X-linked intellectual disability-associated mutations in synaptophysin disrupt synaptobrevin II retrieval

Citation for published version:

Digital Object Identifier (DOI):
10.1523/JNEUROSCI.0636-13.2013

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Publisher's PDF, also known as Version of record

Published In:
Journal of Neuroscience

General rights
Copyright for the publications made accessible via the Edinburgh Research Explorer is retained by the author(s) and / or other copyright owners and it is a condition of accessing these publications that users recognise and abide by the legal requirements associated with these rights.

Take down policy
The University of Edinburgh has made every reasonable effort to ensure that Edinburgh Research Explorer content complies with UK legislation. If you believe that the public display of this file breaches copyright please contact openaccess@ed.ac.uk providing details, and we will remove access to the work immediately and investigate your claim.
Synaptophysin is an integral synaptic vesicle (SV) protein that accounts for ∼10% of total SV protein cargo. Deletion of synaptophysin results in the defective retrieval of synaptobrevin II (sybII) from the plasma membrane during endocytosis, coupled with a slowing in the speed of endocytosis. Synaptophysin has been implicated in X-linked intellectual disability, with a recent study identifying four separate synaptophysin gene mutations in families affected by the disorder. To determine how these mutations may affect synaptophysin function, we expressed them in cultured neurons derived from synaptophysin knock-out mice. Two distinct truncating mutants were mislocalized throughout the axon and phenocopied the arrest of sybII retrieval in synaptophysin knock-out cultures. The remaining two mutants displayed a nerve terminal localization but did not support efficient sybII retrieval. Interestingly, one mutant fully rescued SV endocytosis kinetics, suggesting that sybII retrieval and endocytosis speed are independent from each other. These studies suggest that the efficient retrieval of sybII by synaptophysin may be key to maintaining synaptic health and perturbation of this event may contribute to the pathogenesis underlying neurodevelopmental disorders such as X-linked intellectual disability.

Introduction

Intellectual disability has a prevalence of ∼2% in the general population (Ropers and Hamel, 2005) and X-linked intellectual disability (XLID; also known as X-linked mental retardation) accounts for ∼5–10% of intellectual disability in males (Lubs et al., 2012). XLID is a heterogeneous group of conditions and, accordingly, a large number of X-chromosome gene mutations have been linked to this disorder (Ropers and Hamel, 2005; Lubs et al., 2012). A large-scale systematic sequencing of families containing multiple individuals with intellectual disability identified four mutations in the gene encoding synaptophysin that segregated with the condition and were potentially causal for the individuals affected (Tarpey et al., 2009).

Synaptophysin is a four transmembrane integral synaptic vesicle (SV) protein comprising ∼10% of total SV protein content (Takamori et al., 2006). Despite its abundance, synaptophysin knock-out mice reproduce normally and have no gross ultrastructural defects (Eshkind and Leube, 1995; McMahon et al., 1996). Synaptophysin knock-out mice do, however, display mild behavioral alterations and defects in learning and memory (Schmitt et al., 2009), suggesting a defect in synaptic function.

Recently, two aspects of presynaptic dysfunction have been identified in synaptophysin knock-out mice. First, nerve terminals from these mice displayed a reduced speed of SV endocytosis (Gordon et al., 2011; Kwon and Chapman, 2011). Second, these mice exhibited a profound deficit in the retrieval of a specific SV cargo from the plasma membrane, the integral SV protein synaptobrevin II (sybII) (Gordon et al., 2011). SybII drives SV fusion via interactions with the plasma membrane SNARE (soluble NSF attachment protein receptor) proteins syntaxin and SNAP-25 (Südhof, 2004) via an α-helical SNARE motif proximal to its transmembrane domain (Sutton et al., 1998).

Because synaptophysin is essential for efficient sybII retrieval, we investigated whether identified XLID mutants display defects in this process. To this end, we replicated XLID mutations in human synaptophysin (hSyp) and determined whether they could rescue function in cultured neurons derived from synaptophysin knock-out mice. We found that all XLID hSyp variants displayed a reduced ability to retrieve sybII from the plasma membrane during endocytosis, with different effects on SV endocytosis kinetics. Therefore, inefficient sybII retrieval may underlie neuronal defects in XLID patients harboring synaptophysin mutations.

Materials and Methods

Materials. hSyp clone cDNA BC064550 was obtained from Source Bioscience. Synaptobrevin II-pHloorin (sybII-pHloorin) and vesicular glutamate transporter 1 (vGLUT1)-pHloorin constructs were provided by Prof. G. Miesenbock (Oxford University) and Prof. R. Edwards (University of California), respectively. Neurobasal media, B-27 supplement, penicillin/streptomycin, MEM, and lipofectamine 2000 were obtained from Invitrogen. All other reagents were obtained from Sigma-Aldrich.

Plasmid preparation. hSyp clone cDNA (full-length human synaptophysin gene plus ∼1500 bp of downstream intronic sequence) was obtained in a pCMV-SPORT6 vector. Primers were generated to encompass the entire hSyp coding sequence plus 1267 bases of downstream sequence (forward primer: TCAGTGCTAGCTGTCGCTGCTGGCCGAC ATGGACG, reverse primer: GAGATCCGCATATCATCGACTCTTC.
TCAGG, restriction sites underlined). The 2 kb PCR transcript was digested with XhoI and BamHI and ligated into a pEGFP-C1 vector backbone (Clontech) in which the coding sequence for EGFP was replaced by mCerulean (mCer; Rizzo et al., 2004) using AgeI and BsrGI enzymes. The hSyp clone contained a point mutation (Pro196Leu), which was reverted back to its original form by mutagenesis (forward: GAG GCAGGGAGACCTTGAGACCTTGG; reverse: CGAGGGCTACAGGGTCTCTACGTCC). Human XLID synaptophysin mutations were then introduced into mCer-hSyp via mutagenesis (mutated bases underlined: 177–178CA/H11022 GT, forward: GGATTGTGCCAAGTAGACCGAGATGTGACCTCAGC, reverse: CTAAGAAGACCTTGAGGTGCCCCCTCG; 829 – 832delGACT, position of deleted bases highlighted, forward: GCTACCAGCCT----ATGGTCAACCAGCCGGC, reverse: GCCGGCTGGTTGACCAT----AGGCTGGTAGC) and confirmed by sequencing.

Cortical neuronal cultures. Synaptophysin knock-out mice were maintained as heterozygous breeding pairs on a C56BL/6J background (Gordon et al., 2011). Dissociated primary cortical neuronal cultures were prepared from both embryonic day 17.5 (E17.5) knock-out and wild-type embryos of either sex and then cotransfected with both mCer vectors and pHluorin reporter using lipofectamine 2000 after 7 d in culture (Gordon et al., 2011). Cells were imaged after 13–16 d in culture.

Fluorescent imaging protocols. Cortical cultures were mounted in a Warner imaging chamber with embedded parallel platinum wires (RC-21BRFS) and placed on the stage of Zeiss Axio Observer D1 epifluorescence microscope. Neurons transfected with mCer vectors were visualized with a Zeiss PlanNeofluar 40× oil-immersion objective (numerical aperture 1.3) at 430 nm excitation, whereas pHluorin reporters were visualized at 500 nm (both using a 525 nm dichroic and long-pass emission filter >535 nm). In all experiments, cultures were stimulated with a train of 300 action potentials delivered at 10 Hz (100 mA, 1 ms pulse width). Cultures were subjected to continuous perfusion with imaging buffer containing the following (in mM): 136 NaCl, 2.5 KCl, 2 CaCl2, 1.3 MgCl2, 10 glucose, and 10 HEPES, pH 7.4. Fluorescent images were captured at 4 s intervals (exposure times ranged between 0.9 and 1.3 s) using a Hamamatsu Orca-ER digital camera and processed offline using ImageJ version 1.43 software. Regions of interest were placed over nerve terminals and the total fluorescence intensity was monitored over time. Only regions that responded to action potential stimulation were selected for analysis. All statistical analyses were performed using Microsoft Excel and GraphPad Prism software. The pHluorin fluorescence change was calculated as ΔF/F₀, and n refers to the number of individual coverslips examined.

Figure 1. XLID mCer-hSyp mutants display different localization profiles. A, Illustration depicting putative mutant hSyp structures. Compared with the full-length wild-type (WT) protein, hSyp59 is a truncation after the first transmembrane domain; hSyp136 is a truncation and frame shift after the first transmembrane domain; hSypG217R is a point mutation in the fourth transmembrane domain (G217R); and hSyp469 is a frameshift resulting in an extension of the C terminus. Synaptophysin knock-out cortical neurons were cotransfected with sybII-pHluorin and either empty mCer vector or mCer-hSyp variants. Representative images show the differential distribution of the hSyp proteins along axonal segments after quenching pHluorin fluorescence with acidic imaging buffer (B, mCer; C, mCer-hSypWT; D, mCer-hSyp59; E, mCer-hSyp136; F, mCer-hSypG217R; and G, mCer-hSyp469). Scale bar, 10 μm. H, Bar graph displaying the CV of mCer fluorescence intensity along axonal segments. Data are presented as mean ± SEM, n = 5 for all. ***p < 0.001, one-way ANOVA with Bonferroni’s multiple-comparison post test for mCer-hSypWT, mCer-hSypG217R, and mCer-hSyp469 against mCer, mCer-hSyp59, or mCer-hSyp136.

The diffuseness of mCer-hSyp variants and sybII-pHluorin fluorescence along axons was determined by calculating the coefficient of variation (CV; Lyles et al., 2006), which was determined by drawing a >100 pixel line over an axonal segment and determining the SD/mean.
fluorescence signal. The CV for sybII-pHluorin was calculated after exposure of the cells to alkaline imaging buffer (50 mM NH₄Cl substituted for 50 mM NaCl) to reveal total sybII-pHluorin fluorescence, whereas mCer-hSyp CV was calculated after exposure to acidic imaging buffer (20 mM HEPES, pH 5.5) to quench contaminating pHluorin fluorescence (in both cases, 829-832delGACT mutation produces a frameshift in the cytoplasmic C-terminal tail of hSyp, resulting in the expression of 156 new amino acids. This mutant is therefore 469 aa long (hSyp₄₆₉), whereas the wild-type hSyp is 313 aa long.

To determine how these XLID mutations might affect hSyp function, mCer-tagged mutants were coexpressed in cultured synaptophysin knock-out neurons with the genetic reporter sybII-pHluorin. We first determined whether XLID mutations could influence the targeting of hSyp to SVs by examining their neuronal localization. The mCer empty vector displays a diffuse localization throughout the axon, whereas wild-type (mCer-hSyp₇₅₃) is distributed in a punctate fashion, indicating its localization to nerve terminals (Fig. 1 B, C). The truncated hSyp mutants mCer-hSyp₅₉ and mCer-hSyp₁₃₆ displayed a similar distribution profile to the empty vector (Fig. 1 D, E), whereas mCer-hSyp₂₂₁₇₇R and mCer-hSyp₄₆₉ mimicked the distribution of mCer-hSyp₇₅₃ (Fig. 1 F, G). To quantify the axonal distribution of hSyp variants, the CV was analyzed. CV quantifies the diffuseness of protein distribution, with a lower CV indicating a homogeneous localization along the axon and a higher CV signifying a punctate distribution (Lyles et al., 2006). When this analysis was performed, the CV of mCer-hSyp₇₅₃, mCer-hSyp₂₂₁₇₇R and mCer-hSyp₄₆₉ was significantly higher than that of mCer, mCer-hSyp₂₅₉, and mCer-hSyp₁₃₆ (Fig. 1 H). Therefore, hSyp₂₅₉ and hSyp₁₃₆ mutations result in mislocalization of the protein, whereas hSyp₂₂₁₇₇R and hSyp₄₆₉ retained a distribution commensurate with a nerve terminal localization.

Figure 2. XLID mCer-hSYP mutants differentially affect the localization of sybII-pHluorin. Synaptophysin knock-out cortical neurons were cotransfected with sybII-pHluorin and either empty mCer vector or mCer-hSyp variants. Representative images show the differential distribution of sybII-pHluorin along axonal segments after exposure to alkaline imaging buffer (A, mCer; B, mCer-hSyp₅₉; C, mCer-hSyp₁₃₆; D, mCer-hSyp₂₂₁₇₇R; F, mCer-hSyp₄₆₉). Scale bars, 10 μm. G, Bar graph displaying the CV of sybII-pHluorin fluorescence intensity along axonal segments. Data are presented as mean ± SEM. All comparisons were performed with one-way ANOVA with Bonferroni’s multiple-comparison post test. mCer-hSypWT, mCer-hSyp₂₂₁₇₇R and mCer-hSyp₄₆₉ against mCer; *p < 0.05 and ***p < 0.001; mCer-hSyp₂₅₉ against mCer-hSypWT, mCer-hSyp₂₂₁₇₇R, and mCer-hSyp₄₆₉; #p < 0.05 and ###p < 0.001; mCer-hSyp₁₃₆ against mCer-hSyp₂₂₁₇₇R and mCer-hSyp₄₆₉.

Results

Synaptophysin XLID mutants display different localization profiles

Mutations in hSyp segregate with XLID in a number of affected families, implicating hSyp in this condition (Tarpey et al., 2009). These mutations affect both the sequence and reading frame of hSyp (Fig. 1A). 177-178CA>G introduces a premature stop codon that truncates hSyp after 59 aa (hSyp₅₉). 274-275insA produces a frameshift that results in 45 new amino acids being expressed and truncates the protein after 136 aa (hSyp₁₃₆). 649G>C introduces an amino acid substitution in the fourth transmembrane domain of the protein (hSyp₂₂₁₇₇R). Finally, the 829-832delGACT mutation produces a frameshift in the cytoplasmic C-terminal tail of hSyp, resulting in the expression of 156 new amino acids. This mutant is therefore 469 aa long (hSyp₄₆₉), whereas the wild-type hSyp is 313 aa long.

To determine how these XLID mutations might affect hSyp function, mCer-tagged mutants were coexpressed in cultured synaptophysin knock-out neurons with the genetic reporter sybII-pHluorin. We first determined whether XLID mutations could influence the targeting of hSyp to SVs by examining their neuronal localization. The mCer empty vector displays a diffuse localization throughout the axon, whereas wild-type (mCer-hSyp₇₅₃) is distributed in a punctate fashion, indicating its localization to nerve terminals (Fig. 1 B, C). The truncated hSyp mutants mCer-hSyp₅₉ and mCer-hSyp₁₃₆ displayed a similar distribution profile to the empty vector (Fig. 1 D, E), whereas mCer-hSyp₂₂₁₇₇R and mCer-hSyp₄₆₉ mimicked the distribution of mCer-hSyp₇₅₃ (Fig. 1 F, G). To quantify the axonal distribution of hSyp variants, the CV was analyzed. CV quantifies the diffuseness of protein distribution, with a lower CV indicating a homogeneous localization along the axon and a higher CV signifying a punctate distribution (Lyles et al., 2006). When this analysis was performed, the CV of mCer-hSyp₇₅₃, mCer-hSyp₂₂₁₇₇R and mCer-hSyp₄₆₉ was significantly higher than that of mCer, mCer-hSyp₂₅₉, and mCer-hSyp₁₃₆ (Fig. 1 H). Therefore, hSyp₂₅₉ and hSyp₁₃₆ mutations result in mislocalization of the protein, whereas hSyp₂₂₁₇₇R and hSyp₄₆₉ retained a distribution commensurate with a nerve terminal localization.
hSyP136 compared with neurons expressing mCer-hSyPWT, mCer-hSyP469, or mCer-hSyP469 (Fig. 2G). Therefore, sybII cannot be efficiently targeted to nerve terminals by either mCer-hSyP59 or mCer-hSyP136.

**XLID mutants do not rescue sybII-pHluorin retrieval**

The altered axonal distribution of sybII-pHluorin in synaptophysin knock-out neurons is due to a defect in sybII retrieval from the plasma membrane during endocytosis (Gordon et al., 2011). Therefore we next investigated whether expression of hSyP XLID mutants also perturbed sybII-pHluorin retrieval. The pHluorin tag reports changes in the pH of its local environment, so the observed fluorescence increase on stimulation is due to SV endocytosis. After stimulation, a fluorescence decrease occurs, representing SV endocytosis followed by SV acidification. Changes in this fluorescent downstroke strictly reports sybII retrieval, because SV acidification is unaffected in synaptophysin knock-out mice (Kwon and Chapman, 2011). Synaptophysin knock-out neurons cotransfected with both mCer-hSyP mutants and sybII-pHluorin were stimulated with a train of 300 action potentials (10 Hz) to trigger SV recycling. SybII-pHluorin fluorescence decreased after stimulation in neurons rescued with mCer-hSyPWT, in contrast to empty vector, in which the decrease in fluorescence was significantly slowed (Fig. 3A). When truncated variants of hSyP were examined, a pronounced defect in poststimulation sybII-pHluorin retrieval was observed for both mCer-hSyP59 and mCer-hSyP136 (Fig. 3A). Therefore, sybII-pHluorin retrieval is not supported by truncated XLID hSyP mutants.

Both hSyP59 and hSyP136 mutants represent severe truncations of synaptophysin; therefore, we predicted that they may be dominant negative when expressed in wild-type neurons. To determine this, we examined the retrieval of sybII-pHluorin in wild-type neurons coexpressing either mCer-hSyP59 or mCer-hSyP136. Expression of either of these mutants produced significant dominant-negative effects on sybII-pHluorin retrieval compared with either mCer-hSyPWT or mCer empty vectors (Fig. 3B). Therefore, expression of truncated XLID hSyP mutants in wild-type neurons perturbs the ability of endogenous synaptophysin to retrieve sybII successfully.

In contrast to the truncated hSyP mutants, hSyP469 displayed a subcellular localization indicative of targeting to SVs. We next investigated whether these mutants could rescue sybII-pHluorin retrieval in synaptophysin knock-out neurons. These mutants displayed a partial rescue of sybII-pHluorin retrieval compared with mCer alone; however, they did not fully rescue to mCer-hSyPWT levels (Fig. 3C). Neither mutant affected sybII-pHluorin retrieval when expressed in wild-type neurons, indicating no interference with endogenous synaptophysin (Fig. 3D). Therefore, the full-length XLID mutants hSyP469 display defects in sybII retrieval despite being correctly localized to nerve terminals.

**hSyP469 differentially regulates the rate of SV endocytosis**

The absence of synaptophysin has no global effect on SV turnover; however, it does reduce the speed of SV endocytosis (Gordon et al., 2011; Kwon and Chapman, 2011). Therefore, we next determined whether XLID hSyP mutants could rescue SV endocytosis kinetics by coexpressing the genetic reporter vGLUT-pHluorin (Voglmaier et al., 2006). We were unable to examine the effect of either mCer-hSyP59 or mCer-hSyP136 because both were toxic when expressed in the absence of exogenous sybII (data not shown). Therefore, we limited our study to mCer-hSyP469 and mCer-hSyP469. After stimulation with 300 action potentials (10 Hz), vGLUT-pHluorin recovery was significantly slower in synaptophysin knock-out neurons expressing the empty mCer vector compared with mCer-hSyPWT (Fig. 4; Gordon et al., 2011). There was no significant effect of vGLUT-pHluorin localization (data not shown), indicating this was purely a kinetic defect. Expression of mCer-hSyP469 failed to rescue vGLUT-pHluorin retrieval kinetics significantly, whereas mCer-hSyP469 fully rescued vGLUT-pHluorin retrieval in a manner identical to mCer-hSyPWT (Fig. 4). Therefore, although both hSyP469 and hSyP469 display defects in sybII-pHluorin retrieval, only hSyP469 is able to fully rescue deficits in the speed of SV endocytosis.
Discussion

Synaptophysin is one of the most abundant proteins on SVs and is required for the efficient retrieval of sybII from the plasma membrane after exocytosis (Gordon et al., 2011). We show here that a range of mutant variants of hSyp identified in a screen of XLID families differentially affected both the localization and function of the protein. None of the XLID hSyp mutants examined could fully rescue sybII retrieval in synaptophysin knock-out neurons. Truncation of hSyp after its first transmembrane domain resulted in a dominant-negative form of the protein, which was mislocalized from nerve terminals and abrogated sybII-pHluorin retrieval, even in wild-type neurons. Full-length hSyp mutants displayed more subtle defects in sybII-pHluorin retrieval and a divergence in their ability to rescue the speed of SV endocytosis.

The hSyp59 and hSyp136 truncation mutants were dominant negative, with their expression in wild-type neurons inhibiting sybII-pHluorin retrieval to levels observed in synaptophysin knock-out neurons. An interesting observation was that these mutants were toxic to neurons unless they were coexpressed with exogenous sybII. In the presence of exogenous sybII, these hSyp mutants exit the secretory pathway, whereas hSyp469, which mimics wild-type hSyp (S. Gordon, unpublished observations), is required for the efficient retrieval of sybII-pHluorin retrieval and vGLUT-pHluorin speed, suggesting a general defect in synaptophysin function. Consistent with this, preliminary experiments to examine the trafficking of this mutant during neuronal activity suggest that its reentry back into nerve terminals is retarded, unlike hSyp469, which mimics wild-type hSyp (S. Gordon, unpublished observations). The selective deficit in sybII-pHluorin retrieval observed with hSyp469 suggests that its extended C-terminal cytosolic domain contains additional motifs that disrupt this event because all other aspects of its function correlate with wild-type hSyp.

The ability of hSyp469 to display a wild-type functional profile with the exception of inefficient sybII-pHluorin retrieval suggests that it is specifically this event that may be deleterious to individuals carrying hSyp mutations in XLID. Consistent with this, all hSyp mutants have an inability to fully rescue sybII retrieval. This effect should not be restricted to sybII-pHluorin because endogenous sybII is mislocalized to the same extent as the reporter in synaptophysin knock-out neurons (Gordon et al., 2011). Inefficient sybII retrieval still results in efficient neurotransmitter release and does not perturb global SV turnover in synaptophysin knock-out mice (McMahon et al., 1996; Gordon et al., 2011; Kwon and Chapman, 2011). The absence of an immediate consequence of perturbed sybII retrieval is potentially due to the excess reservoir of sybII present on SVs. Current estimates suggest that there are ~60–70 copies of sybII on a SV (Takamori et al., 2006), however, <10 (possibly even only 1–3) copies of sybII are required for SV fusion (Mohrmann et al., 2010; van den Boogaart et al., 2010; Sinha et al., 2011). Therefore, rather than an immediate reduction in neurotransmission, it is likely that deficient sybII retrieval will have a subtle effect on synaptic efficiency and that it is mediated via hydrophobic interactions through their transmembrane domains (Yelamanchili et al., 2005; Bonanomi et al., 2007; Feldk and Leube, 2008).
over time. This may be exacerbated during high-intensity stimulation, resulting in small deficiencies in plastic changes at the synapse due to experience. Consistent with this, the only behavioral alteration identified in synaptophysin knock-out mice to date is a mild deficit in learning and memory (Schmitt et al., 2009).

The discovery of a series of mutations in hSyp during a large-scale study into familial XLID has linked synaptophysin to this disorder (Tarpey et al., 2009). Although they only account for a small percentage of the XLID cases, these mutations were highly penetrant, implicating synaptophysin in disease causation for these patients. We show in this study that all hSyp mutants examined were dysfunctional for the retrieval of sybII during endocytosis, providing a possible mechanistic basis for the condition. These XLID mutations have provided clues to the mechanism of action of synaptophysin in sybII retrieval and have illustrated that synaptophysin may control sybII retrieval independently of SV endocytosis kinetics. Finally, our results provide a valuable insight into how small perturbations in the efficiency of presynaptic function could translate into human disease.

References


