) the SNARE complex interaction; 3) homo-/hetero-synaptotagmins interaction. An important issue is whether these interactions are Ca²⁺ dependent.

Initially, only the C₂A domain of synaptotagmin was found to bind phospholipid in a Ca²⁺ dependent manner and this interaction has been showed to be in an electrostatic way instead of by the phospholipid head group (Zhang X, et al., 1998; Davletov B, et al., 1998). This notion was later partially corrected after the observation that Ca²⁺ triggers direct insertion of Ca²⁺ binding loop 3 into lipid bilayers by a quenching experiment (Chapman ER and Davis AF, 1998). This study showed that lipid-embedded quencher can decrease tryptophanyl fluorescence of the C2A residues (F_{231,234}W) substitution. So it is now believed that the C₂A domain interacts with phospholipid through electrostatic interaction, which can be further stabilized by the hydrophobic interaction between the C₂A domain and the plasma membrane (Gerber SH, et al., 2001). The early study of immobilized GST-isolated C₂B domain did not show its Ca²⁺ dependent interaction with phospholipid (Schiavo G, et al., 1995; Bai J, et al., 2000), because the initial synaptotagmin cDNA encoded a point mutation that leads to a defective C₂B domain (Perin MS, et al., 1990; Ubach J, et al., 2001). A properly purified C₂B domain indeed can bind phospholipid in Ca²⁺ dependent manner (Ubach J, et al., 2001; Fernandez I, et al., 2001) and further more, the C₂B domain was found to be able to insert into lipid bilayers if it is linked to the C₂A domain (Bai J, et al., 2002). Therefore both C₂ domains can interact with phospholipid cooperatively, there should be a certain mechanism for the domains to distinguish plasma membrane from vesicular membrane. The interaction between synaptotagmin and inositol polyphosphates, which are exclusively present on the plasma membrane has been carefully studied (Bai J, et al., 2000; Bai J, et al., 2004a). Indeed, PIP₂ (phosphatidylinositol 4,5-bisphosphate, a type of inositol polyphosphates) was shown to steer the reconstituted synaptotagmin to penetrate into PIP₂ –harboring bilayers in presence of Ca²⁺ *in vitro*. The polybasic region in the C₂B domain of synaptotagmin was found responsible for the interaction with PIP₂ (Bai j, et al., 2004a).

Synaptotagmin-phospholipid interaction was proven by biochemical experiments *in vitro*. Their consequential effect on physiological synaptic transmission has

been started now. A study of the C₂A domain of synaptotagmin showed that neutralizing a single positive residue in the C₂A domain (R₂₃₃Q) leads to a two-fold decrease in Ca²⁺ dependent phospholipid binding affinity, parallel with a half reduction of synaptic transmission efficiency in hippocampal neurons (Fernandez-Chacon R, et al., 2001). Similar correlation was found in two other strains of knock-in mice (D₂₃₂N and D₂₃₈N), where no change in Ca²⁺ dependent phospholipid binding was observed along with normal synaptic transmission (Fernandez-Chacon R, et al., 2002). These elegant studies suggest that synaptotagmin-phospholipid interaction is quite essential for vesicle release.

That both C₂ domains with the similar 3D structure show the redundant phospholipid binding activity *in vitro* leads to a question: are they redundant in physiological condition for synaptic transmission as well? Several studies tried to resolve this question. For example, the neutralization of some Asp residues in Ca²⁺ binding sites of the C₂B domain severely diminished fast neurotransmitter release (Robinson IM, et al., 2002; Nishiki T and Augustine GJ, 2004b), while mutation studies carried out in the C₂A domain showed a shift in Ca²⁺ sensitivity of synaptotagmin without changing fast synaptic transmission (Stevens CF and Sullivan JM, 2003; Mackler JM, et al., 2002). Similarly, a study using the C₂B domain truncated synaptotagmin mutant in *Drosophila* found a reduced but not eliminated synchronous release together with completely abolished the Ca²⁺ cooperativity (Yoshihara M and Littleton TJ, 2002). These results taken together, suggest that the physiological functions of the C₂ domains of synaptotagmin clearly are unequal and non-redundant.

The Ca²⁺ dependent binding of synaptotagmin to syntaxin (Li C, et al., 1995; Kee Y and Scheller RH, 1996) was discovered to occur at the sequences of the C₂A domain that surround the Ca²⁺ binding sites (Shao X, et al, 1997). The disruption of a single Ca²⁺ binding site abolished this binding and it was found that positively charged residues near Ca²⁺ binding sites are required for syntaxin binding (Ubach J, et al., 1998). The binding site in syntaxin is thought to map to

the transmembrane domain and H3 domain (corresponding to the region of syntaxin that assembles into SNARE complex; Chapman ER, et al., 1995; Kee Y and Scheller RH, 1996). Since it was also found that synaptotagmin can facilitate the SNARE complex formation *in vitro* and a mutation (Y₃₆₄N) in synaptotagmin disrupting the conformation change required for synaptotagmin oligomerization results in a decrease but not loss of the SNARE assembly *in vivo* (Littleton JT, et al., 2001). Therefore, it was speculated that synaptotagmin regulates SNARE assembling upon Ca²⁺ influx and pulls the membranes closer simultaneously (Davis AF, et al., 1999). The finding that synaptotagmin can bind to the C-terminal of SNAP-25 in presence of Ca²⁺ and influence secretion in PC12 cells reinforced this speculation (Zhang X, et al., 2002).

However, recently it has been reported that the SNARE complex can be copurified with synaptotagmin from brain material in the absence of Ca²⁺. The Ca²⁺ independent binding site of synaptotagmin to the t-SNARE heterodimer is localized to the polybasic region of the C₂B domain (Shin OH, et al., 2003; Rickman C and Davletov B, 2003; Rickman C, et al, 2004). The fusion of reconstituted v-/t-SNARE proteoliposomes *in vitro* by synaptotagmin facilitating SNARE complex formation in the absence of Ca²⁺ was also reported (Mahal LK, et al., 2002). Alternatively, another study showed the analogue of Ca²⁺ ion, Sr²⁺, binding to the Ca²⁺ binding sites in the C₂B domain of synaptotagmin can trigger vesicle release, which occurs through the Sr²⁺ dependent synaptotagmin-phospholipid interaction while bypassing the synaptotagmin-SNARE complex interaction (Shin OH, et al., 2003). This observation is an indirect evidence to support the notion that synaptotagmin-SNARE interaction is not essential for vesicular release.

The Ca²⁺-promoted self-association of synaptotagmin has gained great attention since its first report (Wendland B and Scheller RH, 1994). First of all, it is necessary to determine the locus of the self-association site(s). By using yeast two-hybrid interaction screen assay, the C₂B domain of synaptotagmin was

identified as the regulator of Ca^{2+} dependent oligomerization (Sugita S, et al., 1996). Later on, a further screening of the C₂B domain of synaptotagmin unveiled the polybasic region (K_{326, 327}) as the oligomerization site (Chapman ER, et al., 1998). By neutralizing this site, Ca^{2+} dependent oligomerization but not membrane binding was disrupted (Wu Y, et al., 2002) and inhibition of secretion from PC12 cells was observed (Desai RC, et al., 2000). Together with these findings, a synaptotagmin mutant (Y₃₆₄N) in *Drosophila*, which showed disruption of the conformation change required for synaptotagmin oligomerization, resulted in a post-docking defect in exocytosis (Littleton JT, et al., 2001) and a drastic reduction of release (Yoshihara M and Littleton JT, 2002).

Based on the above description, there are now two proposed models to explain the mechanism of action of synaptotagmin in vesicle fusion. One is described as the following (Bai J and Chapman ER, 2004): 1) Before Ca^{2+} influx, synaptotagmin targets on plasma membrane through the interaction with PIP₂; 2) In the presence of Ca^{2+} , PIP₂ steers the Ca^{2+} binding pockets of both C₂ domains of synaptotagmin to insert into the plasma membrane; simultaneously, synaptotagmin interacts with t-SNAREs to help the SNARE complex assemble through self-oligomerization; 3) The tightened SNARE complex together with the oligomerized synaptotagmins pulls the vesicular membrane into close proximity to the plasma membrane and overcome the energy barrier for membrane fusion; 4) Fusion pore forms and neurotransmitters release. The second model is as the following (Rettig J and Neher E, 2002; Sudhof TC, 2004): 1) Before Ca^{2+} influx, complexin is bound to fully assembled SNARE complex (regulated by Sec1/Munc-18 like proteins) and synaptotagmin constitutively associates with the SNARE complex. The synaptic vesicle membrane and plasma membrane are forced into close proximity by SNARE complex assembly, which shows an unstable intermediate state (hemi-fuse state); 2) Ca^{2+} influx triggers the Ca^{2+} binding loops of synaptotagmin to insert into plasma membrane, which further destabilizes the fusion intermediate and mechanically perturbs to open the fusion pore. 3) Neurotransmitters release from vesicles through the fusion pore. The

prominent difference between these two models is whether the SNARE complex forms before or after Ca^{2+} influx, and whether it is synaptotagmin dependent or relies more on other molecules.

1.5 The aim of this study and work overview

The aim of this study is to understand the mechanism of action of synaptotagmin for exocytosis better. As described above, there are until now three main contributors of synaptotagmin known: phospholipid, SNARE complex and synaptotagmin itself. In this study, the Ca^{2+} dependent phospholipid interaction is the central question. Especially, until the project was started, only a few electrophysiological investigations of synaptotagmin in murine neurons had been started (Geppert M, et al., 1994; Fernandez-Chacon R, et al., 2001). The main approach is to rescue synaptotagmin null neurons with synaptotagmin carrying various mutations and postulate the functions of the mutated residues by comparing mutants and wild type synaptotagmin rescued neurons. In this way, I try to uncover the possible interactions between synaptotagmin and phospholipid or synaptotagmin itself and subsequently deduce the mechanism of action of synaptotagmin in exocytosis.

There are several studies in this thesis: A) a basic characterization of synaptotagmin knock out (sytKO) neurons with comparison to WT neurons; B) truncation of either C_2 domains of synaptotagmin to evaluate their importance in synaptic transmission; C) neutralization of the Ca^{2+} binding sites of each domain to better understand the role of the Ca^{2+} dependent synaptotagmin-phospholipid interaction in vesicle release; D) replacing the hydrophobic residues in the Ca^{2+} binding sites with tryptophans to further clarify the importance of synaptotagmin-phospholipid interaction and the contribution of each C_2 domain for synaptic vesicle fusion; E) replacing each synaptotagmin C_2 domain with the corresponding C_2 domain from synaptotagmin isoform (synaptotagmin 7) to gain the insight of the importance of these C_2 domains in synaptic transmission.

2. Materials and methods

2.1 Experimental approach

The experimental design here is to investigate the physiological functions of a synaptic protein by overexpressing the exogenous protein or its mutants on the cultured murine hippocampal neurons (Ashery U, et al., 1999).

When a hippocampal neuron is grown on the isolated micro-island formed by astrocytes, the axon of the neuron is forced to grow within the dendritic region of the cell itself to form a large number of autaptic synapses. The parameters, such as kinetics, pharmacological properties, miniature currents, etc in both the excitatory and inhibitory autapses show little differences between cultured neurons and slices preparation (Bekkers JM and Stevens CF, 1991). In such a culture system, the total quantal size estimation is possible, since the origin of all synapses on the neuron is known.

The patch clamp technique initially developed for single ion channel current measurement (Neher E and Sakmann B, 1976) was adapted for whole cell recording, which is obtained by establishing a giga-seal and breaking a patch beneath the pipette tip with a strong pulse of suction (Hamill OP, et al., 1981). In the voltage clamp mode, the membrane potential is held constant (at about -70mV in resting condition) and the current flowing through the ion channels on the membrane is measured. With a brief depolarization at the soma in whole-cell voltage clamp mode, the basic scheme of synaptic transmission can be obtained as evoked postsynaptic currents by action potential induced neurotransmitter release. It is thought that usually one or no vesicle in the readily releasable pool (RRP) per synapse can be released by an action potential. To quantify the vesicular release probability (normalizing evoked release charge to total RRP charge), the RRP size is measured by hypertonic solution perfusion (i. e. 500 mM

sucrose for 4 seconds) through the fast flowing pipette. Although the exact mechanism of release mediated by hypertonic solution is not clear, it is believed that a Ca^{2+} independent mechanical stress on presynaptic cytoskeleton decreases the energy barrier for vesicle fusion (Stevens CF and Tsujimoto T, 1995; Rosenmund C and Stevens CF, 1996). Change in vesicular release probability is expected to alter synaptic strength (i. e. short term plasticity). In cultured hippocampal neurons, high frequency stimulation (i. e. 10 Hz) usually leads to a marked activity-dependent depression, which is mainly due to a depletion of RRP. Since the molecule studied here is synaptotagmin, a protein involved in Ca^{2+} sensing for vesicular release, another parameter worth considering is the Ca^{2+} sensitivity of the synapses. Technical difficulties (i. e. inaccessibility to the presynaptic terminal in this preparation, difficulty of monitoring the presynaptic Ca^{2+} transient, etc.) restrain the direct measurement of the synaptic Ca^{2+} sensitivity. The alternative way is to measure the apparent Ca^{2+} sensitivity by exogenous application of various Ca^{2+} concentrations (0.5 -12 mM).

The overexpression method based on the Semliki Forest virus (SFV) makes it possible to express exogenous proteins in the cultured hippocampal neurons. The gene of the interest can be ligated to a DNA cloning vector encoding nonstructural SFV gene for replicase, reverse transcriptase and helicase. After in vitro transcription, resultant RNA along with the helper vector is electroporated into a host cell line (i. e. BHK-21 cells, baby hamster kidney cells) for virus production. Enhanced yellow or green fluorescent protein is used here as a marker to detect the transfected neurons. The high viral expression efficiency of the protein makes the physiological measurement possible after 12 hours transfection on the cultured neurons.

2.2 Materials

2.2.1 Chemicals and solutions for neuronal culture

5-Fluro-2'-deoxyuridin	
Albumin, bovine	
Agarose Typ II-A	
Cystein	
Poly-D-Lysine	
Trypsin Inhibitor	
Uridine	-- from Sigma Co.
B27-Supplement	
DMEM (Dulbecco's modified Eagle medium)	
Glutamax-I Supplement	
HBSS (Hanks Balanced Salt Solution)	
N2-Supplement	
NBA (Neurobasal A)	-- from Gibco BRL Co.
MITO	
Collagen	-- from Collaborative Biomedical products Co.
Penicillin/Streptomycin	-- from Boehringer Mannheim Co.
Papain	-- from Worthington Biomedical Co.
Typsin/EDTA (Ethyldiaminetetraacetic acid)	-- from Biochrom Co.
FBS (Fetal Bovine Serum)	-- from Seromed Co.

Coating mixture

Acetic acid (17mM)	300 µl
Poly-D-Lysine (0.5mg/ml)	100 µl
Collagen (1mg/ml)	100 µl

Full medium (for astrocyte culture)

DMEM	180 ml
Fetal Calf Serum (FCS)	20 ml
Penicillin/Streptomycin	400 µl
MITO	200 µl
Store at 37°C, 5% CO ₂ incubator	

FUDR stock

5-fluoro-2'-deoxyuridine	25 mg
Uridine	62.5 mg
DMEM	12.5 ml

Neuron culture medium

NBA	100 ml
B27-supplement	2 ml
Glutamax	1 ml
Penicillin/streptomycin	200 µl

Enzyme digestion solution

Cystein	2 mg
DMEM	10 ml
CaCl ₂ (100mM)	0.1 ml
EDTA (50mM)	0.1 ml
Papain	25 u/ml

Bubbling with carbogen (95% O₂ and 5% CO₂) for 15min before using.

Enzyme inhibition solution

Albumin	25 mg
Trypsin-Inhibitor	25 mg
Full Medium	10 ml

2.2.2 Materials for molecular biology

Those semliki forest virus (SFV) plasmids carrying synaptotagmin 1 (syt or syt1) wild type or mutant genes listed below were generated by Dr. Shin from Prof. Thomas C. Sudhof's lab. (pSFV1: the SFV plasmid; IRES, Internal Ribosome Entry Site; EGFP/EYFP: Enhanced Green/Yellow Fluorescence Protein)

SFV plasmids

pSFV1 – sytWT –IRES EYFP
pSFV1 – sytΔC ₂ A –IRES EYFP
pSFV1 – sytΔC ₂ B –IRES EYFP
pSFV1 – sytC ₂ A3DA –IRES EYFP
pSFV1 –sytC ₂ B3DA –IRES EYFP
pSFV1 –sytC ₂ AB6DA –IRES EYFP
pSFV1 –sytC ₂ A3W –IRES EYFP

syt inserts

Wild type syt;
Deletion of the C ₂ A domain (135-265), the C ₂ B domain (266-421) linked directly to Trans Membrane Region (1-134) of WT syt;
Deletion of the C ₂ B domain (266-421) from WT syt;
Asps at 178, 230, 232 position of the C ₂ A domain replaced with Alas;
Asps at 309, 363, 365 position of the C ₂ B domain replaced with Alas;
Asps at 178, 230, 232, 309, 363, 365 position replaced with Alas;
Met at 173, Phes at 231, 234 position of the C ₂ A domain replaced with Trps;

pSFV1 –sytC ₂ B3W –IRES EYFP	Val at 304, Tyr at 363, Ile at 367 position of the C ₂ B domain replaced with Trps;
pSFV1 –sytC ₂ AB6W –IRES EYFP	Met at 173, Phes at 231, 234, Val at 304, Tyr at 363, Ile at 367 position replaced with Trps.
pSFV1 –sytR ₂₃₃ Q –IRES EYFP	Arg at 233 position replaced with Gln;
pSFV1 –sytK ₃₆₆ Q –IRES EYFP	Lys at 366 position replaced with Gln;
pSFV1 –syt1(syt7 C ₂ B) –IRES EGFP	the C ₂ B domain (266-421) of syt1 replaced with the C ₂ B domain (260-403) of syt7;
pSFV1 –syt1(syt7 C ₂ A) –IRES EGFP	the C ₂ A domain (135-265) of syt1 replaced with the C ₂ A domain (135-258) of syt7;
pSFV1 –syt1(syt7 C ₂ AB) –IRES EGFP	Both C ₂ domains (135-421) of syt1 replaced with the two C ₂ domains (135-403) from syt7;

Besides these pSFV constructs, a few more SFV plasmids with syt mutants were made by myself:

SFV plasmids

syt inserts

pSFV1 –sytWT –IRES EGFP	
pSFV1 –sytΔC ₂ A –IRES EGFP	
pSFV1 –syt2KA –IRES EGFP	Lyses at 326, 327 position of the C ₂ B domain replaced with Alas;

Semliki forest virus plasmids

pSFV1 and its Helper-2
 BHK-21 (Baby hamster kidney -21) cell line
 -- from Gibco BRL Co.

Restriction enzymes

SpeI
 BamHI
 BssHII
 Eco47III
 -- from New England BioLabs Co.

Other chemicals

Taq DNA polymerase (pfu)
 XL-1 Competent cells
 -- from StrataGene Co.

DEPC (Diethylpyrocarbonate)
 MOPS (4-Morpholinopropanesulphonic acid)
 Na-acetate
 Glycerin
 Phenol
 Chloroform
 --from Sigma Co.

dNTPs (Solution Mix of dATP, dGTP, dTTP and dCTP)

dATP (3. 2 -deoxyadenosine-5 Triphosphate)
dGTP (4. 2 -deoxyguanosine-5 Triphosphate)
dTTP (2. 2 -deoxythymidine-5 Triphosphate)
dCTP (1. 2 -deoxycytidine-5 Triphosphate)
-- from InvitroGene Co.

T4 DNA ligase
SOC medium
SP6 RNA polymerase
RNase inhibitor
--from Gibco BRL Co.

MiniPrep box
MaxiPrep box
Gel purification box
PCR purification box
--from Qiagen Co.

Formaldehyd
Formamid
-- from BioRad Co.

PCR primers for mutagenesis

2KA For: 5'-AAGAAGGCAGCGACGACGATTAAGAAGAAC-3'
2KA Rev: 5'-CGTCGTCGCTGCTTCTTCAGCCTCTTACC-3'
-- for 2KA point mutation in C2B domain;

C₂B For: 5'-GAGAAACTGCAGAGCGCTGAGAAAGAAGAG-3'
C₂B Rev: 5'-AGCGCTCTGCAGTTTCTCCTCTTCCTTGGG-3'
-- for C2A domain deletion;

syt For: 5'-TATGGATCCGCCACCATGGTGAGTGCCAGTCATCC-3'
syt Rev: 5'-TATGCGCGCTTACTTCTTGACAGCCAGCAT-3'
-- for full length Syt.
-- from lbc GmbH

2.2.3 Chemicals for electrophysiology

<u>Internal solution (in mM)</u>		<u>External solution (in mM)</u>	
KCl	136	NaCl	140
MgCl ₂	0.6	KCl	2.4
K ₄ EGTA	1	CaCl ₂	4
GTP-Na	0.3	MgCl ₂	4
ATP-Mg	4	Glucose	10
HEPES	17.8	HEPES	10
Phosphocreatin	12		
Creatin-Phosphokinase	50 u/ml		
	-----		-----
	pH 7.4, Osm 315;		pH 7.4, Osm 315.

EGTA (Ethylene glycol-bis(β -aminoethyl ether)
-N,N,N',N' tetra-acetic acid)
CsCl
SrCl₂
Sucrose
-- all from Sigma Co.

TTX (Tetrodotoxin)
NBQX (2,3-Dihydroxy-6-nitro-7-sulphamoylbenzo[f]quinoxaline)
-- from Tocris Co.

2.2.4 Electrophysiological hardware

Digitizer (Digidata 1322A)
Amplifier (Axopatch 200B, MultiClamp 700B)
-- from Axon Co.

Microscope (IX51)
-- from Olympus Co.

Drug Application System
-- from Warner Co.

Glass Pipette
($\varnothing_{\text{inner}} \times \varnothing_{\text{outer}} \times \text{Length}$, 0.86x1.5x80 mm)
-- from Science Products GmbH

Pipette Puller (P-97)
-- from Sutter Instrument Co.

2.2.5 Data analysis software

Clampex 9.0 (for data acquisition) --from Axon Co.

Axograph 4.9 (for data analysis) --from Axon Co.

Kaleidagraph 3.0
(for data analysis and graph presentation) --from Abelbeck Software

Claridraw (graph presentation) --from Claris Co.

2.3 Methods

2.3.1 Mutagenesis of synaptotagmin (syt) mutants

Taking pSFV1-Syt 2KA-IRES EGFP Construction as an example:

The codons for Lysines (Lys, K) at the 326th, 327th position of amino acid sequence of Syt are replaced with two DNA codons for Alanine (Ala, A) in the two primers (2KA for and 2KA rev). Another two primers (Syt for and Syt rev) matching two terminals of Syt DNA sequence were also designed.

Two rounds of PCR programs were performed. The first round PCR procedure is listed as following:

PCR cocktail:		PCR program:	
Templet (pSFV-syt WT-IRES EGFP, 10ng/μl)	1 μl		
Primers (Syt for & 2KA rev, 20pmol/μl)	2.5 μl/each		
[or (Syt rev & 2KA for, 20pmol/μl)	2.5 μl/each]		
dNTP (2.5mM/μl)	4 μl		
10x PCR buffer	5 μl	94 °C	1 min
Taq Enzyme	0.5 μl	44 °C	1 min
H ₂ O	34.5 μl	72 °C	1 min
	-----		-----
	50 μl		x 25 runs

Following the above PCR procedure, two PCR products were generated, P1 and P2. Then the second PCR procedure was applied as following:

PCR cocktail:		PCR program:	
Templets (P1 & P2, 10ng/ μ l)	1 μ l/each	A) 94 °C	1 min
Primers (Syt for & Syt rev, 20pmol/ μ l)***	2.5 μ l/each	48 °C	1 min
dNTP (2.5mM/ μ l)	4 μ l	72 °C	1.5 min
10x PCR buffer	5 μ l	-----	
Taq Enzyme	0.5 μ l		x 1 run
H ₂ O	33.5 μ l		

	50 μ l	B) 94 °C	1 min
		44 °C	1 min
		72 °C	3 min

			x 25 runs

*** The primers were added after PCR program A

Syt2KA PCR product and the plasmid vector (pSFV1-IRES-EGFP) were cut with restriction enzymes (BamH1 and BssHII separately) and then ligated in a ratio of 3:1, at 16 °C, overnight. On the second day, the ligation reaction was transformed to competent cells and plated on LB medium containing Ampicillin. Plates were kept at 37 °C, overnight. Bacterial colonies growing on the plates were selected and cultured in the LB medium, 37 °C overnight. Plasmid DNAs of colonies were extracted and characterized with restriction enzymes (BamHI and SpeI). Colonies with right inserts were maxipreped and later confirmed by DNA sequencing.

2.3.2 Semliki forest virus (SFV) replication

This work was done by technicians, Dirk Reuter and Hui Deng in our lab, just briefly described here:

2.3.2.1 mRNA *in vitro* preparation

4 μ g DNA (pSFV-1 plasmid containing synaptotagmin mutant) and 5 μ g helper DNA were linearized with SpeI to produce a 5' overhang. The linearized DNA

was purified by extraction with phenol-chloroform and ethanol precipitation. DNA restriction digest was vortexed with 150µl DEPC H₂O, 200 µl Phenol and 200µl chloroform. After centrifuge for 10 min at 14,000 rpm, the upper phase (containing DNA) was transferred to a fresh tube with 200 µl chloroform. After another centrifuge step (5min, 14,000 rpm), DNA was recovered from the upper phase by precipitation for 16 hours at -20 °C with 500 µl ethanol in the presence of 20 µl 3 M sodium acetate. The DNA was pelleted by centrifugation at 14,000 rpm for 15-30 mins, washed with 500 µl 70% ethanol and redissolved in 13 µl DEPC treated H₂O. For in vitro transcription, the DNA was mixed with RNA polymerase buffer (8 µl), SP6 RNA polymerase (2 µl), RNase inhibitor (1 µl) and DEPC H₂O (16 µl) for 1hours at 37 °C. Afterwards, the DNA-RNA mix was added with 36 µl DEPC-treated H₂O and 4µl DNase (50 u) and incubated at 37 °C for 20 min. The resulting RNA was purified from protein by extraction with phenol and chloroform as described above for DNA. The precipitated RNA was collected, desiccated and dissolved in 20 µl Rnase free water. 1 µl RNA was denatured at 65 °C for 10 min, and then checked on gel.

2.3.2.2 Electroporation of BHK-cells and harvest of viruses

The BHK-21 cells grown confluent up to 80-90% were split with trypsin (0.05%)-EDTA (0.02%) solution. Dissociated cells were spun down at low-speed centrifuge at 1,500 rpm for 5 min. After washing with ice-cold PBS, the cells were resuspended in the same buffer to the density of 10⁷/ml. Then 10µg of each of the RNAs were mixed with 0.8ml of cell suspension in a tube. These cells were electroporated with 25ms 300V pulse once, then transferred into a tube with 9ml NBA medium and plated in cell culture flask. After incubation at 37 °C for 24 to 30 hours, the cells were centrifuged at 3,000 rpm for 10 min. The medium supernatant containing viruses was collected in 450µl tube and frozen at -80 °C before using.

2.3.3 Hippocampal neurons culture

The characteristic features of the *syt*^{-/-} mice different from *syt*^{-/+} or WT new born mice are that the former have less milk in stomachs and the sizes are usually smaller comparing to the latter. Besides this, when the tail of *syt*^{-/-} mouse was pinched, it will give a weaker and irregular sound. As to other parameters for distinguishing the *syt*^{-/-} mice from the *syt*^{-/+} or WT ones, both genotyping and electrophysiology are applicable.

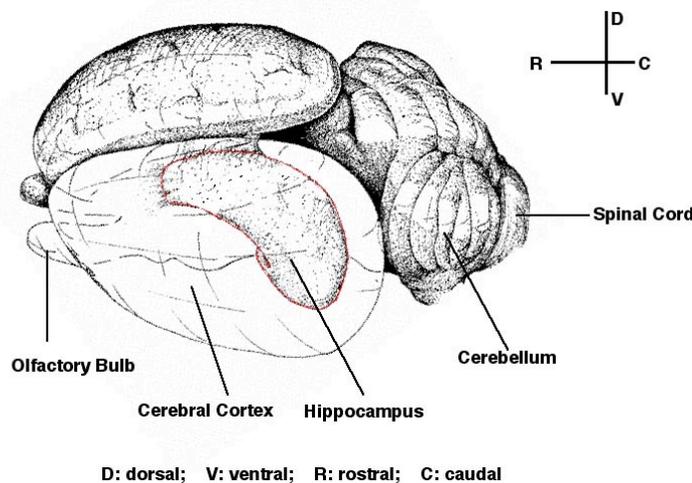


Figure 2.1 Stereo diagram of rat brain depicts the position of hippocampus. (Mouse brain is similar to it, picture is adapted from prof. John Jefferys' website, <http://www.neuroscience.bham.ac.uk/neurophysiology/research/hippocampus.htm>)

The procedure for hippocampus dissection out of mouse brain is quite simple. The mouse brain was cut down through the neck, then the skin and inner skull covering the brain were peeled off. The brain (fig. 2.1) was transferred quickly into cold HBSS medium. Under microscope, the two cortexes were pulled apart with slimmer forceps until the banana shaped hippocampus is visible. Then the hippocampus was taken out, put in enzyme digestion solution (500 μ l) and kept shaking at 700 rpm, 37 °C for 1 hour. Afterward, digestion solution was replaced

with the same volume of enzyme inhibition solution and kept shaking at 37 °C for 15 min. Well digested neurons were homogenously triturated and plated into 6 well plate containing confluent astrocyte microisland in low density (3-4 K/well). Cells were kept growing for 10 days before starting electrophysiological recording.

2.3.4 Astrocyte culture

The microisland autaptic neuron culture is the standard system in our lab for electrophysiological investigation. There are several steps to build up it: First of all, the sterilized glass coverslip was covered with a thin layer of agarose to prevent cell growing on it, then a regular collagen/PDL substrate dots were stamped on it, which are the microislands for astrocytes growing. Astrocytes were plated to form a confluent monolayer on the microislands, and later the neurons in low density were scattered individually on microislands to grow and form synapses between its own axon and dendrites.

The cleaned sterilized glass coverslips (\varnothing 30 mm) were coated with a thin layer of 0.15% agarose gel. After drying, coating mixture was stamped on the top of agarose gel with a rubber stamp with protruding pins of regularly spaced squares (200x200 μ m) to form microislands. The plates were sterilized with UV light before plating astrocytes.

A half of the cortex from newborn wild type mouse was digested in 1 ml enzyme digestion solution at 37 °C for 1 hour (shaking at 700 rpm). After digestion, the cortex is transferred to a tube with 0.5 ml inhibition enzyme solution at 37 °C for 15 min (shaking at 700 rpm). After homogenizing the digested cortex, the cells were plated on 75 cm² flask in 10 ml full medium growing for 1 week until approaching confluence. Confluent astrocytes dissociated with trypsin (10 ml) were suspended and then centrifuged at 1,600 rpm for 5min. Astrocytes resuspended in 10 ml full medium were plated into glass coverslips in the density

of 30 K/well and kept growing. After approaching confluent microislands, astrocytes were controlled with FUDR (20 μ l/well).

2.3.5 Electrophysiological characterization of syt mutants rescued neurons

2.3.5.1 Electrophysiology setup

The electrophysiology setup consists of two parts: a pharmacological manipulation part and data acquisition part. The pharmacological manipulation part consists of a microscope for localizing the neurons for patching, a manipulation system for positioning the electrode and fast solution flowing system (pipette shifting in 100 ms range) for drug application. The data acquisition part is composed of a digitizer for transforming the acquired analog data to digital data, an amplifier for amplifying the recording signals from patched neurons and a computer for data storage.

The open tip resistances of glass pipettes were about 2.0~3.5 M Ω in KCl based internal solution. Cells were whole-cell voltage clamped at -70 mV with the amplifier under control of the Clampex program. Currents were low-pass filtered at 2 or 5 kHz and stored at either 10 or 20 kHz. The series resistance was compensated to 70–80 %. Only cells with series resistances below 10 M Ω were analyzed.

2.3.5.2 Viral transfection on syt knock out neurons

After about 10 day's culture, neurons usually show prominent EPSC response. EPSC time course difference between WT and sytKO neurons helps distinguish the genotypes of plated neurons at this period.

The viruses were activated with 100 μ l α -chymotrypsin for 30 min and then inactivated with addition of 100 μ l Aprotinin to the mixture. Virus solution was added into culture plate 12~18 hours before starting electrophysiological recording. The fluorescence intensity of infected neurons (due to the expression of EG(Y)FP in virus constructs) indicated the infection efficiency and only those cells with bright fluorescence were recorded.

2.3.5.3 EPSC synchronous and asynchronous components analysis

The EPSC time course has two distinct components, which indicate the heterogeneous vesicular release modes: synchronous and asynchronous release. To quantify the amplitude of the components and their time constants, EPSC is integrated to show the charge accumulation. Double exponential curve fit was performed to acquire those parameters. The formula of double exponential is listed below:

$$A = A_{\text{total}} + A_0 * \exp(-t / \tau_s) + A_1 * \exp(-t / \tau_{\text{as}})$$

2.3.5.4 Readily releasable pool (RRP) size and vesicular release probability (Pvr) definition

RRP size of a neuron can be quantified by hypertonic solution stimulation, while the mechanism of it is not clear, maybe because high osmotic pressure decrease membrane fusion energy barrier (Rosenmund C and Stevens CF, 1996). As to the Pvr, it is defined as following:

$$\text{Pvr} = \text{EPSC charge} / \text{RRP charge}$$

The patched neuron was voltage clamped at -70 mV with a constant external solution flowing (~ 1 ml/min). A single evoked response preceded 4 s 500 mM sucrose application with an interval of 3 s. The charge of the single response and

the charge of transient invert current by sucrose are quantified as EPSC charge and RRP charge respectively (Fig. 2.2).

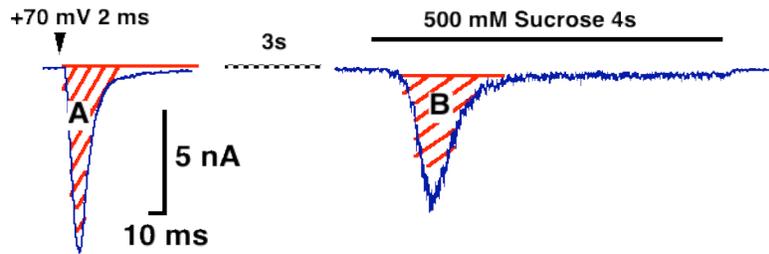


Figure 2.2 Definition of EPSC charge and readily releasable pool (RRP) size. As shown on the left, EPSC charge is calculated as the area A in red shadow; RRP size defined with 500 mM sucrose stimulation is calculated as the area B in red shadow (right side).

2.3.5.5 Evoked response recovery after RRP depletion

After hypertonic solution depleting the RRP, some reserve pool vesicles in the presynaptic terminal are thought to become fusion competent, refilling the RRP. During the RRP recovering period, action potential (AP) evoked response recovers gradually simultaneously.

To measure the EPSC recovery after RRP depletion, the experimental design was shown in Fig. 2.3. The first action potential (AP) evoked response preceded 4 s 500 mM sucrose application for RRP depletion. After that, various time intervals (ΔT s, 200 ms, 400 ms, 800 ms, 1 s, 2 s... etc.) were generated before the second action potential was initiated. The 2nd AP evoked EPSC charge was normalized to the 1st EPSC, representing the EPSC recovery.

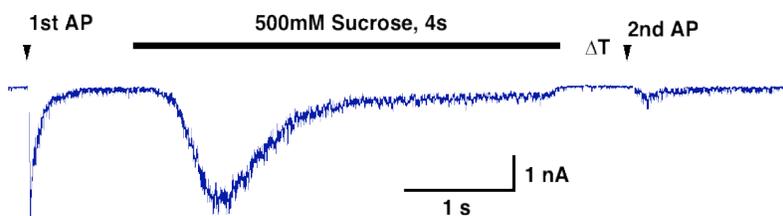


Figure 2.3 Experimental design for EPSC recovery measurement after RRP depletion in *sytko* neurons.

2.3.5.6 Short term plasticity (STP) of neurons

A consecutive AP stimulation in high frequency usually will change the synaptic transmission efficiency, for instance, increasing or decreasing vesicular release probability, vesicular release becoming more asynchronous or more synchronous, etc. All these are called the short-term plasticity of neurons. An investigation of neuronal STP can provide information for the working efficiency of those molecules involved in this process (for review, Zucker R and Regehr WG, 2002).

Neuronal STP was generated with a 10 Hz AP trains for 5 s. The individual evoked EPSC amplitude was normalized to the first response during the train and the time course of the normalized EPSC amplitudes were plotted (Fig. 2.4).

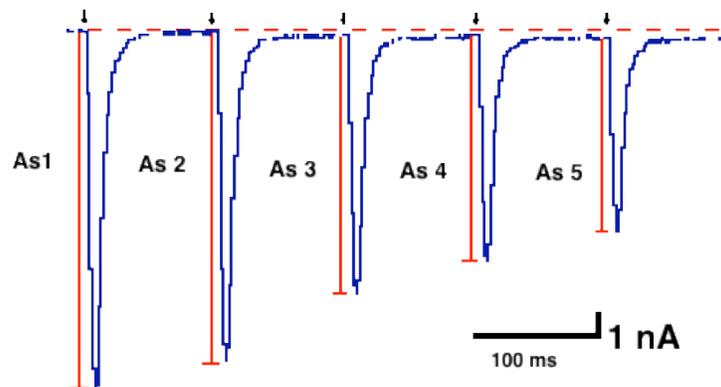


Figure 2.4 The EPSC amplitude measurement for quantifying STP. Arrow represents stimulation; As_i ($i=1,2,3\dots$) is the amplitude of the i th EPSC.

2.3.5.7 Spontaneous vesicular release analysis

In the presence of 300 nM TTX in external solution, the Na^{2+} channels required for firing APs were completely blocked. The recorded events represent the spontaneous vesicular release or miniature EPSC. To determine spontaneous vesicular release rate, 50 consecutive sweeps of 2 s recording were performed.

For data analysis, first of all, a standard mEPSC template with variable amplitude was defined. Its rise time (80% of the amplitude) was set as 0.5ms and exponential decay time constant as 3ms. The Detection criterion is calculated from the template scaling factor (Scale, peak amplitude of the event), and from the goodness-of-fit (SSE, the sum of squares for error) between the scaled template and the data, which is defined as the following:

$$\text{Detection} = \text{Scale} / \sqrt{\text{SSE} / (N-1)}$$

Where, sqrt, square root function

Since $\sqrt{\text{SSE}/(N-1)}$ approximates the noise standard deviation, the detection criterion is related to the signal-to-noise ratio for the detected events. Usually, Detection is set as 3.5, a reasonable threshold for events with a significant deviation from the noise (Fig. 2.5 A). The mean EPSC was calculated by averaging all detected events (Fig. 2.5 B). The mini rate was the frequency of events occurring, which was calculated as the following:

$$F_{\text{mepsc}} = \text{Number of events} / \text{recording time scale (100s)}$$

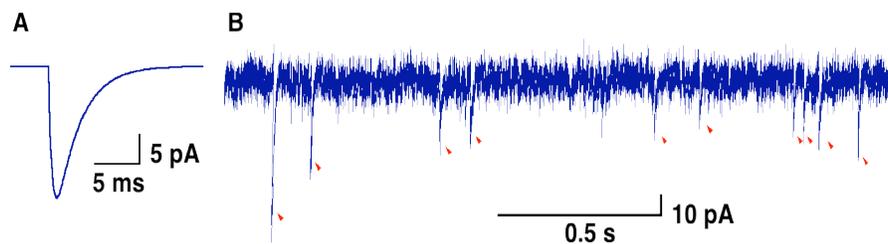


Figure 2.5 mEPSC analysis A. The template mEPSC given by exponential function; B Events detected with the mEPSC template in a sweep of 2s recording (Red arrows point out those detected events).

2.3.5.8 Apparent Ca^{2+} sensitivity measurement

Vesicle release efficiency upon Ca^{2+} influx is greatly affected by the Ca^{2+} sensitivity of the Ca^{2+} sensor(s). The direct method measuring presynaptic Ca^{2+} concentration at the release site is not available in hippocampal neurons.

However, apparent Ca^{2+} sensitivity can be detected using various external Ca^{2+} concentrations.

EPSCs under normal external solution (in mM, 4 Ca^{2+} , 4 Mg^{2+}) were recorded before and after certain Ca^{2+} concentration solution application; 6 to 9 traces were recorded in each condition (Fig. 2.6).

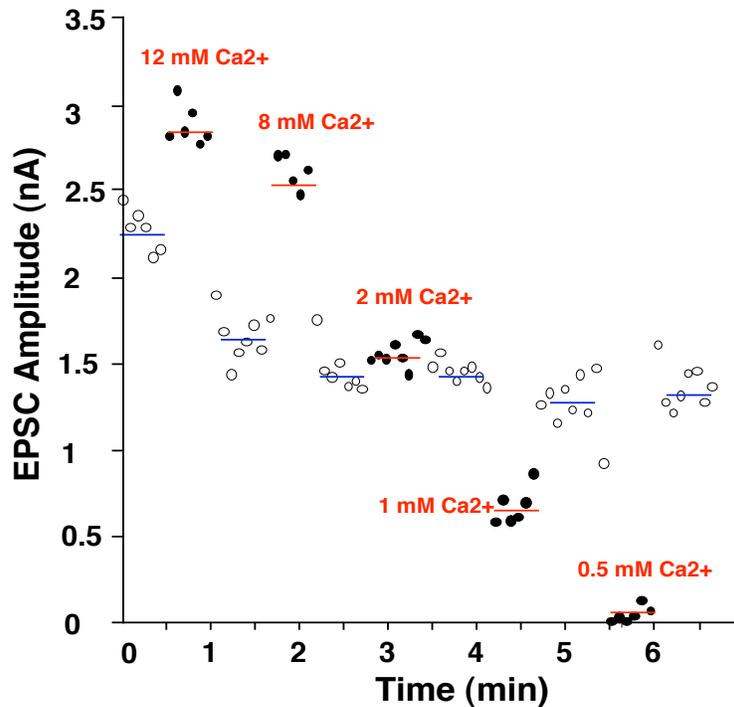


Figure 2.6 EPSC amplitudes in various external Ca^{2+} concentrations recorded from a single neuron. Circle dots represent EPSCs in control solution (4 mM Ca^{2+} , 4 mM Mg^{2+}) and filled dots represent external solution with various Ca^{2+} concentrations (0.5, 1, 2, 8, 12 mM Ca^{2+} , in presence of 1 mM Mg^{2+}). Blue dashed bars are mean control responses and red dashed bars are mean values of EPSC in different Ca^{2+} concentrations.

The mean value of blue dashed bars before and after EPSC amplitude in certain Ca^{2+} concentration is defined as the control EPSC amplitude. EPSC amplitude in certain Ca^{2+} concentration (red dashed bar value) is normalized to the control

amplitude, and is plotted against external Ca^{2+} concentrations. Data points are fitted with Hill equation:

$$Y=Y_{\max}/(1+(K_d/[\text{Ca}^{2+}])^n)$$

Here K_d is the Ca^{2+} dissociated constant; $[\text{Ca}^{2+}]$ is the external Ca^{2+} concentration; n is the Ca^{2+} cooperativity.

2.3.6 Data analysis and experimental bias minimization

Cultured neurons show a relatively high variability in EPSC and RRP size measurement due to variable geometry of microdots and the number of synapses formed. Additionally, the value of these parameters will increase with neuronal culture days *in vitro* due to the increase in synapse number. To resolve this variability problem, I usually recorded more than 15 neurons for one parameter, and collected similar number of cells in the control and the test group per day. Neuronal recording is restricted in 10th –16th days' culture *in vitro*, unless it is noted in the text. For other parameters, such as vesicular release probability, I found that it is less sensitive to neuronal development (Fig. 3.3B).

For the comparison of two groups of data to determine whether they are likely to have come from the same underlying population that have the same mean value, unequal variance Student's t-test (two-tailed distribution) was performed. For comparison of more than two groups of data, Kruskal-Wallis (KW) nonparametric ANOVA test was performed to give a conservative estimation whether the difference in groups is significant. Based on the KW nonparametric test results, Dunn's multiple comparisons test specifies the pairs of groups with significant difference.

3. Results

The functional significance of synaptotagmin 1 (syt or syt1) for exocytosis has been depicted both in the *Drosophila* and Murine systems by knock out techniques. In *Drosophila* neuromuscular junctions, the vesicular neurotransmitter release was severely impaired by eliminating of syt (Littleton JT, et al., 1993). In the Murine central neuronal synapses, the lack of syt leads to much slower time course of evoked response (Geppert M, et al., 1994).

This study consists of two parts, namely: A) a detailed analysis of the phenotype of syt knock out (sytKO) hippocampal neurons by evaluating the effect of syt in Ca^{2+} evoked response. Furthermore, additional parameters were also examined, such as, the readily releasable vesicle pool (RRP), evoked response recovery after RRP depletion, apparent Ca^{2+} sensitivity and presynaptic Ca^{2+} buffering effect. B) an in depth structure/function study of syt using a viral rescue approach to overexpress exogenous syt carrying amino acid mutations in sytKO neurons.

3.1 Basic characterization of sytKO hippocampal neurons

3.1.1 Neonatal features of sytKO mice

The sytKO mouse strain was generated in Prof. Thomas C. Sudhof's lab. The behavior phenotype of these mice has been previously described (Geppert M, et al., 1994) and my observation of the mice is in full agreement with the description. The following is a brief characterization of the sytKO phenotype:

The sytKO mice delivered by syt +/- parents usually die on the first day of birth. As described in section 2.3.3, the newborn pups lacking syt were characterized by an absence of milk in stomach and a morphologically smaller size as

compared to their syt heterozygous or wild type littermates. No evident morphological dysfunction in neuronal development has been observed in cultured hippocampal neurons due to knocking out syt.

3.1.2 Postsynaptic response (PSC) time course of the excitatory and inhibitory sytKO hippocampal neurons

In order to examine the function of presynaptic proteins, such as syt, the initial test is to verify whether the evoked vesicular release in central neurons is affected by removal of this protein.

Using standard whole-cell patch clamping mode, parallelly cultured sytKO and wild type neurons were stimulated with a 2 ms, 70 mV membrane depolarization pulse at a frequency of 0.2 Hz and the subsequent somatic excitatory postsynaptic current (EPSC) was recorded (Fig. 3.1 Left). The delayed EPSC response in syt null neurons is consistent with the previous report (Geppert M, et al., 1994), but the characteristics of evoked response in inhibitory hippocampal neurons was not examined previously.

The same experiment was performed in inhibitory hippocampal neurons. Interestingly, the evoked inhibitory postsynaptic current was also slower (Fig. 3.1 right).

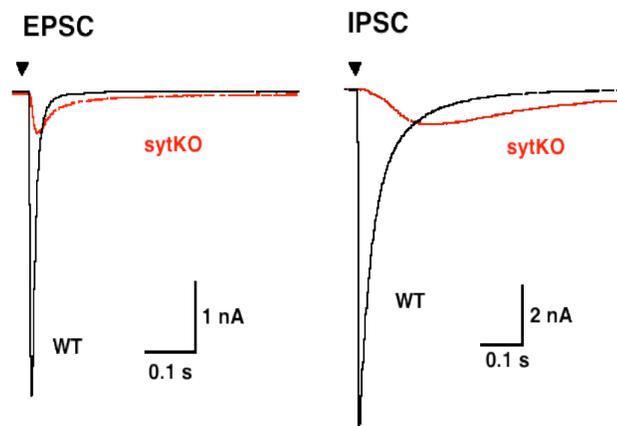


Figure 3.1 PSC traces recorded from excitatory and inhibitory neurons reveal slower time course by knocking out syt. (Black arrows indicate the depolarization pulse)

The one second PSCs cumulative charges were fitted with double exponential equation (section 2.3.5.3) and the time constants of two components in each type of hippocampal neurons are listed in the following table:

Table 3.1 Time constants of the components of PSCs

Hippocampal neurons	τ_{fast} (ms)	τ_{slow} (ms)
WT excitatory	~7	~170
sytKO excitatory	~38	~310
WT inhibitory	~36	~150
sytKO inhibitory	~69	~600

The slower evoked response of both types of hippocampal neurons by knocking out syt suggests that syt has a similar function in these neurons. Furthermore, these data show that both the fast and slow components of the evoked response are slowed down by knocking out syt in hippocampal neurons, indicating that syt may play a role not only in the synchronous release but also in the asynchronous release. In the following studies, most experiments were performed on excitatory hippocampal neurons unless otherwise indicated.

3.1.3 The evoked vesicular release and the readily releasable pool (RRP) in sytKO neurons

Evoked vesicular release efficiency is determined both by the vesicular release speed and the amount of released vesicles. Knocking out syt leads to slower vesicular release as shown in above section, whether the number of released vesicles is altered or not is not clear. In order to clarify this question, the charges of EPSC from parallel wild type and sytKO neuronal culture were compared.

The EPSC traces from both groups were integrated in a period of 1 s and the cumulative charges were calculated. Clearly there is a gradual increase in EPSC charge during neuronal development in both sytKO and WT neurons (Fig. 3.2 A) and the evoked response of sytKO neurons is smaller than that of WT ones throughout the days of measurement. The average EPSC charge for WT (from the 8th to 14th day) is 55.1 ± 4.1 pC (n=93) and for sytKO neurons is 19.7 ± 2.5 pC, (n=89) (t-test $p < 0.001$, Fig. 3.2 B). By fitting the EPSC time course with the double exponential equation, the amplitude of each component for sytKO is $Q_{\text{fast}} = 9.3 \pm 1.1$ pC and $Q_{\text{slow}} = 11.3 \pm 1.4$ pC; while for the WT the values are $Q_{\text{fast}} = 55.2 \pm 3.9$ pC and $Q_{\text{slow}} = 5.7 \pm 0.5$ pC. This shows mainly a reduction in the fast component amplitude together with an increase of slow component amplitude in sytKO neurons. Additionally, no change in either amplitude or frequency of miniature EPSCs was found in sytKO neurons compared to WT neurons throughout the neuronal development (data not shown). This suggests that the reduction of evoked release is neither due to defects of postsynaptic receptors nor contents of vesicles ready for fusion in sytKO neurons.

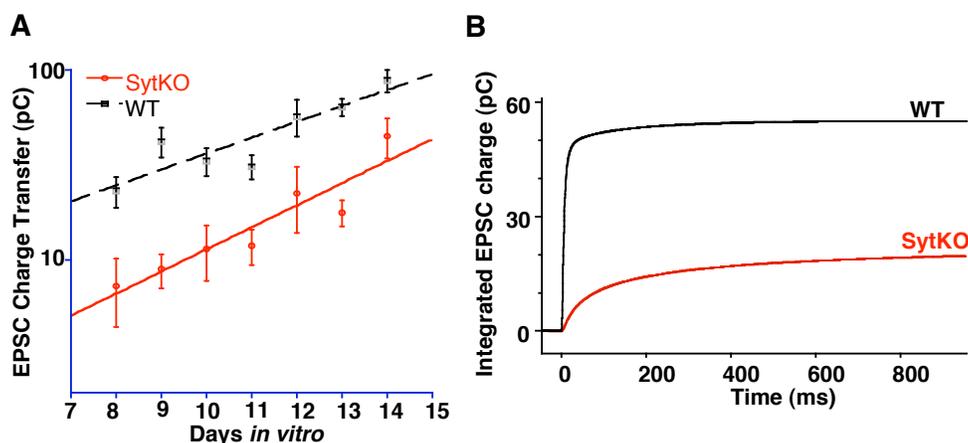


Figure 3.2 Parallel comparison of EPSC charge recorded from the sytKO and the WT hippocampal neurons. A, Developmental increase of EPSC charges of the sytKO and the WT neurons. Data were fitted with single exponential equation. Cells were recorded from the 8th to 14th days after neuronal culture and each data point is the mean value of 10-15 cells. (Student's t-test indicates that EPSC charge of sytKO neurons is significantly different from that of WT neurons in each day's comparison. For 8th, 9th, 10th, 11th and 13th day, $p < 0.001$ and for 12th, 14th day, $p < 0.05$) B, The average integration of EPSC charges of the sytKO and the WT neurons (WT $n=93$ and sytKO $n=89$, data from one batch of neuronal culture).

To rule out the possibility that the reduction of EPSC charge is due to a defect in other steps of vesicle recycling preceding exocytosis, such as vesicular priming, vesicular refilling, the RRP size was quantified by hypertonic solution application.

A 4s pulse of 500 mM sucrose was applied to the patched neuron and the transient inward current was measured. No difference in RRP size was found between sytKO neurons and WT neurons (Fig. 3.3 A). The mean RRP size of the sytKO neurons was 451 ± 46 pC, $n=83$, and the mean value for the WT neurons was 471 ± 39 pC, $n=90$. Student's t-test suggests no difference of RRP size between sytKO neurons and WT neurons in each day's comparison. The similar RRP sizes calculated from these two groups suggests that the EPSC charge reduction in sytKO neurons is not due to a shortage of fusion competent vesicles.

Since both EPSC charge and RRP size will increase along with the neuronal development (Fig. 3.2 A and 3.3 A), the variance of these values is relatively high, which makes the comparison between sytKO and WT neurons become less reliable with development. The vesicular release probability (Pvr) of each type of neurons was calculated by normalizing EPSC charge to RRP size to consolidate the above findings (Fig. 3.3 B). The relative constant Pvr in each individual day of measurement suggests that there is a reduction of release efficiency in sytKO neurons compared to WT neurons.

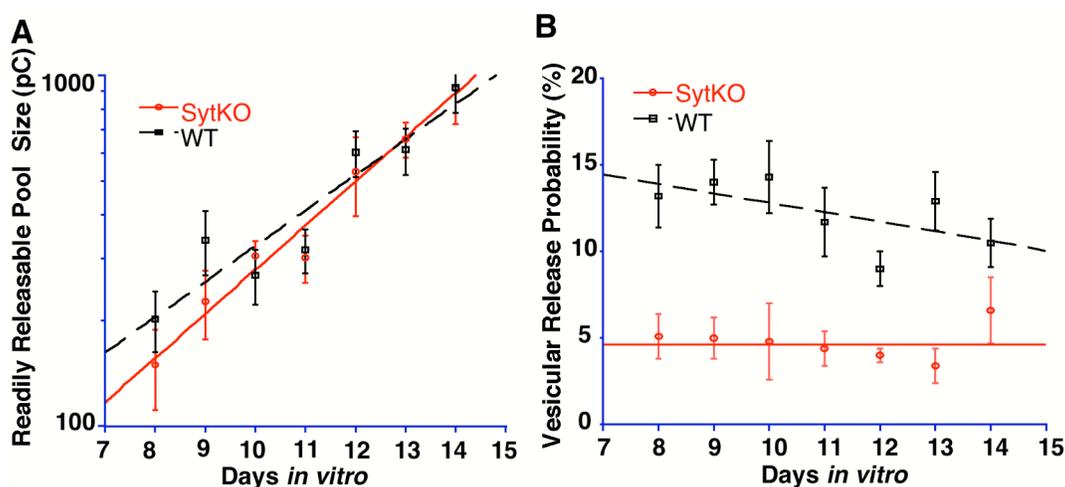
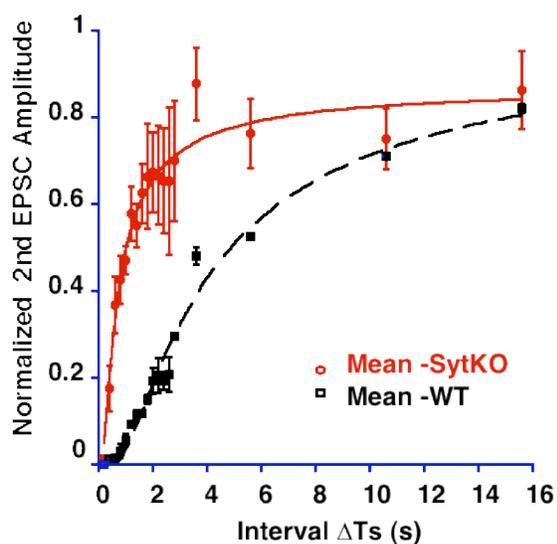


Figure 3.3 RRP size and Pvr comparison between sytKO and WT neurons. A) Unchanged RRP size in sytKO neurons compared to WT neurons (Data were fitted with single exponential equation.); B) Neuronal development independent Pvr in sytKO and WT neurons. Each data point represents the mean value of 10-15 cells (Student's t-test suggests that Pvr of sytKO neurons is significantly different from WT neurons in each day's comparison (except the 14th day), $p < 0.01$) Data were from one batch of neuronal culture and fitted with linear equation).

3.1.4 EPSC recovery following Ca^{2+} independent RRP depletion in sytKO neurons

Since knocking out syt mainly reduced the amount of evoked fast vesicular release without affecting the total number of the fusion competent vesicles in all synapses, sytKO neurons is a very good model to study the characteristics of the slower release (so called, asynchronous release). Different fusion competent vesicles release modes in sytKO and WT neurons may be based on different refilling kinetics. Based on this rationale, the EPSC recovery after vesicle pool depletion was measured as described in section 2.3.5.5.

Figure 3.4 the recovery of EPSC after RRP depletion in sytKO neurons and WT neurons (sytKO n=10, WT n=3). (Data were collected from 16-day old sytKO neurons and 11-day old WT neurons respectively.)



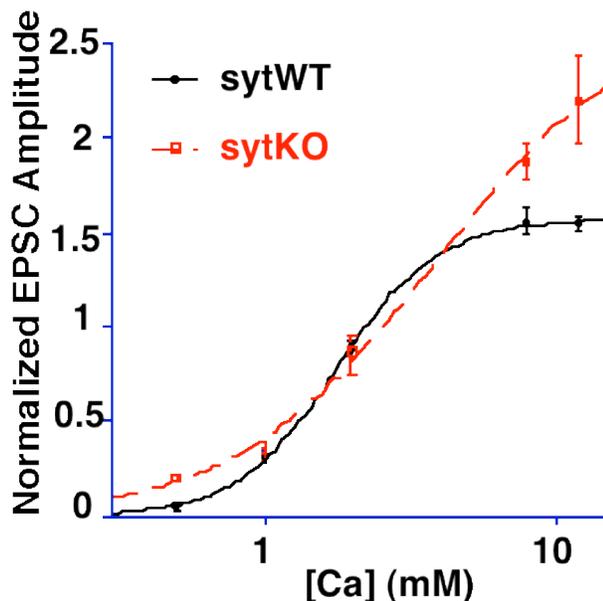
As shown in Fig. 3.4, the EPSC recovery after RRP depletion developed faster in sytKO neurons than in WT neurons. By fitting these data with a single exponential equation, τ_{sytKO} was 0.57 s and τ_{WT} was 3.4 s. Since the evoked vesicle release in sytKO neurons is predominantly asynchronous, the faster recovery observed above may imply that the asynchronous vesicles have a faster refilling rate than the synchronous vesicles. However, the data were recorded from cultures with different day *in vitro* and the number of WT neuron is small, so this interesting finding needs further confirmation.

3.1.5 Different Ca^{2+} sensing properties of fusion competent vesicles between WT and sytKO neurons

3.1.5.1 Decreased apparent Ca^{2+} sensitivity by knocking out syt in hippocampal neurons

The reduction of evoked responses in sytKO neurons (Fig. 3.2) may be due to decreased Ca^{2+} sensitivity of the vesicles in the absence of syt. To evaluate this possibility, the apparent Ca^{2+} sensitivity was measured in sytKO neurons. By varying the exogenous Ca^{2+} concentration and studying its effect on vesicular release efficiency, one can elucidate the possible role of syt in Ca^{2+} sensing for exocytosis.

Figure 3.5 Apparent Ca^{2+} sensitivity of sytKO neurons and sytWT rescued neurons. (Data were fitted with Hill equation, Ca^{2+} cooperativity for sytKO, 1.3 ± 0.2 , $n=6$; sytWT 2.5 ± 0.1 , $n=16$)



As shown in Fig 3.5, by fitting the Ca^{2+} dose response data with the Hill equation, the K_d of Ca^{2+} for sytWT rescued neurons is 1.8 ± 0.04 mM (similar to a previous report in WT hippocampal neurons, $K_d = 1.9 \pm 0.2$ mM, Fernandez-Chacon R, et al., 2001) and for SytKO is 3.8 ± 1.2 mM. By knocking out syt, the apparent Ca^{2+} sensitivity was decreased about two fold, which explains the low release efficiency in sytKO neurons compared to WT cells.

It is important to take into consideration certain factors that may affect accuracy of the apparent Ca^{2+} sensitivity measurement. The first factor is that 12 mM Ca^{2+}

cannot saturate the EPSC response in sytKO neurons. Ideally it will be better to measure the EPSC response in a higher Ca^{2+} concentration (i. e. 16 mM Ca^{2+}) to generate a correct fit for these data. Since high Ca^{2+} concentration can cause the reduction of the excitability of the axon and thereby negatively affect the EPSC response due to poor action potential propagation. Therefore the recordings become more unreliable by increasing Ca^{2+} concentration. Second, the data set is from one culture of neurons, to consolidate the finding, another set of experiment would be desirable.

3.1.5.2 Inhibition of vesicular release with pipette injection of EGTA in sytKO neurons

Synchronous release and asynchronous release are thought to be regulated by different Ca^{2+} sensors (Goda Y and Stevens CF, 1994). It has also been suggested that these two components are dominated by the distance of vesicles from Ca^{2+} channels (Neher E, 1998). Vesicles located closer to Ca^{2+} channels experience a rapid Ca^{2+} transient rise, thus they will be released synchronously; The longer time for Ca^{2+} diffusion to reach those vesicles located further from Ca^{2+} channels helps explain the asynchronous release.

EGTA is a widely used Ca^{2+} binding buffer. When a high concentration of EGTA is applied to presynaptic terminals, it causes a narrower range of Ca^{2+} diffusion from the Ca^{2+} channels, together with a competition against Ca^{2+} sensor to bind to Ca^{2+} ions.

To understand the mechanism of synchronous and asynchronous release, the experiment of EGTA (1 mM or 50 mM) injection via patch pipette was performed. After patching a cell, EPSCs were recorded with 0.2 Hz stimulation for 10 min in both sytKO and WT neurons. Every five consecutive EPSC responses were averaged as one data point shown in the Fig 3.6.

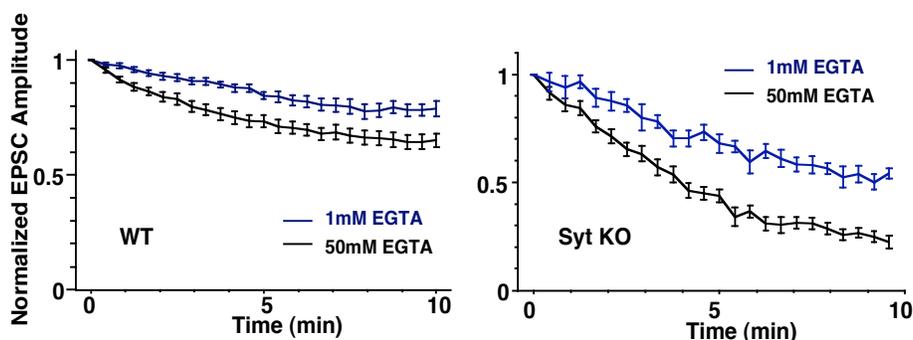


Figure 3.6 Pipette injected EGTA inhibits evoked neurotransmitter release. (For WT, 1 mM EGTA n=14, 50 mM EGTA n=19; For sytKO, 1 mM EGTA n=13, 50 mM EGTA n=15)

The inhibition of neurotransmitter release in the sytKO neurons is stronger than the WT neurons under 1 mM/ 50 mM EGTA condition, which indicates that asynchronous release is more easily inhibited by EGTA compared to synchronous release.

The reduction of EPSC by a high concentration of EGTA in the sytKO neurons may be due to either buffering the Ca^{2+} transient during its diffusion to releasable vesicles or shorter onset time for Ca^{2+} binding EGTA comparing to unknown Ca^{2+} sensor on vesicles. If we can find another Ca^{2+} buffer, which has similar Ca^{2+} onset time as EGTA but lower Ca^{2+} affinity, then perhaps the mechanism can be better explained.

An alternative explanation can be that asynchronous released vesicles have lower Ca^{2+} sensitivity compared to synchronous released vesicles (section 3.1.5.1). When high concentration of EGTA exists in the presynaptic terminals, the asynchronous released vesicles that need high concentration of Ca^{2+} to release will be affected more severely than the synchronous released vesicles that can detect lower Ca^{2+} concentration.

3.2 Functional/structural analysis of syt by over-expressing syt mutants in sytKO neurons

The transfection of the cultured sytKO hippocampal neurons with Semliki forest virus (SFV) carrying wild type syt construct can restore sytKO EPSC time course to wild type level (Han WP, et al., 2004). The physiological function of syt can be studied in detail by taking the advantage of the rescue approach.

The experimental design for this study was initiated in 2002, when there were few reports about the functions of syt using murine neurons as a model. The mechanism of action of syt in exocytosis was better illustrated with the progress of this project and the fast development of relevant studies in this field (Stevens CF and Sullivan JM, 2002; Nishiki T and Augustine GJ, 2004b). Although during my study period, other labs have reported some findings of syt by similar approach, the parameters that I have examined are not completely overlapped.

The experimental design for syt functional study is to try to reveal the residues crucial for the functions of syt by using site directed mutagenesis. (A) Since syt is a protein with two Ca^{2+} binding domains in the cytosolic part, truncation of either C_2 domain to evaluate the loss of function of syt can be the starting point to reveal the importance of the C_2 domain for the function of syt. (B) To gain deeper insight of the function of syt, those aspartates in either C_2 domain which have been shown to be important for Ca^{2+} dependent syt-phospholipid interaction in *in vitro* biochemical studies (Zhang X, et al., 1998; Davletov B, et al., 1998; Ubach J, et al., 2001; Fernandez I, et al., 2001) were neutralized. Additionally, this can be helpful to reveal the physiological importance of syt-phospholipid interaction. (C) The hydrophobic residues in the top Ca^{2+} binding loops (Loop 1 and 3) of the two C_2 domains, which have been reported to insert into phospholipid membrane in *in vitro* studies (Chapman ER and Davis AF, 1998; Bai J, et al., 2002) were investigated by mutating them to the bulky hydrophobic amino acid, tryptophan,

to test whether a gain of function mutant can be acquired. This study can give further implications on the physiological importance of syt-phospholipid interaction. (D) It has been shown that the polybasic region of the C₂B domain interacts with multiple molecules (Chapman ER, et al., 1998). Therefore by neutralizing these basic residues to abolish the interactions, one can evaluate whether these interactions, especially syt self-oligomerization, are essential for synaptic transmission. (E) Finally, a study of syt1/7 chimera constructs was performed, which not only shed some light on the physiological functions of the C₂ domains of syt7, but also gave hints on the physiological importance of the C₂ domains of syt1.

3.2.1 The importance of the two C₂ domain of syt

Semliki forest virus carrying full length syt or syt lacking either C₂ domain was transfected in cultured autaptic sytKO neurons. The direct evaluation of these constructs is via the EPSC amplitude and time course of release. The RRP size quantified by hypertonic solution application is also a good parameter for revealing their functions.

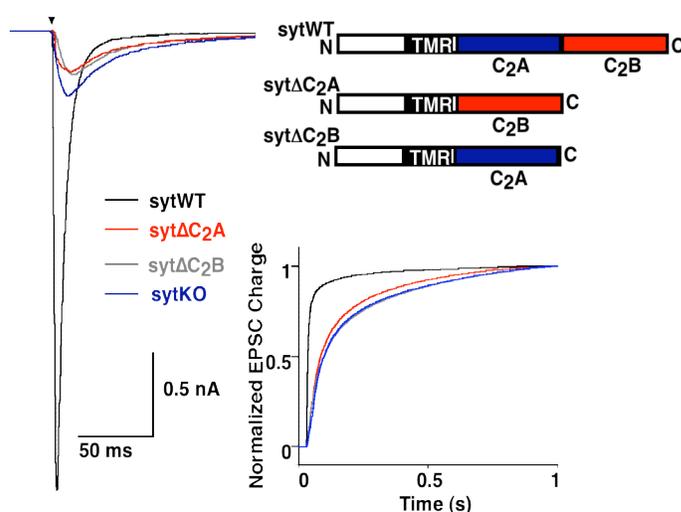


Figure 3.7 EPSC traces of sytKO neurons rescued with sytWT, syt C₂A fragment (sytΔC₂B) or syt C₂B fragment (sytΔC₂A). Insert shows the EPSC time course of different mutants. Black arrow represents the 2 ms, +70 mV depolarization of the neuron. (Subsequent figures will mainly use integrated EPSC curve to emphasize the time course of release, which is the major factor in revealing the function of syt.)

Constructs transfected in sytKO neurons with loss of either C₂ domain failed to rescue fast neurotransmitter release (Fig. 3.7). The total evoked EPSC charge of truncated constructs was reduced to about 50% of that in sytWT rescues (sytWT 22.7 ± 2.4 pC, n=49; sytΔC₂B 13.8 ± 1.4 pC, n=57; sytΔC₂A 12.0 ± 2.4 pC, n=53; sytKO 19.6 ± 1.7 pC, n=52). These indicate that both C₂ domains are indispensable for syt fulfilling its function.

Hypertonic solution was used to quantify the RRP size of these mutants, as shown in Fig 3.8 A. Deletion of the C₂A domain leaves the RRP size unchanged (sytΔC₂A compared to sytKO), while any syt rescue constructs containing the C₂A domain reduced the RRP size to about 60% (sytΔC₂B 315 ± 38 pC; sytWT 260±25 pC; compared to sytKO 512 ± 48 pC). This suggests that overexpression of the C₂A domain of syt can reduce RRP size. In Fig 3.8 B, the vesicle release probability (P_{vr}), as calculated by normalizing EPSC charge to RRP size, is increased more than two fold if sytKO neurons are rescued with sytWT construct (sytKO 4.3 ± 0.4%; sytWT 9.5 ± 0.7%), but neurons transfected with truncated syt constructs have smaller P_{vr} than sytWT rescued neurons (sytΔC₂B 6.8 ± 0.7%; sytΔC₂A 3.1 ± 0.7%).

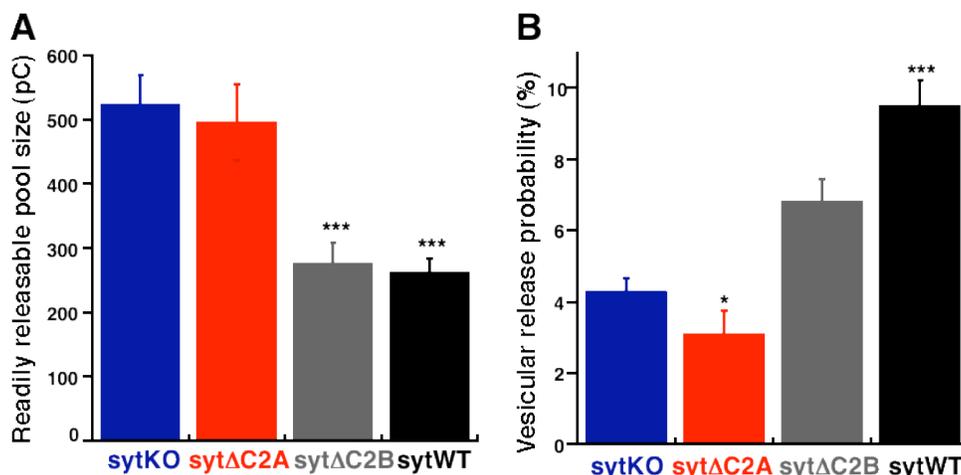


Figure 3.8 A. RRP size of the syt truncated mutants or sytWT rescued neurons and sytKO neurons (***) indicates KW nonparametric test and Dunn's multiple comparison test, $p < 0.001$, each rescue compared to sytKO neurons; B. Vesicular release probability (Pvr) of three constructs rescued neurons compared to sytKO neurons (* and *** indicate KW nonparametric test and Dunn's multiple comparison test, $p < 0.05$ and $p < 0.001$ respectively; t-test shows that the Pvr of sytΔC₂B rescue is significantly different from that of sytWT rescue, $p < 0.05$). sytKO $n = 52$, sytΔC2A $n = 53$, sytΔC2B $n = 55$, sytWT $n = 49$. Data are collected from three batches of neuronal cultures.

It is important to note that sytWT rescued neurons have similar EPSC charge as sytKO neurons (sytWT 22.7 ± 2.4 pC, $n = 49$ and sytKO 19.6 ± 1.7 pC, $n = 52$), which seems inconsistent with the finding in section 3.1.3, where the EPSC charge of sytKO neurons is much smaller than that of WT ones (Fig. 3.2). However, the reduction of RRP size in sytWT rescued neurons compared to sytKO neurons (Fig. 3.8 A) explains this discrepancy, because in section 3.1.3, the RRP size of WT neurons is similar to that of sytKO neurons (Fig. 3.3). The viral overexpression of sytWT leads to reduced EPSC charge and RRP size, but has no significant effect on the vesicular release probability (sytKO $4.8 \pm 0.5\%$, $n = 83$ and WT $12.2 \pm 0.6\%$, $n = 90$ in section 3.1.3; sytKO $4.3 \pm 0.4\%$, $n = 52$ and sytWT $9.5 \pm 0.7\%$, $n = 49$, in this section).

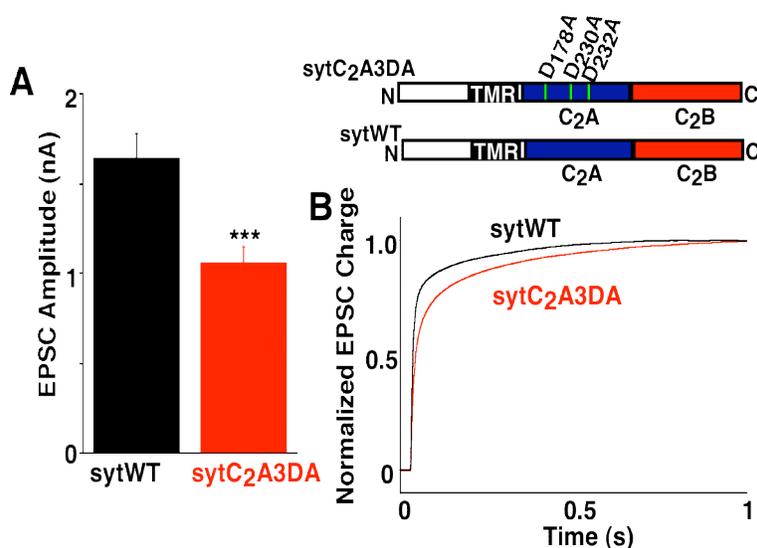
3.2.2 Differential roles of the Ca^{2+} binding sites in two C_2 domains for fast vesicular release (partial contribution from Jeong Seop Rhee)

Each C_2 domain has five Asp residues in the top loop1 and 3 that contribute to the Ca^{2+} mediated phospholipid binding (Shao X, et al., 1996). Neutralizing the 2nd to 4th Asp residues in the C_2A domain ($\text{D}_{172, 230, 232}\text{A}$) or the corresponding Asp residues in the C_2B domain ($\text{D}_{303, 363, 365}\text{A}$) decreases the Ca^{2+} dependent syt-phospholipid interaction *in vitro* (Ok-Ho Shin, personal communication). To evaluate the consequence of these mutations in physiological conditions, the following experiments were performed.

3.2.2.1 Neutralizing the 2nd, 3rd and 4th Asp to Ala in the C_2A domain (Abr. syt $\text{C}_2\text{A3DA}$)

Syt $\text{C}_2\text{A3DA}$ rescued sytKO neurons produces fast synaptic response like sytWT, but the statistics showed about a 40% reduction in EPSC amplitude of this mutant (sytWT 1.64 ± 0.14 nA; syt $\text{C}_2\text{A3DA}$ 1.05 ± 0.09 nA). By comparing the normalized cumulative EPSC charge of sytWT and syt $\text{C}_2\text{A3DA}$ rescued neurons, the latter has a relatively higher asynchronous release component (Fig. 3.9).

Figure 3.9 Basic EPSC characteristics of syt $\text{C}_2\text{A3DA}$ mutant. A. EPSC amplitudes of sytWT and syt $\text{C}_2\text{A3DA}$ rescued neurons (sytWT n=58; syt $\text{C}_2\text{A3DA}$ n=82, data were collected from 5 batches of neuronal cultures and *** indicates t-test $p < 0.001$). B. Normalized cumulative EPSC charge in a period of 1 s.



The RRP size and vesicular release probability of the rescued *sytKO* neurons were also quantified and Student's t-test showed no significant differences between *sytC₂A3DA* and *sytWT* rescued neurons in the tested parameters (data not shown). These results suggest that the Ca^{2+} binding sites in the *C₂A* domain regulate synchronous release efficiency. Neutralizing these binding sites leads to a smaller synchronous release but larger asynchronous release without affecting the total release.

3.2.2.2 Neutralizing the 2nd, 3rd and 4th Asp to Ala in the *C₂B* domain (Abr. *sytC₂B3DA*)

In contrast *sytKO* neurons transfected with *sytC₂B3DA*, a mutant that neutralizes three Asps in the *C₂B* domain, does not rescue the fast synaptic transmission. The EPSC charge is reduced to about 50% in this mutant in contrast to that of *sytWT* rescued neurons, while the RRP size was not changed. The *sytC₂AB6DA* construct, with the six Asps neutralized in both the *C₂A* and the *C₂B* domain, was tested simultaneously with the *sytC₂B3DA*. As expected, no rescue was found in the *sytC₂AB6DA* mutant and no change in either EPSC charge or RRP size compared to *sytKO* neurons (Fig 3.10).

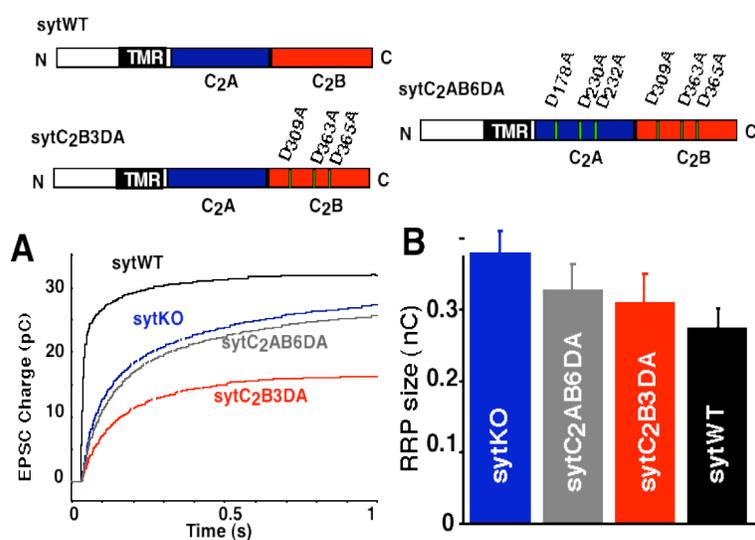


Figure 3.10 Basic characteristics of *sytC₂B3DA* and *sytC₂AB6DA* mutants. A. cumulative EPSC charge of mutants, *sytWT* rescued neurons and *sytKO* neurons. B. RRP size of neurons rescued by the constructs and *sytKO* neurons (*sytKO* n=70, *sytC₂AB6DA* n=51, *sytC₂B3DA* n=42 and *SytWT* n=64. Data were collected from 3 batches of neuronal cultures).

Since neutralization of these sites completely eliminates the fast component of EPSC, from these data, it is clearly shown that the Ca^{2+} binding sites in the C_2B domain is essential for evoked synchronous release.

In summary, although both C_2 domains can bind Ca^{2+} ions, the physiological functions of the binding sites are not equivalent. The Ca^{2+} binding sites in the C_2A domain regulate the ratio of synchronous release component and asynchronous release component without affecting the total release efficiency, while the Ca^{2+} binding sites in the C_2B domain is essential for maintaining synchronous release.

3.2.3 The role of hydrophobic residues in Ca^{2+} binding loops of the two C_2 domains (partial contribution from Jeong Seop Rhee)

There are three hydrophobic residues in the Ca^{2+} binding loops (L1, L3) of each C_2 domain, Met₁₇₃, Phe_{231, 234} in the C_2A domain and Val₃₀₄, Tyr₃₆₄, Ile₃₆₇ in the C_2B domain. Ala replacement of Met₁₇₃ residue, Trp replacement of Phe_{231, 234} residues or Cys replacement of Ile₃₆₇ residue in previous studies indicated that both domains can insert into the phospholipid membrane via Ca^{2+} binding loops (Gerber SH, et al., 2001; Chapman ER and Davis AF, 1998; Bai J, et al., 2002), although the physiological effect of this membrane insertion is unknown. To test whether syt-membrane insertion contributes to the overall function of syt in synaptic vesicular release, three constructs of syt mutants were generated (by Ok-Ho Shin): Tryptophan replacement of M₁₇₃, P_{231, 234} in the C_2A domain (sytC₂A3W), Tryptophan replacement of V₃₀₄, Y₃₆₄, I₃₆₇ in C_2B domain (sytC₂B3W) and Tryptophan replacement of all six hydrophobic residues in both C_2 domains (sytC₂AB6W). Biochemical evidence shows that all three W mutants can enhance syt-membrane interaction (Fig. 4.1).

3.2.3.1 SytC₂AB6W significantly enhances synaptic transmission

The initial analysis of evoked postsynaptic currents (EPSCs) showed that syt6W rescued fast neurotransmitter release was similar to the sytWT rescue construct. The mean EPSC amplitudes of sytWT and syt6W were comparable (sytWT 2.2 ± 0.2 nA, $n=56$; sytC₂AB6W 2.0 ± 0.2 nA, $n=46$; Fig. 3.11). This indicated that the 6W mutation did not change the overall function of syt.

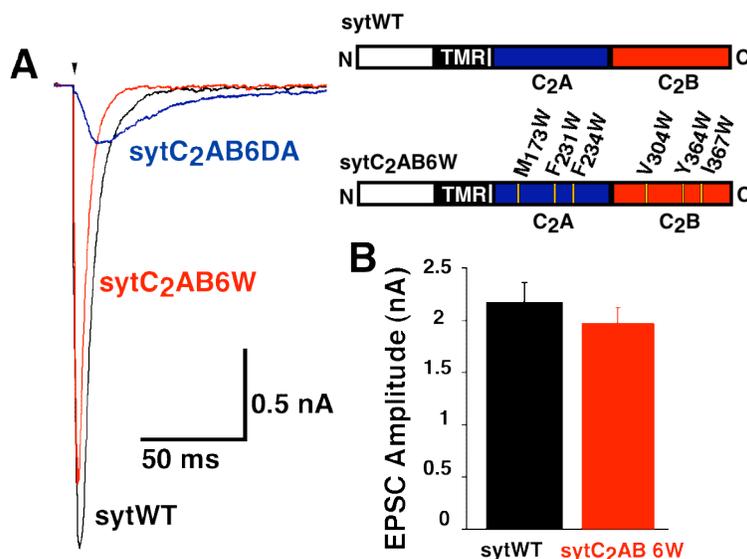


Figure 3.11 Exemplary EPSCs of sytWT and sytC₂AB6W mutant recorded in normal external solution. A. Raw EPSC traces of these two constructs and sytC₂AB6DA as a non-rescued negative control; B. Mean EPSC amplitudes of sytWT and sytC₂AB6W. Black arrow represents 2 ms, +70 mV depolarization of the neurons.

Next we specifically studied several release parameters by a side-by-side experiment comparing sytC₂AB6W and sytWT. First, we tried to answer the question of whether the sytC₂AB6W mutant could affect the synaptic transmission efficiency by varying external Ca²⁺ concentrations. As described in the section 2.3.5.8, EPSCs were recorded in 0.5-12 mM Ca²⁺ at a constant 1 mM Mg²⁺ condition and later normalized to the response amplitudes with control Ca²⁺ concentration (4 mM Ca²⁺, 4 mM Mg²⁺). A drastic left shift in the apparent Ca²⁺ sensitivity in contrast to sytWT was found. As the raw traces show in Fig. 3.12 A,

with lower external Ca^{2+} (0.5 mM), only about 50% reduction of the EPSC response in $\text{sytC}_2\text{AB6W}$ mutant compared to the barely detectable EPSC in sytWT was observed. By fitting the dose response data with a standard Hill equation (Fig. 3.12 B), we observed a decrease in Ca^{2+} cooperativity (sytWT 2.5 ± 0.1 vs $\text{sytC}_2\text{AB6W}$ 1.4 ± 0.2) as well as an approximate 3 fold increase in the apparent Ca^{2+} affinity (sytWT 1.80 ± 0.04 mM vs $\text{sytC}_2\text{AB6W}$ 0.59 ± 0.04 mM). This clearly indicates that the increasing hydrophobicity at the top loop of the C_2 domains enhances the synaptic transmission, suggesting that Ca^{2+} dependent membrane penetration is key in syt function. The decreasing Ca^{2+} cooperativity suggests that the interaction of $\text{sytC}_2\text{AB6W}$ with the membrane becomes less Ca^{2+} -dependent compared to sytWT .

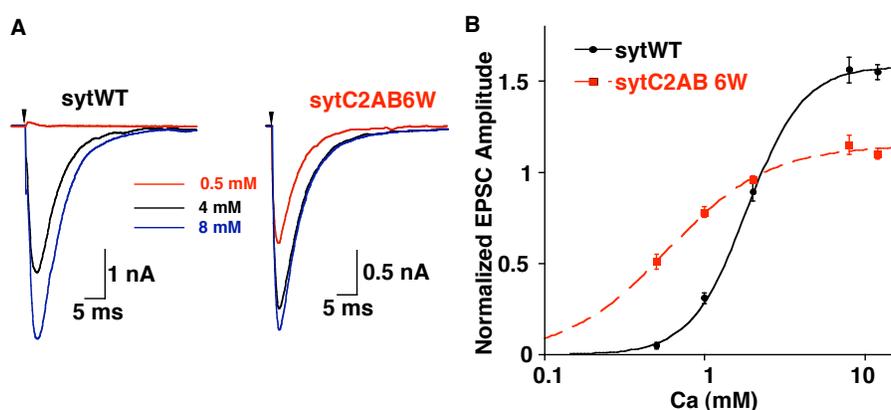


Figure 3.12 Excitatory synapses expressing $\text{sytC}_2\text{AB6W}$ mutant showed an enhanced apparent Ca^{2+} sensitivity of release. A. Exemplary EPSCs from sytWT rescues (left) and $\text{sytC}_2\text{AB6W}$ rescues (right), measured at 0.5 mM (green trace), 4 mM (black) and 8 mM external Ca^{2+} . Black arrows represent 2 ms, +70 mV depolarization of the neurons. B. External Ca^{2+} dependent EPSC responses in sytWT and $\text{sytC}_2\text{AB6W}$ rescues. Hill Equation fit indicates a three-fold increase in apparent Ca^{2+} sensitivity of evoked release in the hydrophobic top loop mutant ($\text{sytC}_2\text{AB6W}$ $n=12$, sytWT $n=18$).

An increase in Ca^{2+} sensitivity should lead to enhanced efficacy of Ca^{2+} triggered fusion and therefore to increased probability of release. To test this idea, a train of action potentials to estimate the efficiency of Ca^{2+} triggered release was performed in neurons rescued with the $\text{sytC}_2\text{AB6W}$ construct. EPSC amplitudes

during 50 consecutive action potentials applied at a frequency of 10 Hz were recorded. In general, unreliable, low release probability synapses displays facilitation, while more efficient synapses show more depression (Zucker R and Regehr WG, 2002). The sytWT rescues showed regular moderate depression of EPSC amplitudes (depression at the end of train $29 \pm 5\%$, $n=46$), and in contrast, the sytC₂AB6W mutant displayed very pronounced depression of the synaptic response ($79 \pm 2\%$, $n=46$, $p<0.01$; Fig. 3.13 A), indicating an enhanced release probability of synaptic transmission in the sytC₂AB6W mutant.

To prove that the enhanced short-term depression mutant correlates with the higher release probability in the sytC₂AB6W mutant, we measured release probability with an independent method. The vesicular release probability can be simply computed by normalizing the charge of EPSC to the charge of RRP. By comparing the sytC₂AB6W rescued neurons with those transfected with sytWT, a significant reduction of the RRP size was found (sytWT: 0.50 ± 0.07 nC, $n=44$; sytC₂AB6W: 0.29 ± 0.04 nC, $n=36$) (Fig 3.13 B). The computed vesicular release probability in the sytC₂AB6W transfected neurons was strongly enhanced (sytWT $5.6 \pm 0.7\%$, $n=44$; sytC₂AB6W: $14.1 \pm 2.6\%$, $n=36$), therefore the increase of vesicular release probability is consistent with the enhanced depression of EPSC during trains of action potentials (Fig 3.13 A).

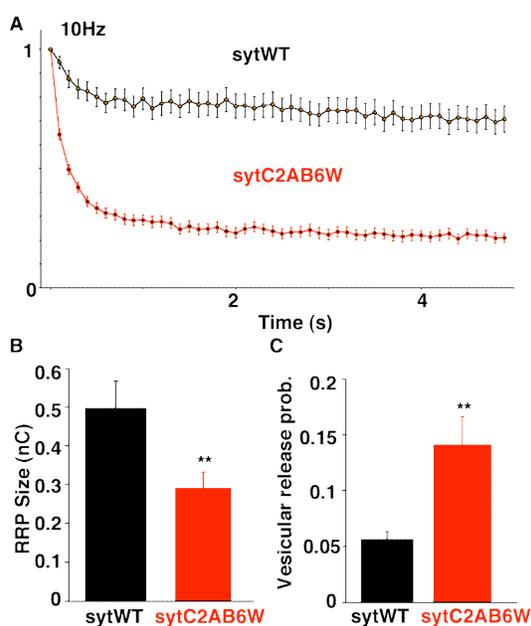


Figure 3.13 Lower release probability predicts heavier short-term depression in sytC₂AB6W mutant. A. Short-term depression of neurons rescued with sytC₂AB6W and sytWT. Each EPSC amplitude during the 10 Hz 5s stimulation train was normalized to the first EPSC response; B. Mean RRP sizes of the two constructs quantified with sucrose; C. Computed vesicular release probabilities of sytWT and sytC₂AB6W mutant. (** indicates t-test $p<0.01$)

Due to the reduction of the readily releasable vesicle pool size in the *sytC₂AB6W* mutant, which could affect Ca^{2+} independent spontaneous release, we measured mEPSC release activity in neurons rescued with *sytWT* and *sytC₂AB6W*. In our experiment, there was a higher mEPSC release rate in the *sytC₂AB6W* mutant than in *sytWT* (*sytWT* 3.2 ± 0.6 Hz, $n=25$; *sytC₂AB6W* 6.0 ± 0.6 Hz, $n=21$, Fig. 3.14 B). Although the increased mEPSC release rate may in principle contribute to depletion of the vesicle pool, the increase in spontaneous mEPSC rate is far too small to explain the 42% reduction of the RRP. Additionally, the normal amplitude and charge of mEPSCs in *sytC₂AB6W* mutant indicates the proper filling of vesicle with glutamate and no postsynaptic receptor dysfunction (*sytWT* 23.9 ± 2.3 pA, $n=25$; *sytC₂AB6W* 23.4 ± 1.3 pA, $n=21$).

3.2.3.2 SytC₂A3W and sytC₂B3W rescue study indicates that the two C₂ domains cooperate in synaptic transmission

The next question to be clarified is whether this synaptic transmission enhancement is conducted by the two C₂ domains in a redundant or additive fashion. To address this question, similar experiments were done by rescuing *sytKO* neurons with the *sytC₂A3W* and the *sytC₂B3W* constructs. If the enhanced synaptic transmission is only relevant to one of the two C₂ domains, one of these constructs should behave as *sytWT* while another one as *sytC₂AB6W*. If both domains act in an additive, non redundant way, their phenotypes should lie in between the two extremes (*sytWT* and *sytC₂AB6W*).

As summarized in Fig. 3.14, all our data point to an additive gain of function phenotype as a function of the number of domains with tryptophan replacement. The EPSC amplitudes in the *sytC₂A3W* and *sytC₂B3W* mutants were again comparable to the *sytWT* and *sytC₂AB6W* (*sytC₂A3W* 1.8 ± 0.2 nA, $n=62$; *sytC₂B3W* 1.9 ± 0.1 nA, $n=72$, compared to Fig. 3.11 above, KW nonparametric test and Dunn's multiple comparison test show no difference between mutants and *sytWT*). The vesicular release probability (*sytC₂A3W*: $8.5 \pm 0.7\%$, $n=37$;

sytc₂B3W 10.4 ± 1.3%, n=42; compared to Fig. 3.13 above), synaptic depression (Fig. 3.14 A), mEPSC rates (Fig. 3.14 B) and apparent Ca²⁺ sensitivity (sytc₂WT 1.79 ± 0.04 mM, sytc₂A3W 0.79 ± 0.04 mM, sytc₂B3W 1.09 ± 0.12 mM and sytc₂AB6W 0.59 ± 0.04 mM Fig. 3.14 C) were in between the phenotypes of sytc₂WT rescue and sytc₂AB6W rescue. These data nicely demonstrates the non-redundant action of both C₂ domains, which strongly indicates that both C₂ domains participate almost equally to the regulation of Ca²⁺ sensitivity and release probability.

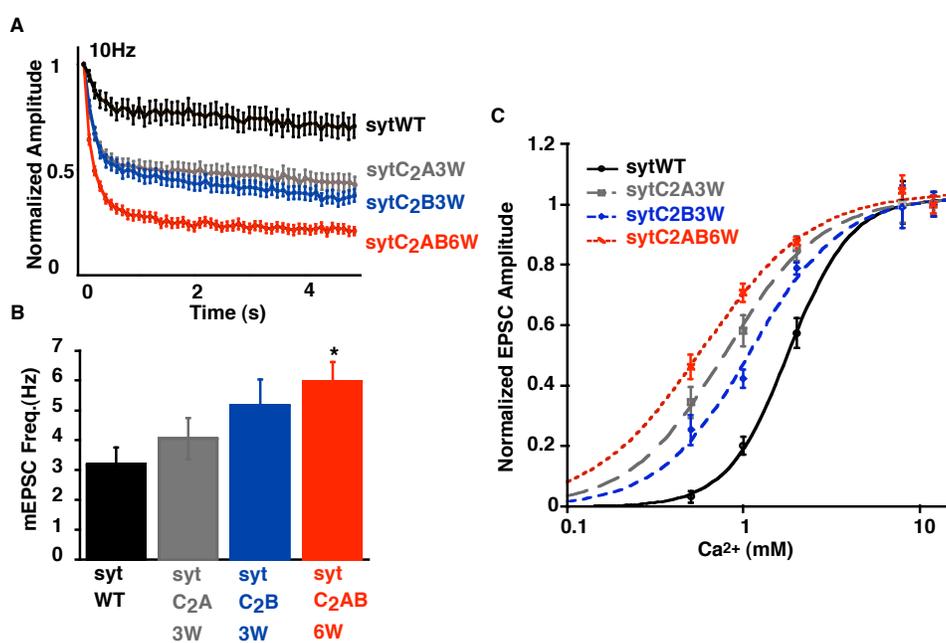


Figure 3.14 Additive effect of two C₂ domains in facilitating synaptic transmission. A, Short-term depression of sytc₂ tryptophan mutants and sytc₂WT. B, mEPSC rate of neurons rescued by the four constructs rescued neurons (sytc₂WT n=25, sytc₂A3W n=27, sytc₂B3W n=23 and sytc₂AB6W n=21. * indicates KW nonparametric test and Dunn's Multiple comparisons test, p<0.05, sytc₂AB6W compared to sytc₂WT). C, External Ca²⁺ dependent EPSC amplitudes of four constructs rescued neurons (Ca²⁺ cooperativity of sytc₂A3W and sytc₂B3W are 1.6 ± 0.2 and 1.7 ± 0.3, between the value of sytc₂WT (2.5 ± 0.1) and sytc₂AB6W (1.4 ± 0.2). sytc₂WT n=16, sytc₂A3W n=9, sytc₂B3W n=12 and sytc₂AB6W n=10).

3.2.4 Asymmetrical distribution of basic residues in the two C₂ domains regulating vesicular release probability

3.2.4.1 Neutralization of polybasic residues in the C₂B domain (K_{326, 327}A)

The polybasic region in the C₂B domain is important for interacting with multiple molecules (i. e. another copy of synaptotagmin, PIP₂ in plasma membrane, AP-2 and Ca²⁺ channels, etc. Chapman ER, et al., 1996; Sugita S, et al., 1996; Desai RC, et al., 2000; Fukuda M, et al., 1994; Sheng ZH, et al., 1997; Kim DK and Catterall WA, 1997). The syt K_{326,327}A (syt2KA) mutant showed a 36% reduction of evoked release in the neuromuscular junctions of flies (Mackler JM and Reist NE, 2001). Syt2KA mutant rescued hippocampal neurons were compared side-by-side to the sytWT construct rescued neurons to evaluate the physiological role of the polybasic region in the C₂B domain of syt.

The efficiency of synaptic transmission is evaluated via the EPSC amplitudes. The mean EPSC amplitudes of the syt2KA mutant were significantly reduced to app. 50% of the wild type control (sytWT 1.05 ± 0.13 nA, n=40; syt2KA 0.46 ± 0.05 nA, n=40; Fig 3.15).

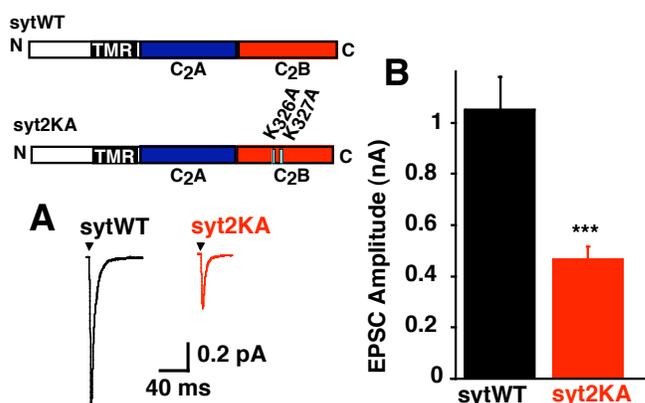


Figure 3.15 The EPSCs recorded from syt2KA and sytWT rescued sytKO neurons. A. typical synaptic responses from sytWT or syt2KA mutant. B. mean EPSC amplitudes of the two constructs (***) indicates t-test, $p < 0.001$).

The EPSC time course of the syt2KA mutant was also compared to the sytWT rescue. EPSCs were integrated and fitted with a double exponential equation. No significant changes in the time constants of both the fast and slow components were detected (sytWT $\tau_{fast} = 8.0 \pm 0.6$ ms, $\tau_{slow} = 252 \pm 27$ ms $n = 17$; syt2KA $\tau_{fast} =$

10.1 ± 1.0 ms, $\tau_{\text{slow}} = 236 \pm 33$ ms $n = 12$; Fig 3.16). The reduction in EPSC amplitude in the *syt2KA* mutant was exclusively due to a decrease in the amplitude of the fast component (*sytWT* $Q_{\text{fast}} = 11.3 \pm 1.4$ pC, $Q_{\text{slow}} = 2.7 \pm 0.4$ pC $n = 17$; *syt2KA* $Q_{\text{fast}} = 6.2 \pm 0.8$ pC, $Q_{\text{slow}} = 2.5 \pm 0.5$ pC $n = 12$; Fig 3.16). These results show that the main effect of the 2KA mutation is a selective reduction of the synchronous release.

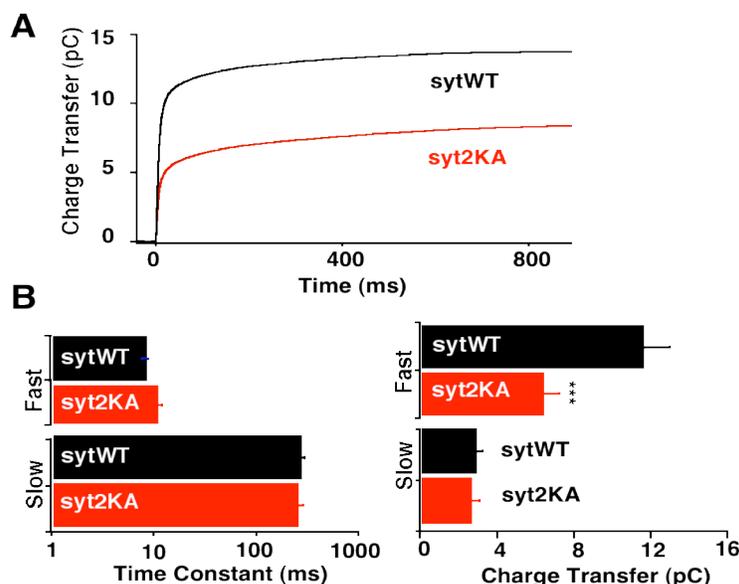


Figure 3.16 Time course of EPSC from *sytWT* and *syt2KA* mutants. A, exemplary cumulative EPSC charge responses from a *sytWT* and a *syt2KA* rescued neurons B, analysis of time constants and amplitudes with the double exponential fitting of the integrated responses (***) indicates t-test, $p < 0.001$).

To define the RRP size, hypertonic sucrose solution (500 mM) was applied to the clamped neuron and the transient component of response was recorded. No significant differences in the RRP size between *sytWT* and *syt2KA* rescued neurons were observed (Fig 3.17 A). From these data, the vesicular release probability (P_{vr}) was calculated and the 2KA mutation showed a reduction in P_{vr} from $7.1 \pm 0.6\%$ ($n = 34$, for *sytWT*) to $4.1 \pm 0.6\%$ ($n = 34$, in *syt2KA*) (Fig 3.17 B). If considering that the 2KA mutation specifically reduced the synchronous release

component of EPSC, the actual reduction in this function was about 50% ($P_{vr_{fast}}$ WT: $5.3 \pm 0.2\%$, $n=17$; Syt2KA: $2.7 \pm 0.1\%$, $n=12$).

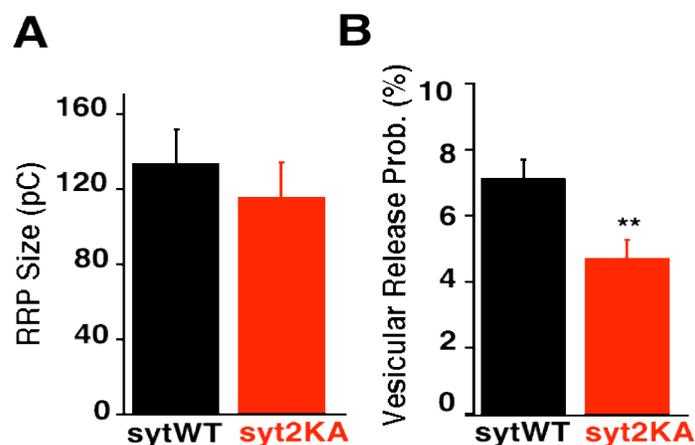


Figure 3.17 Readily releasable pool size and vesicular release probability of the syt2KA or sytWT rescued neurons. A, similar readily releasable pool size of sytWT and syt2KA rescued neurons. B, mean vesicular release probability of wild type and 2KA mutant (sytWT $n=34$; syt2KA $n=34$, ** indicates t-test $p<0.01$).

It is worth noting that the mEPSCs amplitudes were not affected by neutralizing these two Lys to Ala residues (sytWT 21.0 ± 1.2 pA, $n=16$; syt2KA 19.9 ± 1.4 pA, $n=12$), indicating that the reduction of EPSC is not due to changes in neurotransmitter content in the vesicle or the sensitivity of the postsynaptic AMPA receptors. Consistent with the unchanged RRP size, the mEPSC frequency was not changed in the syt2KA mutant compared to the sytWT (sytWT 2.4 ± 0.4 Hz, $n=16$; syt2KA 1.9 ± 0.5 Hz, $n=12$).

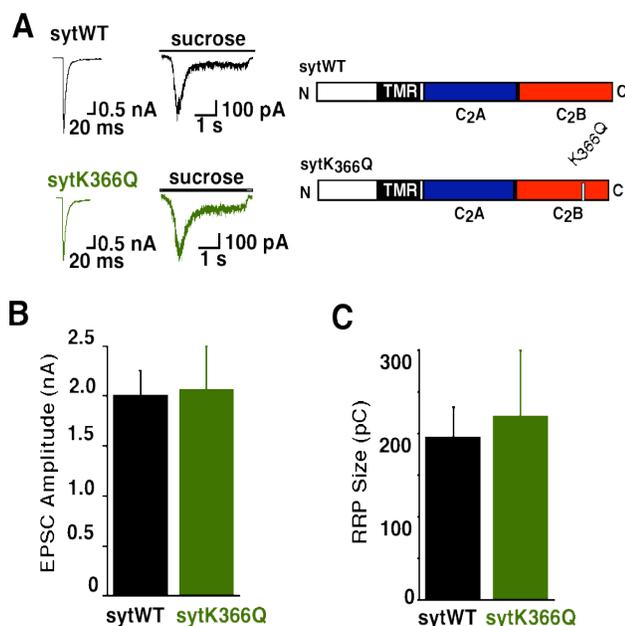
3.2.4.2 Point mutation of Lys366 (K₃₆₆Q) in the C₂B domain

The similar characteristics of synaptic transmission between the neutralized polybasic stretch in the C₂B domain and the previously studied basic residue mutation R₂₃₃Q in the C₂A domain (Fernandez-Chacon R, et al., 2001) leads to speculation of the roles of the basic residues in the C₂ domains. The

corresponding basic residue of R233 in the C₂B domain, Lys366 was also investigated. A mutation with neutralizing Lys366 in the C₂B domain (sytK₃₆₆Q) was compared to sytWT by rescuing in the sytKO neurons.

As to the initial test of evoked EPSC response, t-test shows no significant difference between sytK₃₆₆Q and sytWT constructs. The mean EPSC amplitude of sytK₃₆₆Q mutant is 2.06 ± 0.44 nA and for sytWT it is 2.00 ± 0.21 nA (sytK₃₆₆Q n=8, sytWT n=9; Fig. 3.18 B). Additionally, the RRP determined by 4 second application of 500 mM sucrose was unchanged in sytK₃₆₆Q mutant compared to sytWT rescues (sytK₃₆₆Q 220 ± 80 pC, n=6 and sytWT 195 ± 37 pC, n=7; Fig. 3.18 C).

Figure 3.18 Synaptic properties of sytK₃₆₆Q and sytWT rescued neurons. A, typical evoked EPSC response and transient synaptic response induced by sucrose; Statistical comparison of EPSC amplitude (B) and RRP size (C) between sytK₃₆₆Q and sytWT.



3.2.4.3 Overview of the characteristics of three mutants (sytR₂₃₃Q, syt2KA and sytK₃₆₆Q) and sytWT rescued sytKO neurons

The vesicular release probability is correlated to short term plasticity with low release probability usually leading to short term facilitation and high release probability resulting in short term depression (as shown in sytC2AB6W study, Fig. 3.13). The 50% reduction of EPSC amplitude and Pvr in syt2KA mutant

compared to sytWT led to the investigation of short term plasticity of these two constructs. A 5 second 10Hz stimulation train was performed and as expected the low release probability mutant syt2KA showed short-term facilitation in contrast to the moderate synaptic depression in sytWT (Fig. 3.19 A).

The resemblance of the synaptic transmission phenotype between the syt2KA and the previously reported sytR₂₃₃Q is very interesting. To directly compare their similarity, a side-by-side experiment of syt2KA, sytR₂₃₃Q and sytWT rescues was conducted. As shown in Fig. 3.19 B, the short-term plasticity of syt2KA and sytR₂₃₃Q was found to be nearly the same.

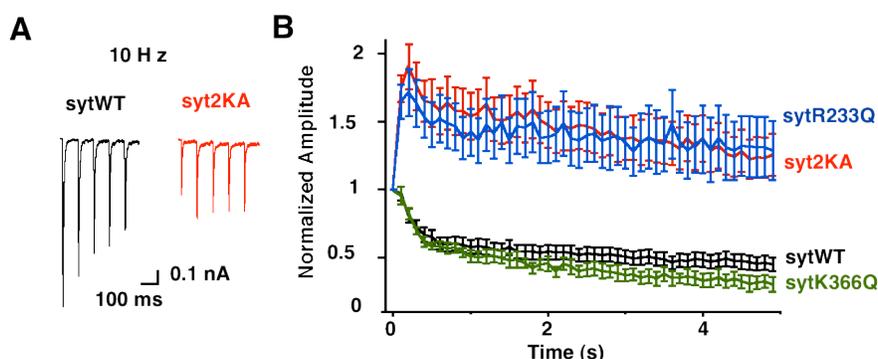


Figure 3.19 Short-term plasticity comparison of three mutants (syt₂₃₃Q, syt2KA and sytK₃₆₆Q) and sytWT. A, raw traces of the initial five consecutive EPSCs of sytWT and syt2KA mutant during a 10Hz action potential train; B, plot of normalized EPSC amplitudes (syt R₂₃₃Q n=35, syt2KA n=35, sytWT n=36 and sytK₃₆₆Q n=8).

Furthermore, to summarize all these characteristics in three mutants, the EPSC amplitude, RRP size and vesicular release probability were all normalized to the values of sytWT (Fig 3.20 A). By varying the Ca²⁺ concentrations in the external solution and later normalizing the EPSCs recorded in these conditions to the one in normal external solution, the Ca²⁺ dose response curve of these four constructs were plotted (Fig 3.20 B). The apparent Ca²⁺ sensitivity of sytR₂₃₃Q decreased about 1.7 fold compared to sytWT, so did syt2KA (sytR₂₃₃Q K_{Cad}= 2.8 ± 0.2 mM; syt2KA K_{Cad}= 2.9 ± 0.5 mM; sytK₃₆₆Q K_{Cad}= 1.7 ± 0.3 mM and sytK₃₆₆Q K_{Cad}= 1.8 ± 0.1 mM).

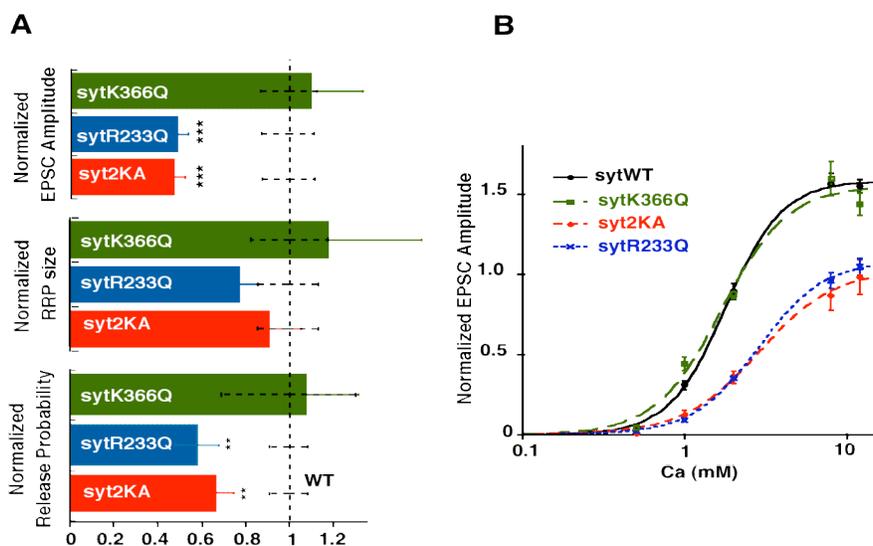


Figure 3.20 Overall comparison of synaptic properties of the three syt basic residue mutants (sytR₂₃₃Q, sytK₃₆₆Q and syt2KA) with sytWT rescue. A, EPSC amplitude, RRP size and Pvr of three mutants were normalized to sytWT (sytWT n=34, sytR₂₃₃Q n=33, syt2KA n= 34; sytWT n=9, sytK₃₆₆Q n=8; *** and ** indicate t-test, p<0.001 and p<0.01 respectively); Note that the comparison of sytWT vs. sytK₃₆₆Q and sytWT vs. sytR₂₃₃Q and syt2KA were done on separate sets of experiments. C. Synaptic response amplitude as a function of external Ca²⁺ concentration (sytWT n=9-15, sytR₂₃₃Q n=9, sytK₃₆₆Q n=8-12, syt2KA n=9-13).

In all the measured parameters, the four constructs can be divided into two groups according to their clearly distinct phenotypes: syt2KA and sytR₂₃₃Q, sytK₃₆₆Q and sytWT. The basic residues in the C₂B domain that are the “function copy” of R233 exist in the polybasic region instead of the corresponding site of R233- K366, which indicates that the basic residues of syt regulating vesicular release probability distribute asymmetrically in the two C₂ domains.

3.2.5 Further analysis of the C₂B domain of syt1

The importance of the two C₂ domains of syt1 in triggering fast synaptic transmission has been shown in section 3.2.1. Both syt fragment mutants (sytΔC₂A and sytΔC₂B) cannot facilitate synchronous vesicular release (Fig. 3.7) by single action potential stimulation. However the analysis of synaptic

transmission during trains of action potential revealed partial rescue activity in *syt* Δ C₂A transfected *sz*tKO neurons.

3.2.2.1 Syt 1 with the deletion of the C₂A domain can partially rescue fast synaptic vesicular release

A train of 10Hz stimulation lasting 5 seconds was performed in *syt* Δ C₂A rescued neurons, and compared to *syt*WT rescued neurons and *syt*KO neurons. Fig.3.21 shows the average EPSC traces of *syt* Δ C₂A, *syt*WT rescues and *syt*KO during 10 Hz stimulation. There was a clear high-frequency stimulation dependent synchronous release activity in *syt* Δ C₂A rescued neurons. As control, the EPSC time course of *syt*WT rescued neurons or *syt*KO neurons did not change prominently (Fig.3.21 B).

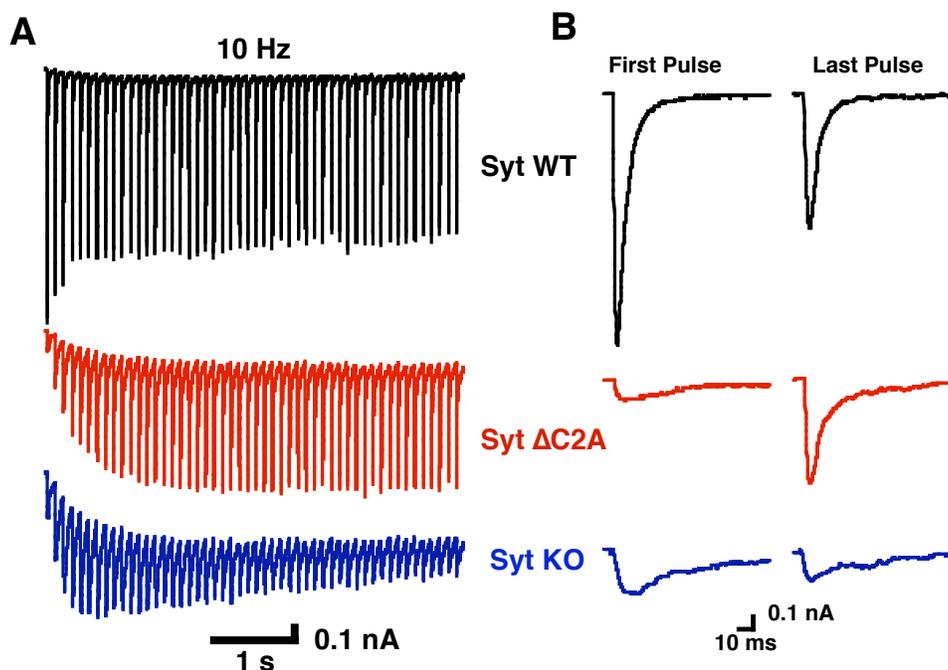


Figure 3.21 High frequency stimulation shifts asynchronous release to synchronous release in *syt* Δ C₂A rescue. A, 50 consecutive EPSC traces of *syt*WT, *syt* Δ C₂A rescued neurons or *syt*KO neurons in 10 Hz stimulation. B, The comparison of the first and last pulses evoked EPSC traces. (*syt*WT, n=11; *syt* Δ C₂A, n=22; *syt*KO, n=15)

In order to quantify this shift of EPSC time course, a further analysis was performed. Since 10 Hz stimulation sets each EPSC trace in the 100ms range, I integrated the 100 ms EPSC traces and fitted them with single exponential equation. In case it gave unsatisfying results, a double exponential equation was performed. The time constants of each cumulative EPSC charge were plotted against time (Fig. 3.22) and were fitted with linear equation. Clearly, all the EPSC integrations of sytWT rescued neurons have two time constants ($\tau_{1st} = 5.9 \pm 0.1$ ms, $\tau_{2nd} = 34.4 \pm 2.0$ ms). However in sytKO neurons, only one time constant of the cumulative EPSC charge was found ($\tau = 36.2 \pm 0.7$ ms). For syt ΔC_2A construct, EPSC integrations of the first three stimulations only can be fitted with a single exponential equation and all the rest have two components ($\tau_{1st} = 7.3 \pm 0.1$ ms, $\tau_{2nd} = 36.3 \pm 1.1$ ms). Student's t-test shows a significant difference between the τ_{1st} of the sytWT and syt ΔC_2A rescued neurons ($p < 0.0001$), which indicates that syt ΔC_2A can only partially rescue fast synaptic transmission in sytKO neurons compared to sytWT rescues.

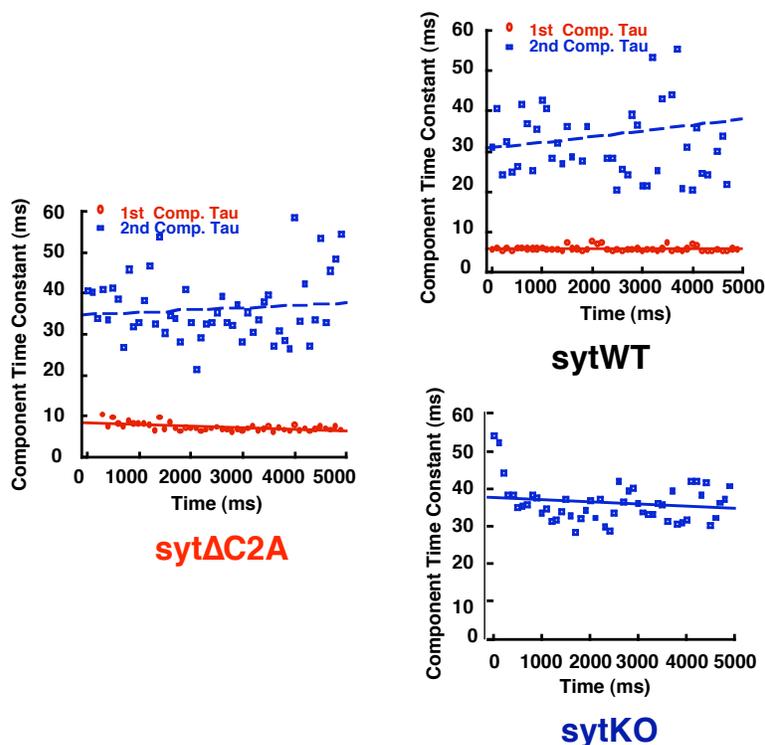


Figure 3.22 high frequency stimulation lead to partial rescue of fast release in syt ΔC_2A rescue. The red dots represent τ of the fast component and the blue dots represent τ of the slow component of the 50 consecutive integrated EPSCs in a period of 100 ms.

3.2.2.2 Syt 1/7 chimerical constructs in the absence of syt1 C₂B domain cannot rescue fast synaptic transmission

The interesting finding of the partial rescue in *syt* Δ C₂A mutant leads to a further investigation of the importance of each C₂ domain. Two critical questions arose from this finding: A) can the C₂B domain of syt1 be replaced with the C₂B domain from other synaptotagmin isoforms, for example the C₂B domain of syt7 and B) Is the C₂A domain of syt1 not essential in fast synaptic transmission?

For the first question, two syt1/7 constructs were designed (by Ok-Ho Shin) and tested, the syt1(syt7 C₂AB) (replacing the cytosolic part of syt1 with that from syt7) and syt1(syt7 C₂B) (replacing the C₂B domain of syt1 with that from syt7).

The evoked EPSC response from neither of the above constructs can mimic wild type rescued neurons (Fig. 3.23) and no EPSC shape shift was found during high frequency stimulation (Data not shown). Together with the finding that overexpression of syt7 in syt1 null neurons cannot rescue fast release (Jeong Seop Rhee, personal communication), the failure of these two constructs in triggering fast synaptic transmission indicates that the C₂B domain of syt1 is the sole molecule in syt1 regulating synchronous release and the C₂ domains of syt7 have distinct function comparing with those of syt1.

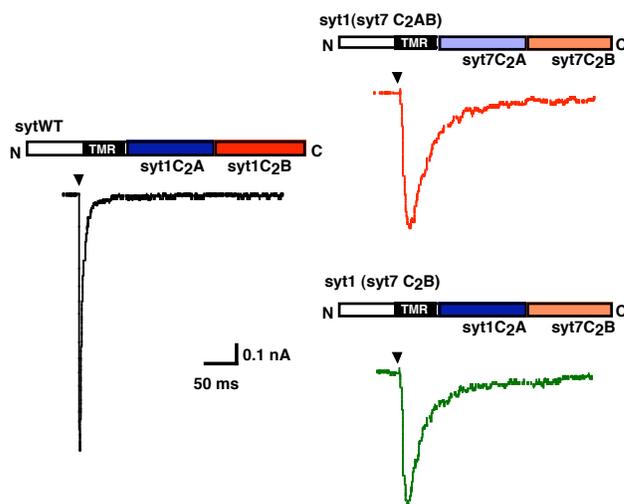


Figure 3.23 EPSC traces of different syt constructs (syt1WT, syt1(syt7 C₂AB) and syt1(syt7 C₂B)) rescued sytKO neurons.

3.2.2.3 Syt1/7 chimerical construct containing syt1 C₂B domain can partially rescue fast synaptic transmission

To answer the question of whether the C₂A domain of syt1 is essential in fast synaptic transmission, a new construct syt1(syt7 C₂A) (replacing syt1 C₂A domain with that from syt7) was designed (by Ok-Ho Shin) and tested in our system.

The initial test of evoked EPSC with the syt1(syt7 C₂A) construct showed synchronous release similar to sytWT rescues (Fig. 3.24 A). A side-by-side experiment of syt1(syt7 C₂A) and sytWT was performed to gain more detailed insight of this construct. The mean EPSC amplitude was reduced about 45% in syt1(syt7 C₂A) mutant compared to sytWT rescue (sytWT 2.52±0.33 nA; syt1(syt7 C₂A) 1.37±0.19 nA).

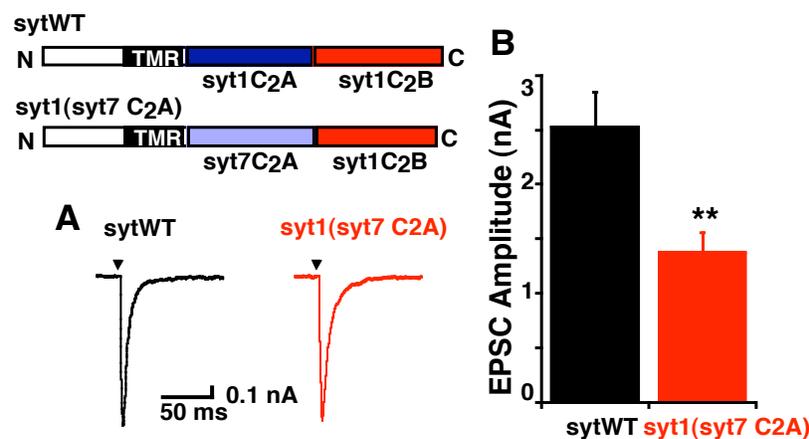


Figure 3.24 EPSC recorded from syt1(syt7 C₂A) or sytWT rescued sytKO neurons. A, a typical EPSC response from these constructs; B, Mean EPSC amplitude recorded from rescued neurons (sytWT, n=22; syt1(syt7 C₂A), n=24, ** indicates t-test p<0.01).

Further analysis of the EPSC cumulative charge was carried out and the characteristics of the two components from both syt1(syt7 C₂A) and sytWT rescued neurons were calculated.

The normalized cumulative EPSC charge of *syt1(syt7 C₂A)* mutant shows that the fast component increases slower than that of *sytWT* rescues but faster than that in *sytKO* neurons. This observation was confirmed in a further double exponential equation analysis. As shown in Fig. 3.25 B, the time constant of the fast component in *syt1(syt7 C₂A)* mutants was twice as the fast component in *sytWT* rescues (*sytWT* $\tau_{\text{fast}} = 8.3 \pm 0.7$ ms, *syt1(syt7 C₂A)* $\tau_{\text{fast}} = 16.9 \pm 1.5$ ms), and the time constant of the slow component remained unaltered.

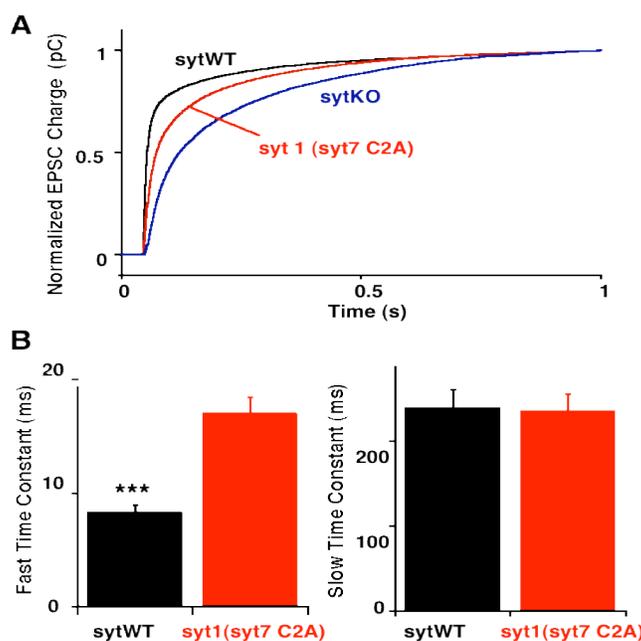


Figure 3.25 *syt1(syt7 C₂A)* mutant partial rescues synchronous release. A, normalized cumulative EPSC time course of *syt1(syt7 C₂A)*, *sytWT* constructs rescued neurons and *sytKO* neurons. B, the time constants of two components given by double exponential curve fit (*sytWT* $n=22$, *syt1(syt7 C₂A)* $n=23$. *** indicates t-test $p < 0.001$).

Besides the time constants, the amplitudes of the two components were also given by double exponential equation. The total charge in the chimerical mutant was about 50% larger than that of *sytWT* rescue (Fig. 3.26 A). This increase in the EPSC charge was contributed mainly from the slow component. As it is

shown in Fig. 3.26 B, no significant differences of the mean EPSC fast component charge were found between sytWT and syt1 (syt7 C₂A) construct (sytWT 19.8±2.1 pC, syt1 (syt7 C₂A) 23.1±2.8 pC); but the EPSC slow component in syt1 (syt7 C₂A) rescued neurons was almost three times as that of sytWT rescued neurons (sytWT 5.5±1.0 pC, syt1 (syt7 C₂A) 15.1±1.9 pC). The specific increase in asynchronous release without affecting the charge of synchronous component in syt1(syt7 C₂A) construct may be the function of the C2A domain of syt7, which has been implicated as the Ca²⁺ sensor for asynchronous vesicular release (Sugita S, et al., 2001; Sugita S, et al., 2002).

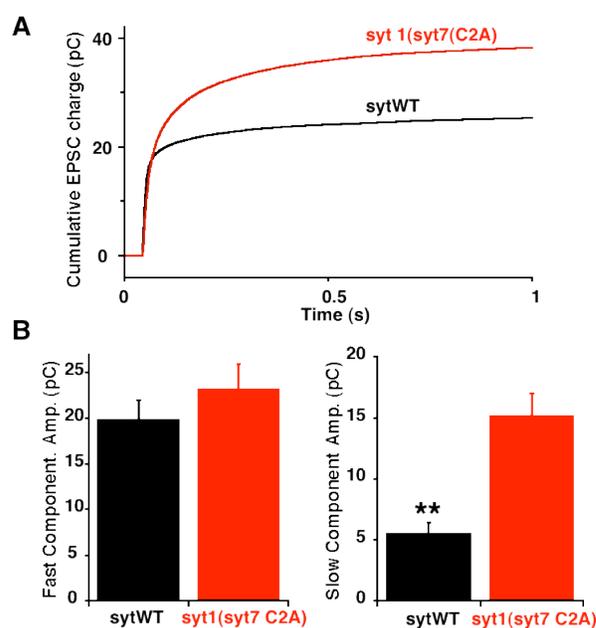


Figure 3.26 syt1(syt7 C₂A) enhances asynchronous release without affecting the amplitude of synchronous component. A, cumulative EPSC curve of syt1(syt7 C₂A) and sytWT constructs rescued neurons. B, the amplitude of two components given by double exponential curve fit (sytWT n=22, syt1(syt7 C₂A) n=23, ** indicates t-test p<0.01).

Although there is an increase of asynchronous release and therefore enhancement of the total vesicular release in the chimerical construct rescued neurons, the exact vesicular release probability cannot be quantified until the total number of primed synaptic vesicles is known.

Similar to the previous experiments, 500 mM sucrose was applied to the patched neurons for 4 seconds to record the transient response, which was quantified as RRP size. As shown in Fig. 3.27 A, the RRP size of the neurons rescued by sytWT is significantly smaller compared to sytKO neurons, while the RRP size in

syt1(syt7 C₂A) rescue is not significantly different from sytKO neurons. Consistent with previous data (Fig. 3.8), these results indicate that overexpression of the syt1 C₂A domain but not the syt7 C₂A domain will affect the homeostasis of RRP.

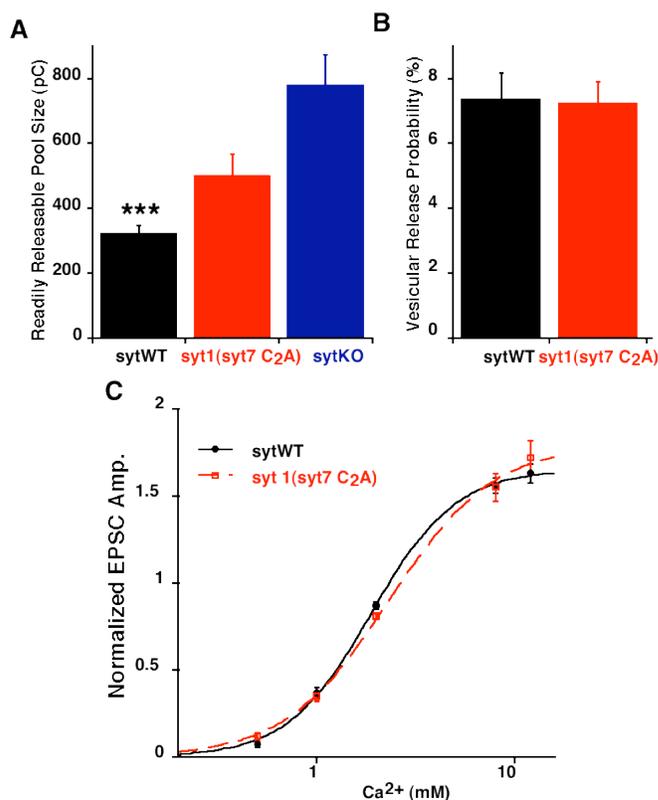


Figure 3.27 neurons rescued by syt1(syt7 C₂A) has similar release probability as sytWT rescue. A, RRP size defined with hypertonic solution application. (***) indicates KW nonparametric test and Dunn's multiple comparisons test $p < 0.001$, sytWT compared to sytKO: No significant difference was found between syt1(syt7 C₂A) and sytWT rescues); B, Vesicular release probability of sytWT and syt1(syt7 C₂A) mutant rescued neurons. sytWT $n=22$, syt1(syt7 C₂A) $n=24$ and sytKO $n=18$; C, External Ca²⁺ dependent EPSC responses.

The vesicular release probability was computed by normalizing the evoked response charge to RRP size. Student's t-test showed no difference in release probability between sytWT and syt1(syt7 C₂A) rescued neurons. Additionally, the apparent Ca²⁺ sensitivity measurement shows no difference between sytWT and the chimerical construct either.

These data taken together indicate that modifying the syt1 C₂A domain by replacing it with the C₂A domain of a syt isoform syt7 did not change the overall efficacy of synaptic vesicle release, while it compromised the release toward slower kinetics. This leads to the conclusion that the C₂A domain participates in regulation of the fast vesicular release.

4. Discussion

4.1 Synchronous and asynchronous vesicular release

Syt has been implicated as the candidate of Ca^{2+} sensor for fast synaptic transmission in many previous reports. For instance, injection of synthetic peptides or antibodies that interfere with syt function greatly attenuates synaptic transmission *in vivo* (Bommert R et al., 1993; Fukuda M et al., 2000; Llinas RR et al., 2005). In addition, knocking out of the syt gene results in a reduction of synaptic response amplitude in various organisms including *C. elegans*, *Drosophila*, and mice (Nonet ML et al., 1993; Littleton JT et al., 1993; Geppert M et al., 1994). Although a crucial for syt in fast synaptic transmission has been well established, the specific function that syt plays in regulating synchronous and asynchronous release has not been investigated. The first part of my investigation serves to better resolve how syt regulates fast and slow release by analyzing the basal electrophysiological characteristics of sytKO hippocampal neurons.

Interestingly, I find that cumulative evoked EPSC charge is reduced in sytKO neurons (Fig. 3.2), which contradicts previous studies. In their studies, EPSC charge was found to be unaltered in sytKO neurons (Shin OH et al., 2003; Nishiki T and Augustine GJ, 2004a). Furthermore, the increase of τ_{fast} and τ_{slow} of 1s PSC integration in sytKO neurons compared to WT neurons (Table 3.1) suggests a role of syt beyond simply regulating fast synaptic transmission. Previous work (Nishiki T and Augustine GJ, 2004a) failed to uncover these differences likely because the EPSC was insufficiently integrated over 400 ms as opposed to 1 s resulting in incorrect estimation of the τ_{slow} by double exponential fit. Although the τ_{fast} in the sytKO neurons (~38 ms) is about as five times as that in the WT neurons (~7 ms), it is still much smaller than the τ_{slow} in the WT neurons (~170 ms), which indicates that the fast asynchronous release component in sytKO neurons is different from the asynchronous release in WT neurons. Alternatively

speaking, the loss of syt generates another form of asynchronous release. The delay of the slow component by knocking out syt may be due to two possibilities: a lost control of syt dependent inhibition of asynchronous release (Yoshihara M and Littleton JT, 2002) or regulation of slow component release by syt and its isoforms.

My results show that syt is not related to vesicle priming since RRP size defined by hypertonic solution application is unchanged (Fig. 3.3 A). However, the recovery of the EPSC after sucrose mediated RRP depletion is more rapid in sytKO neurons compared to WT neurons (Fig. 3.4). This observation suggests that either vesicle priming is accelerated or more likely that syt independent release (asynchronous release) recovers faster after RRP depletion. This is added evidence for a molecular heterogeneity within the pool of readily releasable vesicles (Murthy VN, et al., 1997; Rosenmund C, et al., 2002; Sakaba T and Neher E, 2001a-b).

According to the initial hypothesis (Goda Y and Stevens CF, 1994), two different Ca^{2+} sensors are responsible for synchronous and asynchronous release respectively. The sensor regulating asynchronous release has higher apparent Ca^{2+} affinity and is therefore capable of detecting the tail of presynaptic Ca^{2+} transient rise. Given this model, in the sytKO neurons the remaining asynchronous component should have higher Ca^{2+} sensitivity. However my results suggest that the apparent Ca^{2+} sensitivity is lower in sytKO neurons. This is also supported by the study that examined the apparent Ca^{2+} sensitivity of asynchronous release in the Complexin I and II knock out hippocampal neurons (Reim K, et al., 2001), where the apparent Ca^{2+} sensitivity of asynchronous release is lower than that of synchronous release. In any case, the change of the vesicle release by the removal of syt appears to be quite complex, as the triggered release become less steeply dependent on Ca^{2+} in sytKO neurons. For example, the vesicle release at low Ca^{2+} concentration (i. e. 0.5 mM) was more efficient in sytKO neurons than in WT neurons (Fig. 3.5).

Another important hypothesis explaining the existence of evoked synchronous and asynchronous release is the possible spatial distribution of the Ca^{2+} source (presynaptic Ca^{2+} channels) in relationship to its target (Ca^{2+} sensors) (Neher E, 1998; Meinrenken CJ, et al., 2002; Meinrenken CJ, et al., 2003). The EGTA pipette injection experiment partially supports this idea (Fig. 3.6). Since high concentration of Ca^{2+} buffer narrows the effective range of Ca^{2+} influx in triggering vesicular release, therefore in this condition, asynchronous release will be inhibited more severely than synchronous release. Additionally, syt may play an important role in associating with Ca^{2+} channels, as the polybasic region of syt has been shown to interact with Ca^{2+} channels (Sheng ZH, et al., 1997; Kim DK and Catterall WA, 1997). However, I found that the syt2KA mutant specifically reduce the fast release amplitude without affecting the time constants of the EPSC (Fig. 3.16), raising doubt as to whether the interaction between syt and Ca^{2+} channels is important for regulating synchronous release. Furthermore, the finding that vesicles can shift from asynchronous release to synchronous release with high frequency stimulation in syt $\Delta\text{C}_2\text{A}$ mutant is hard to be explained by the spatial distribution of vesicles and Ca^{2+} channels hypothesis, because according to this hypothesis, the gradual elevation of Ca^{2+} concentration by high frequency stimulation inclines to trigger higher asynchronous release instead of higher synchronous release. This phenomenon can be explained in an alternative way: because the high EGTA concentration decreases the evoked Ca^{2+} transient amplitude, this leads to more inhibition of asynchronous released vesicles with lower Ca^{2+} sensitivity compared to synchronous released vesicles with higher Ca^{2+} sensitivity. Then one may argue that asynchronous released vesicles with lower Ca^{2+} sensitivity can not reconcile the above finding in syt $\Delta\text{C}_2\text{A}$ mutant, since elevation of presynaptic Ca^{2+} concentration will lead to more asynchronous release instead of higher level of synchronous release. While the possible explanation of the phenotype of syt $\Delta\text{C}_2\text{A}$ can be that synchronous release is determined by the syt C_2B domain-phospholipid interaction, and Ca^{2+} sensitivity of the vesicles is determined by full-length syt. For vesicles carrying syt $\Delta\text{C}_2\text{A}$

mutant, they can still undergo synchronous release, but the shortage of syt C₂A domain impaired their Ca²⁺ sensibility.

Overall, my results indicate that whether vesicles undergo synchronous or asynchronous release is more likely due to the distinct Ca²⁺ sensitivities of the vesicles instead of the spatial distribution of Ca²⁺ channels and vesicles. Clearly, the origin of synchronous and asynchronous release in evoked EPSC response is very complex and still remained to be determined.

4.2 The mechanism of action of syt in triggering vesicular release

Although many molecules interact with syt *in vitro*, including SNAP-25, syntaxin, phospholipid, AP-2 and Ca²⁺ channels (Zhang X, et al., 2002; Tucker WC, et al., 2004; Shao X, et al., 1997; Fernandez-Chacon R, et al., 2001; Chapman ER, et al., 1998; Wu Y, et al., 2003), the *in vivo* partners of syt are not clear. Two main parts of my study clearly support the notion that the role of syt-phospholipid interaction is critical for synaptic vesicular release. Both the basic residue mutants (syt2KA, sytR₂₃₃Q), as well as the tryptophan replaced mutants (sytC₂A3W, sytC₂B3W and sytC₂AB6W) show parallel changes in biochemical Ca²⁺ dependent syt-phospholipid binding assays (performed by my collaborators, Ok-Ho Shin and Thomas C. Sudhof, discussed in the below) and Ca²⁺ triggered vesicle release. Additionally, the tryptophan replacement mainly altered the hydrophobic interaction properties of syt instead of changing the ionic protein-protein interaction, therefore the gain of function in these tryptophan mutants is due to enhancing the syt-phospholipid interaction rather than syt-protein binding.

Another major point in my study is related with the relative contribution of the two C₂ domains for evoked vesicle release. Neutralizing aspartates in the Ca²⁺ binding sites, consistent with prior studies (Robinson IM, et al., 2002; Nishiki T

and Augustine GJ, 2004b), revealed an essential role of the C₂B domain for synchronous release. In addition, although the Ca²⁺ binding sites in the C₂A domain have been suggested to be not essential for fast release (Stevens CF and Sullivan JM, 2003; Mackler JM, et al., 2002 and Fig. 3.9), I find that fast release is also defective in the sytΔC2A rescued neurons with low frequency stimulation (0.2Hz). This indicates that the C₂A domain may structurally accompany the C₂B domain for syt to fulfill its function. Furthermore the additive and non-redundant effect of the tryptophan replacement in the C₂A and C₂B domain (sytC₂A3W, sytC₂B3W compared to sytC₂AB6W) suggests that the C₂A domain-phospholipid interaction is similarly important as the phospholipid interaction mediated by the C₂B domain. The indispensable role of the C₂A also lies in that it can participate in regulating the homeostasis of readily releasable pool (Fig. 3.8A and Fig. 3.27A).

4.2.1 Neutralization of Asp in the Ca²⁺ binding pockets of syt C₂ domains suggests unequal contribution of the two C₂ domains in mediating the efficiency of vesicular release

Consistent with a previous study of the syt C₂A domain (Stevens CF and Sullivan JM, 2003), neutralization of the 2nd to 4th Asps in the C₂A domain leads to a reduction but not elimination of fast release (Fig. 3.9). This mutation in the C₂A domain is shown to greatly reduce Ca²⁺ dependent plasma membrane binding *in vitro* (Ok-Ho Shin, personal communication). These results suggest that Ca²⁺ dependent phospholipid binding of the C₂A domain is not essential for synchronizing vesicle release. Further support comes from previous report of R₂₃₃Q mutant, where a reduction but not elimination of fast evoked response parallel with a decreased Ca²⁺ dependent syt-phospholipid binding was found (Fernandez-Chacon R, et al., 2001). Although the Ca²⁺ dependent syt-membrane interaction in the C₂A domain cannot determine fast release, it may regulate asynchronous release, since the sytC₂A3DA mutant shows a higher asynchronous release component but a similar vesicular release probability

compared to sytWT (section 3.2.2.1). The study of sytC₂B3DA and sytC₂AB6DA also support this idea. As shown in Fig.3.10 A, the sytC₂B3DA mutant reduced the EPSC charge, while sytC₂AB6DA had a comparable EPSC charge as sytWT rescued neurons, indicating the loss of control of the asynchronous release in sytC₂AB6DA mutant.

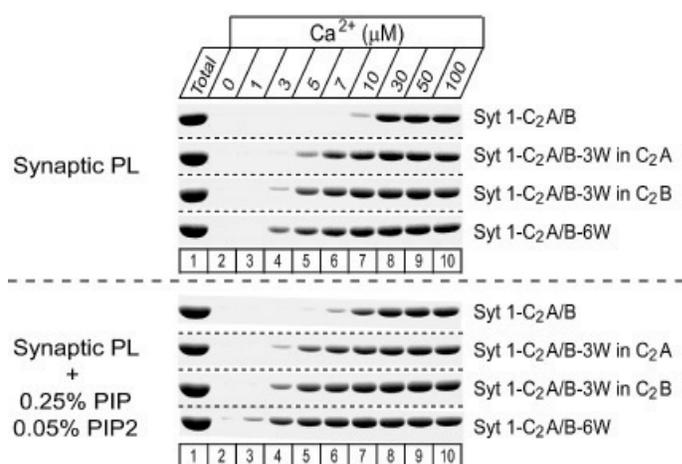
In contrast to the phenotype of sytC₂A3DA mutant, mutating the 2nd to 4th Asps in the C₂B domain eliminated synchronous release, which is consistent with a recent study (Nishiki T and Augustine GJ, 2004), showing that the 2nd and the 3rd Asps in the C₂B domain determine synchronous release. However, the time constants of the two components in the neurons rescued by sytC₂B3DA or sytC₂AB6DA is similar to that in the sytKO neurons (data not shown), in contrast to previous studies that the fast component is still detectable (Nishiki T and Augustine GJ, 2004). Additionally, neutralization of these Asps of the C₂B domain also greatly reduced Ca²⁺ dependent plasma membrane binding affinity *in vitro*, which suggests the importance of the C₂B-plasma membrane interaction in fast vesicular release.

In summary, the Ca²⁺ dependent syt-membrane interaction in the C₂ domains has distinct functions. The interaction in the C₂A domain can regulate but not determine synchronous release efficiency and inhibit asynchronous release, while the interaction in the C₂B domain determines synchronous release in all or none fashion.

4.2.2 Tryptophan replacement experiment reveals the importance of syt-membrane interaction in vesicular release efficiency and the cooperation of the two C₂ domains in fulfilling the functions of syt

There are three classes of interactions within syt, which have been found to determine/affect the functions of syt *in vitro*: A) the five aspartates in each C₂ domain functioning as the essential domains for Ca²⁺ mediated phospholipid binding; B) the basic residues distributed in the top loops or flanking side of syt that interacts with multiple molecules; C) the hydrophobic residues in the loop region, thought to undergo Ca²⁺ dependent insertion into the phospholipid membrane (Chapman ER and Davis AF, 1998; Bai J, et al., 2002). By replacing these hydrophobic residues with the most hydrophobic amino acid, tryptophan, ionic mediated protein-syt interaction in these regions should be unlikely affected, but the Ca²⁺ dependent phospholipid binding will be enhanced.

Previous analysis was performed by Ok-Ho Shin to determine the Ca²⁺ dependent syt-phospholipid binding of these tryptophan mutants *in vitro* (Fig. 4.1). As predicted by the design, a gradual increase of the Ca²⁺ dependent phospholipid binding was found in these three mutants. This suggests that the tryptophan mutation can drastically enhance the Ca²⁺ dependent phospholipid binding ability of syt. Consistent with the biochemical finding, my data showed enhanced synaptic release efficiency in all three tryptophan mutants. The nice correlation between biochemical and electrophysiological findings further reinforces the idea that syt-phospholipid interaction is crucial for syt to induce vesicular release.



Binding buffer: 50 mM HEPES pH 6.8, 100 mM NaCl, 4 mM EGTA, 2 mM Mg²⁺
 Synaptic PL: 41% PC, 32% PE, 12% PS, 5% PI, and 10% cholesterol

Figure 4.1. Ca²⁺ dependent phospholipid binding of different syt tryptophan mutants comparison with the sytWT (data provided by Ok-Ho Shin, for detailed methodological explanation, see Shin OH, et al., 2002.)

The three fold increase in the apparent Ca^{2+} sensitivity in $\text{sytC}_2\text{AB6W}$ mutant leads to another interesting question: how is the EPSC time course of this mutant comparing to sytWT rescue? The idea behind the question is based on the previous model that evoked asynchronous release is regulated by another Ca^{2+} sensor with higher Ca^{2+} affinity (Goda Y and Stevens CF, 1994). If a higher affinity Ca^{2+} sensor for asynchronous release exists, we may expect a certain change (i. e. increase in asynchronous release) in the evoked release time course in the neurons rescued by “super syt” ($\text{sytC}_2\text{AB6W}$). The deconvolution of evoked EPSC time course between the sytWT and the $\text{sytC}_2\text{AB6W}$ rescued neurons overlaps. A more detailed analysis of the time constants of synchronous and asynchronous release and the contribution of each component to total release reveals no change between the sytWT and the $\text{sytC}_2\text{AB6W}$ rescued neurons as well (Fig 4.2). These data suggest that the Ca^{2+} sensitivity of the asynchronous release Ca^{2+} sensor may be more than three-fold higher than that of syt. Alternatively, the explanation can be that syt solely plays a role in regulating synchronous vesicular release.

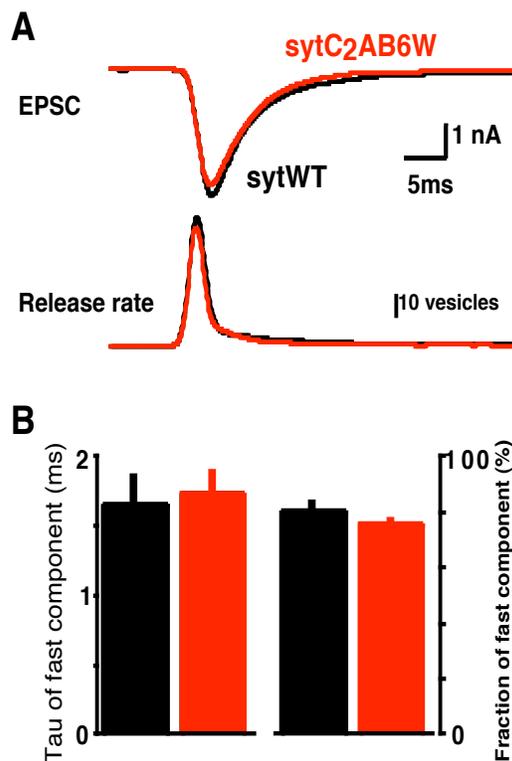


Figure 4.2 The high Ca^{2+} sensitivity mutant does not yield significant changes in the time course of neurotransmitter release. A. Top, exemplary EPSCs from SytWT (black) and Syt $\text{C}_2\text{AB6W}$ rescues (red); Below, EPSCs deconvolved with mean mEPSC time course to reveal the vesicular release rate. B. Release time course were fitted by two exponential equation. Bar plot of mean time constants (left) and relative amplitude of the fast component of release (right). Student's t-test shows no difference between sytWT (black) and $\text{sytC}_2\text{AB6W}$ (red) (The slow component of release also did not reveal any change in its time course, not shown here).

The finding that the sytC₂A3W and the sytC₂B3W both display a similar behavior in the short term depression and an increase of apparent Ca²⁺ sensitivity indicates the important function of the C₂A domain in synaptic transmission. Previous studies of syt in *Drosophila* suggested that the C₂A domain is not important for synaptic function (Mackler JM, et al., 2002). However other studies implicated the Ca²⁺ binding region of the C₂A domain as part of the Ca²⁺ sensor molecule (Stevens CF and Sullivan JM, 2003). Here, our study clearly shows that the C₂A domain is important for syt function and that both C₂A and C₂B domains contribute almost equally to regulate the Ca²⁺ sensitivity and probability of vesicle release.

Another finding is the gradual increase of mEPSC frequency in the order of sytWT < sytC₂A3W < sytC₂B3W < sytC₂AB6W. This observation can be correlated to the gradual increase of the apparent Ca²⁺ sensitivity in the three tryptophan mutants, since the elevation of the Ca²⁺ sensing ability of these mutants may let the vesicles start releasing in residue Ca²⁺ level. To test this hypothesis, the rescued neurons (with sytWT or sytC₂AB6W) were incubated in 50 μM EGTA-AM for 15 min (37 °C) in order to accumulate a high concentration of EGTA in the presynaptic terminals, and then mEPSCs were recorded in presence of 300 nM TTX. To our surprise, Student's t-test indicated no change of spontaneous release rate either in the sytWT or in the sytC₂AB6W group after EGTA-AM application (The mEPSC frequency after EGTA-AM application was normalized to the mEPSC frequency before EGTA-AM application, sytWT 93.8 ± 12.5%, n=17; sytC₂AB6W 81.1 ± 16.2%, n=19). The unchanged mEPSC frequency suggests that the spontaneous release rate is Ca²⁺ independent. Another experiment recording mEPSC of sytC₂AB6W rescued neurons in the presence of 0 mM Ca²⁺ and 4 mM Ca²⁺ was performed by Dr. Rhee JS, to further test this idea. In this experiment, the spontaneous release rate was unchanged in either condition (data not shown), which also support the previous conclusion that the spontaneous release rate is Ca²⁺ independent in sytC₂AB6W. In summary, the increased mEPSC frequency in sytC₂AB6W mutant is not due to its three-fold

increase in the apparent Ca^{2+} sensitivity compared to sytWT. Possible explanation can be that the sytC₂AB6W mutant may enhance Ca^{2+} independent phospholipid interaction thus to increase spontaneous vesicle fusion rate.

4.2.3 Asymmetrical distribution of basic residues for regulation of release probability in the C₂A and C₂B domain suggests different orientation for the C₂ domains upon Ca^{2+} dependent membrane interaction

The effects of the syt2KA mutation in my study correlating with results previously obtained in the neuromuscular junctions in flies (Mackler JM, et al., 2001), generalize that perturbing the polybasic region leads to a significant decrease in vesicular release. In addition, the high resolution of the electrophysiological analyses of mammalian neuronal cultures allowed us to characterize in details a variety of synaptic parameters that led us to uncover the parallelism with the phenotype caused by the R₂₃₃Q mutation. The observation that basic residues regulating vesicular release probability distribute asymmetrically in the two C₂ domains led to a further analysis of the origins of these phenotypes.

Ok-Ho Shin explored the Ca^{2+} dependence of phospholipid binding to a syt fragment containing both C₂-domains (C₂A/B fragment) at various Ca^{2+} concentrations in R₂₃₃Q and 2KA mutants. In addition, he analyzed how increasing PIP and PIP₂ concentrations affect this Ca^{2+} dependence.

In the absence of PIP and PIP₂, phospholipid binding to the WT synaptotagmin 1 C₂A/B fragment required Ca^{2+} and the observed apparent Ca^{2+} affinity was significantly decreased by the R₂₃₃Q mutation (Fig. 4.3 the left column), as described previously (Fernandez-Chacon et al, 2001). The 2KA mutation also decreased the apparent Ca^{2+} affinity, which suggests that the polybasic region is involved in Ca^{2+} -dependent phospholipid binding to syt. Addition of increasing amounts of PIP and PIP₂ increased the apparent Ca^{2+} affinity of all proteins, and

the higher PIP/PIP₂ concentrations induced some degree of Ca²⁺-independent binding that was abolished by the 2KA mutation but not by the R₂₃₃Q mutation (Fig. 4.3 the middle and right columns). Under all conditions tested in this series of experiments, both the R₂₃₃Q and 2KA mutations decreased the apparent Ca²⁺ affinity of the C₂A/B fragment. The extent of this decrease was most similar at the intermediate PIP/PIP₂ concentrations (Fig. 4.3 the middle column). These results show that the similar decrease in the apparent Ca²⁺ sensitivity of release induced by these two mutations (Fig. 3.20 B) can be correlated with a similar alteration of Ca²⁺-dependent phospholipid binding. On the other hand, the two mutations had clearly distinct effects on the Ca²⁺-independent binding observed at the higher PIP/PIP₂ concentrations, which hence do not correlate with the similarity of these two mutants in the examined electrophysiological parameters.

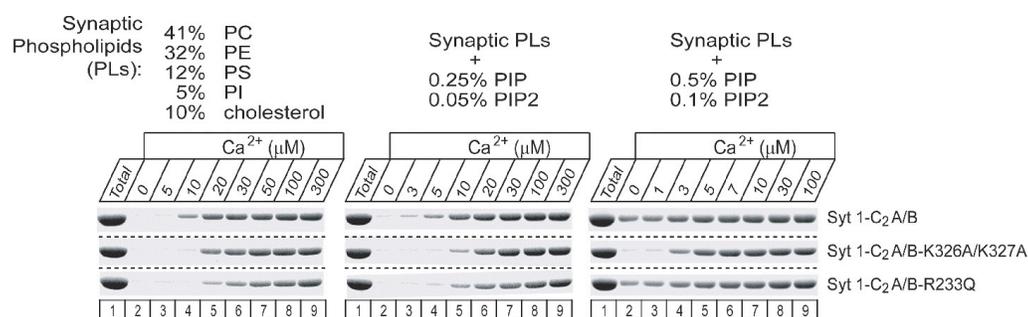


Figure 4.3 the Ca²⁺ dependent phospholipid binding of syt2KA and sytR₂₃₃Q mutants comparison with sytWT (data provided by Ok-Ho Shin).

Dr. Shin further studied the importance of electrostatic forces to the syt-phospholipid interaction by analyzing phospholipid binding in the absence and presence of Ca²⁺ as a function of the ionic strength, varying also the PIP/PIP₂ concentrations as in the previous set of experiments. At low ionic strength (50 mM NaCl) the phospholipid binding to the sytWT C₂A/B fragment in the absence of Ca²⁺ and PIP/PIP₂ was observed (Fig. 4.4 the left column). This result demonstrates that the ability of syt interacting with membrane in the absence of Ca²⁺ does not depend specifically on polyphosphoinositides. As expected, increasing the ionic strength decreased the binding observed in the absence and presence of Ca²⁺, but both types of interactions became more resistant to NaCl

with increasing concentrations of PIP/PIP₂. These results show that binding of the synaptotagmin C₂A/B fragment to phospholipids in both the absence and presence of Ca²⁺ depends on a delicate energetic balance where electrostatic interactions play a critical role.

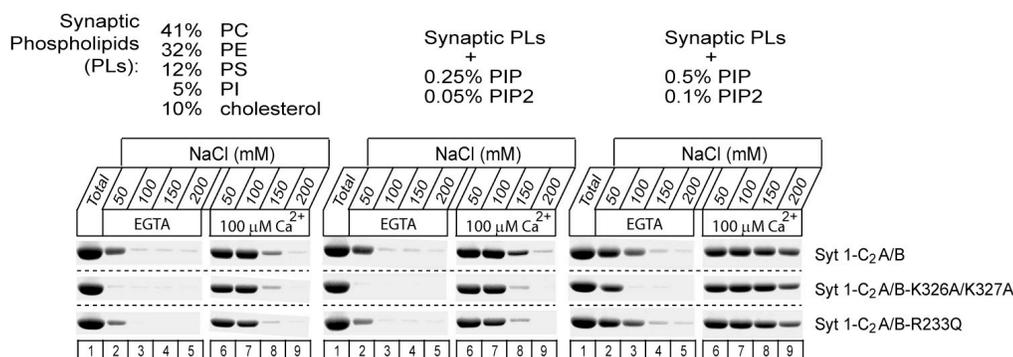


Figure 4.4 the ionic strength dependent phospholipid interaction of syt2KA and sytR₂₃₃Q comparison with sytWT (Data provided by Ok-Ho Shin .).

The study here implicates that Ca²⁺ dependent phospholipid binding of syt plays an important role for proper synaptic transmission. The observation that release is decreased instead of abolished by the 2KA mutation indicates that interactions are impaired but not completely abolished by this mutation. Indeed, these biochemical studies showed that Ca²⁺-induced phospholipid binding fits this criterion, unlike many interactions showed to be abrogated by the 2KA mutation. The decrease in the observed Ca²⁺ affinity correlating with the decrease in the apparent Ca²⁺ sensitivity of release caused by the 2KA mutation further supports this idea. The fact that the phenotype induced by the 2KA mutation can be correlated with the effects on Ca²⁺-induced phospholipid binding, indicates that any other interaction mediated by the polybasic region is less critical for the function of syt in release.

Initially, syt was believed to bind to lipids only in the presence of Ca²⁺, but the observation of a Ca²⁺-independent interaction with PIP₂-containing vesicles lead recently to the proposal that this interaction steers its membrane penetration activity and facilitates the rapid time scale of release (Bai J, et al., 2004b). The

data here show that PIP₂ is not strictly required for Ca²⁺-independent binding of the C₂A/B fragment to phospholipids (Fig. 4.4, the left column), and that little binding occurs at physiological ionic strengths in the presence of amounts of phosphoinositides that are likely to be close to those present on synaptic membranes (but see McLaughlin et al., 2002). In addition, the effects of the R₂₃₃Q and 2KA mutations on this interaction do not correlate with their *in vivo* phenotypes. Thus, it appears that the Ca²⁺-independent lipid binding is not important for syt function, although we cannot rule out the possibility that such interaction occurs *in vivo* and the lack of a correlation with the electrophysiological data is due to a dominant effect of the Ca²⁺-induced interaction. In any case, it seems unlikely that the Ca²⁺-independent membrane binding facilitates the synchronous mode of release, since the 2KA mutation did not change the time course of fast release (Fig. 3.16 B).

Further more the study of basic residue Lys366 in the C₂B domain also indicates a correlation between biochemical and electrophysiological assays: the Ca²⁺ dependent phospholipid binding of the sytK₃₆₆Q construct was similar to the sytWT results (Fig. 4.5). The observation that the polybasic region participates in Ca²⁺-dependent phospholipid binding to the C₂A/B fragment, together with the different effects of the R₂₃₃Q and K₃₆₆Q mutations on binding, show that there are important differences in the mode of binding of the two C₂-domains to the lipids. The lack of an effect of the K₃₆₆Q mutation on binding does not imply that the Ca²⁺-binding loops are not involved in binding, since this observation just indicates that interactions between the Lys366 side chain and the lipids do not make a measurable energetic contribution to binding. However, this finding does reinforce the notion that the Ca²⁺ dependent phospholipid binding of the basic residues of syt regulates vesicular release efficiency and the asymmetric distribution of these effective residues in the two C₂ domains suggest a different orientation of the two C₂ domains upon coming Ca²⁺ signal.

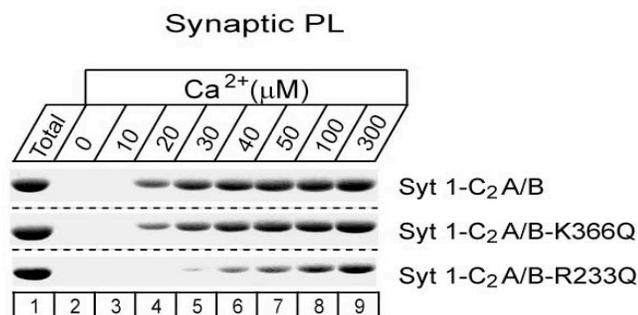


Figure 4.5 Ca²⁺ dependent phospholipid interaction of sytK₃₆₆Q and sytR₂₃₃Q in comparison with sytWT (Data provided by Ok-Ho Shin .).

Synaptic PL: 41% PC, 32% PE, 12% PS, 5% PI,
10% cholesterol
Binding buffer: 50 mM HEPES pH 6.8,
100 mM NaCl, 4 mM EGTA, 2 mM Mg²⁺

Although all these mutations (Asps neutralization, basic residues neutralization, hydrophobic residues replacement with tryptophans) cannot fully reveal the mechanism of action of syt during vesicular release, the notion that syt facilitates vesicular fusion through its interaction with phospholipid in a Ca²⁺ mediated way was strongly supported. Phospholipids are not the sole molecules that interact with syt, but other protein(s) that have shown interaction with syt *in vitro* may more likely play a minor contribution to the mechanism of action of syt for vesicle release.

4.3 Discussion of syt1/7 chimera study

The first important finding in this syt1/7 chimera study is that syt1C₂B domain is essential for synchronous release. This notion has been proved in several studies, both in drosophila and murine preparations (Robinson IM, et al., 2002; Nishiki T and Augustine GJ, 2004b). Here I showed its importance using alternative methods. As shown in sytΔC₂A study, the high frequency stimulation of sytΔC₂A rescued neurons can shift EPSC time course from asynchronous release to synchronous release (Fig. 3.21), while there are still two defects of this mutant: A) The lower Ca²⁺ sensitivity in this mutant compared to sytWT rescue; B) Insufficient fast component rescue. One explanation of these defects may be originated from the structural shortage of the C₂A domain in sytΔC₂A. Another

mutant (syt1(syt7 C₂A)), by replacing syt1C₂A domain with syt7 C₂A domain had an insufficient fast component rescue without changing the apparent Ca²⁺ sensitivity (Fig. 3.25 and Fig. 3.27 C). This finding suggests the structural support of the C₂A domain for fast synaptic release, since slight difference between the structure of syt7 C₂A domain and syt1 C₂A domain leads to a significant effect on fast release time course. Furthermore the Ca²⁺ dependent syt-phospholipid assay showed a higher Ca²⁺ affinity of the syt7 C₂A domain compared to syt1 C₂A domain (Sugita S, et al., 2002; Shin OH, et al., 2002), while the similar apparent Ca²⁺ affinity of syt1 (syt7 C₂A) mutant and syt1 WT rescues raises doubts of the idea that syt1 C₂A domain is part of the Ca²⁺ sensor (Stevens CF and Sullivan JM, 2003).

Another finding that syt1 C₂A domain can regulate the RRP size (as shown in Fig 3.8 A) was supported in syt1 (syt7 C₂A) rescue experiment. The neurons with overexpression of syt1 C₂A domain (syt Δ C₂B or sytWT rescue) have significantly reduced RRP size compared to sytKO neurons but the overexpression of syt7C₂A domain (syt1 (syt7 C₂A)) shows a comparable RRP size to sytKO neurons (Fig. 3.27 A). The observation of lack of inhibition of RRP size by overexpression of syt7 C₂A domain compared to syt1 C₂A domain suggests that the C₂A domains of syt1 and syt7 have distinct functions in regulating the homeostasis of RRP.

The last important finding is that asynchronous component was increased in syt1 (syt7 C₂A) mutant. Syt7 has been implicated as the Ca²⁺ sensor for asynchronous release because of its higher Ca²⁺ affinity for phospholipid binding (Sugita S, et al., 2002) and the finding here showed that syt7 C₂A domain may be responsible for it. The failure of rescuing fast synaptic response in both syt1 (syt7 C₂AB) and syt1 (syt7 C₂B) domain also suggested that syt7 C₂B domain has distinct function compared to syt1 C₂B domain. Whether syt7 C₂B domain also contributes to regulate asynchronous release, it is not clear.

5. Summary and conclusion

My thesis project explored the relationship between the structure and the physiological function of synaptotagmin 1 (syt), a putative Ca^{2+} sensor for vesicular release. The technique of conventional whole-cell voltage clamp and the cultured syt null (sytKO) mouse hippocampal neuron autapses transfected with Semliki forest virus carrying the mutated syt, were applied in this study.

The abundant information about syt gained from biochemical *in vitro* studies together with the controversial suggested mechanisms of action of syt in exocytosis deduced from these studies require a direct investigation of the physiological role of syt *in vivo*. In this study, three questions are mainly concerned: A) What are the possible functions of syt in vesicle recycle by studying sytKO neurons? B) Are the C_2 domains of syt redundant and what are their roles in synaptic transmission? C) What is the mechanism of action of syt in exocytosis?

The severely impaired synaptic transmission, especially the dramatic reduction of synchronous release component without altering the total fusion competent vesicles in sytKO neurons suggests the important role of syt for fast vesicle release. The faster recovery of asynchronous release in sytKO neurons compared to the recovery of synchronous release in WT neurons after the Ca^{2+} independent RRP depletion, indicates the heterogeneity of the fusion competent vesicle pool. The apparent Ca^{2+} sensitivity measurement and pipette injection of high concentration of EGTA in sytKO neurons reinforces the notion of distinct characteristics of synchronous and asynchronous release. These findings together suggest that synaptotagmin is the Ca^{2+} sensor for fast vesicle release and readily releasable vesicles with/without syt can display distinct properties in exocytosis.

The viral overexpression of exogenous mutated synaptotagmins in sytKO neurons clarified the non-redundant role of the two C₂ domains of syt in vesicle release. The C₂ domain truncation study showed the complete tertiary structure of synaptotagmin is important to keep efficient and fast vesicle release; The neutralization of Ca²⁺ binding sites in either C₂ domain study revealed the essential role of the C₂B domain for synchronizing vesicle release; Combining the above results and the syt1/7 chimera studies, the important function of the C₂A domain in controlling RRP size and regulating the asynchronous release component was clarified. The study of the basic residues in the C₂ domains supported the notion that the C₂ domains contribute unequally for syt fulfilling its function in vesicular release, which was supplemented by the study of tryptophan replaced mutants, showing that both C₂ domains can cooperatively contribute to synaptic transmission.

Through this study, together with the biochemical findings, the mechanism of action of synaptotagmin in vesicular release may be understood better. In general, the model that syt-phospholipid interaction regulates the last step of vesicle fusion was supported, although the importance of the interaction between syt and the SNARE complex in this step cannot be ruled out. The basic residues study suggested that the R₂₃₃ and K_{326,327} residues in two C₂ domains bind equally to the plasma membrane in Ca²⁺ dependent way and this interaction was kept in a delicate balance state. Also in this study, the physiological consequence of the Ca²⁺ independent syt-PIP₂ interaction and the Ca²⁺ dependent syt oligomerization was shown to be unessential for fast synaptic transmission. The tryptophan replacement study showed a gain of function of syt in synaptic transmission and reinforced that the Ca²⁺ dependent syt-membrane insertion is critical for synaptic transmission.

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