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In addition to disrupting the regulated intramembranous proteolysis of key substrates, mutations in the presenilins also alter calcium homeostasis, but the mechanism linking presenilins and calcium regulation is unresolved. At rest, cytosolic Ca\(^{2+}\) is maintained at low levels by pumping Ca\(^{2+}\) into stores in the endoplasmic reticulum (ER) via the sarco ER Ca\(^{2+}\)-ATPase (SERCA) pumps. We show that SERCA activity is diminished in fibroblasts lacking both PS1 and PS2 genes, despite elevated SERCA2b steady-state levels, and we show that presenilins and SERCA physically interact. Enhancing presenilin levels in Xenopus laevis oocytes accelerates clearance of cytosolic Ca\(^{2+}\), whereas higher levels of SERCA2b phenocopy PS1 overexpression, accelerating Ca\(^{2+}\) clearance and exaggerating inositol 1,4,5-trisphosphate–mediated Ca\(^{2+}\) liberation. The critical role that SERCA2b plays in the pathogenesis of Alzheimer’s disease is underscored by our findings that modulating SERCA activity alters amyloid β production. Our results point to a physiological role for the presenilins in Ca\(^{2+}\) signaling via regulation of the SERCA pump.

Introduction

PS1 and PS2 are highly conserved integral membrane proteins that localize predominantly to the ER. Mutations in the PS1 and PS2 genes that cause autosomal-dominant early-onset Alzheimer’s disease (AD) disrupt several cellular pathways, including altered γ-secretase–mediated cleavage of the amyloid precursor protein (APP) to form amyloid β (Aβ) peptides (Duff et al., 1996) and disruption of intracellular Ca\(^{2+}\) homeostasis (LaFerla, 2002; Demuro et al., 2005). Ca\(^{2+}\) signaling disruptions manifest as enhanced filling of ER Ca\(^{2+}\) stores (Leissring et al., 1999b), attenuation of capacitive Ca\(^{2+}\) entry stores (Leissring et al., 2000; Yoo et al., 2000; Smith et al., 2002; Herms et al., 2003), and by exaggerated liberation of Ca\(^{2+}\) from the ER by the second messenger inositol 1,4,5-trisphosphate (IP\(_3\); Leissring et al., 1999b; Yoo et al., 2000; Smith et al., 2002; Stutzmann et al., 2004). Given that mutations in presenilin disrupt intracellular Ca\(^{2+}\) signaling, we set out to determine whether presenilins may serve a physiological role in intracellular Ca\(^{2+}\) homeostasis.

In support of a role in Ca\(^{2+}\) homeostasis, overexpression of wild-type PS1 or PS2 in Xenopus laevis oocytes causes enhanced IP\(_3\)-mediated Ca\(^{2+}\) release, an effect that is exacerbated by mutations in both genes (Leissring et al., 1999b). However, it remains unclear whether the exaggerated IP\(_3\)-evoked responses result from modulation of the IP\(_3\) signaling pathway, such as sensitization of IP\(_3\) receptors by presenilins, or as a consequence of overfilling of ER stores. Recently, the presenilins have been reported to be able to form ER leak channels, and it has been reported that mutations in the presenilins disrupt this function (Tu et al., 2006). However, it is unclear how leak channel formation could account for the numerous reports of wild-type presenilin overexpression increasing IP\(_3\)-mediated calcium release.

Ca\(^{2+}\) pumps, along with Ca\(^{2+}\) release channels, are the key components of Ca\(^{2+}\) regulatory systems in neuronal and nonneuronal cells (Berridge et al., 2000). The sarco ER Ca\(^{2+}\)-ATPase (SERCA) pumps have the highest affinity for Ca\(^{2+}\) removal from the cytosol and, together with plasma membrane Ca\(^{2+}\)-ATPases and transporters, determine the resting cytosolic Ca\(^{2+}\) concentration. Three differentially expressed genes encode at least five isoforms of the SERCA pump. SERCA1a and -1b are expressed in skeletal muscle, whereas SERCA2a is expressed in cardiac muscle (Aubier and Vières, 1998). SERCA2b, which has a C-terminal extension, is ubiquitously expressed in smooth muscle tissues and nonmuscle tissues including neurons (Baba-Aissa et al., 1998). SERCA3 has limited expression in various nonmuscle tissues (Baba-Aissa et al., 1998).
Given that overfilled ER Ca\textsuperscript{2+} stores are one consequence of most PS1 mutations, we hypothesized that presenilin may regulate SERCA pump activity. In this paper, we used both gain-of-function and loss-of-function genetic approaches to show that presenilins are required for proper functioning of SERCA activity in both mammalian cell lines and \textit{X. laevis} oocytes. Notably, we find that presenilins physically associate with SERCA, and modulation of SERCA function via genetic or pharmacological means results in altered Aβ production. Furthermore, SERCA2b knockdown mimics the Ca\textsuperscript{2+} dynamics seen in presenilin-null cells. Collectively, these results suggest that presenilins regulate and are necessary for normal functioning of the SERCA2b pump, most likely through a direct protein–protein interaction, and that SERCA activity itself impacts Aβ generation.

**Results**

**Elevated cytosolic Ca\textsuperscript{2+} levels and attenuated ER Ca\textsuperscript{2+} stores in presenilin-null cells**

We previously showed that presenilin mutations lead to enhanced filling of ER Ca\textsuperscript{2+} stores (Leissring et al., 1999a,b). To further explore the role of endogenous presenilin in intracellular Ca\textsuperscript{2+} signaling, we investigated ER Ca\textsuperscript{2+} stores in immortalized mouse embryonic fibroblast (MEF) cells from presenilin double-knockout (PSDKO) mice (Herreman et al., 1999). Cytosolic Ca\textsuperscript{2+} signals were recorded in Fura-2-AM–loaded cells before and during stimulation with 1 μM thapsigargin, a potent irreversible inhibitor of the SERCA pump (Lytton et al., 1991).

PSDKO fibroblasts displayed elevated resting cytosolic Ca\textsuperscript{2+} levels compared with control cells (Fig. 1, A and B). Application of thapsigargin in the bath perfusion promoted a transient rise of cytosolic [Ca\textsuperscript{2+}] signal as a consequence of constitutively active Ca\textsuperscript{2+} leakage from the ER, providing a signal proportional to the amount of Ca\textsuperscript{2+} sequestered in the ER, although it does not take into account differences in Ca\textsuperscript{2+} efflux across the plasma membrane. PSDKO fibroblasts showed reduced responses to thapsigargin as compared with control fibroblasts (Fig. 1 B). These results are consistent with diminished SERCA activity, as it is this ER Ca\textsuperscript{2+} pump which helps to maintain low cytosolic resting Ca\textsuperscript{2+} level by actively pumping Ca\textsuperscript{2+} from the cytosol into the ER stores, thereby regulating the Ca\textsuperscript{2+} levels between the two compartments.

To determine the respective contribution of the two presenilins, we next investigated Ca\textsuperscript{2+} responses in PS1-deficient (PS1KO) or PS2-deficient (PS2KO) fibroblasts. Basal cytosolic Ca\textsuperscript{2+} levels were elevated in the PS2KO cells at comparable levels to those observed in the PSDKO fibroblasts. Likewise, the PS2KO cells also showed diminished responses after treatment with thapsigargin. In contrast, the PS1KO cells showed small or no changes in basal Ca\textsuperscript{2+} levels but did show diminished thapsigargin-mediated responses (Fig. 1, A and B). Therefore, although both PS1 and 2 appear to regulate intracellular Ca\textsuperscript{2+} homeostasis, it appears to be PS2 that plays a larger role in maintaining low cytosolic Ca\textsuperscript{2+} levels and appropriate filling of ER Ca\textsuperscript{2+} stores. We next looked at ionomycin-evoked calcium release in control and PSDKO cells (Fig. 1 C). Ionomycin is an ionophore that causes the release of Ca\textsuperscript{2+} from most intracellular stores. Application of 1 μM ionomycin in the absence of extracellular Ca\textsuperscript{2+} evoked smaller rises and areas
PS1, PS2, or both together rescued both the basal and thapsigargin-evoked Ca\(^{2+}\) levels to the same degree (Fig. 2, A and B).

SERCA2b steady-state levels are elevated in presenilin-null cells

The observed phenotype of elevated basal cytosolic Ca\(^{2+}\) and reduced ER Ca\(^{2+}\) store content in presenilin-null cells is consistent with either reduced levels of SERCA2b or a reduction in functional activity of SERCA pumps (Zhang et al., 2006). Surprisingly, we found that SERCA2b steady-state levels, the isoform of SERCA found in brain neurons, were elevated, rather than diminished, in the PSDKO fibroblasts (Fig. 2, C and E), suggesting that SERCA activity was impaired in the absence of presenilins and that the cells attempt to compensate by increasing SERCA expression. The presence of either PS1 or PS2 is sufficient to prevent this increase in SERCA2b steady-state levels as shown in PS1KO and PS2KO cell lines (Fig. 2, D and E). Given our hypothesis that SERCA activity was impaired in the absence of presenilins, we attempted to mimic the Ca\(^{2+}\) phenotype seen in PSDKO cells via siRNA knockdown of SERCA2b in CHO cells. Knockdown of SERCA2b levels resulted in elevated basal Ca\(^{2+}\) levels, and a marked decrease in thapsigargin evoked Ca\(^{2+}\) release (Fig. 2 F).
expression system to monitor the clearance of Ca\(^{2+}\) ions from the cytosol after a transient influx across the plasma membrane. For this purpose, oocytes were induced to express the Ca\(^{2+}\)-permeable nicotinic acetylcholine receptor (nAChR) that served as a “Ca\(^{2+}\) switch,” allowing precisely controlled cytosolic Ca\(^{2+}\) transients to be evoked by pulsing the membrane potential to strongly negative voltages to increase the electrochemical driving force for Ca\(^{2+}\) entry. Oocytes were loaded with the Ca\(^{2+}\)-sensitive dye Oregon Green BAPTA 1 and were voltage-clamped at a holding potential of 0 mV to minimize Ca\(^{2+}\) influx. In the presence of 100–500 nM acetylcholine, a brief (300 ms) hyperpolarizing pulse to −150 mV produced a transient Ca\(^{2+}\) fluorescence signal because of Ca\(^{2+}\)

This phenotype was remarkably similar to that seen in the PS-DKO cell line, giving further credence to presenilin regulation of SERCA function. It should be noted that it is unlikely that changes in SERCA function directly modulate basal cytosolic Ca\(^{2+}\) levels but that they probably do so through changes in other Ca\(^{2+}\) influx pathways such as store-operated Ca\(^{2+}\) entry.

**PS1 and PS2 mimic SERCA2b-accelerated cytosolic Ca\(^{2+}\) clearance**

Based on these data from presenilin-null cell lines, we moved to a more regulatable system to directly establish whether presenilins modulate SERCA pump activity. We used the X. laevis oocyte

![Figure 3. PS1 and PS2 accelerate the clearance of cytosolic Ca\(^{2+}\) after entry via muscle nAChR channels. (A) Ca\(^{2+}\)-dependent fluorescence changes (ΔF/ΔF\(_{0}\)) after 300-ms hyperpolarizing pulses to induce Ca\(^{2+}\) entry through nAChR expressed in the plasma membrane. Traces show mean data from >35 recordings in multiple oocytes injected 3 d earlier with αβγγ nAChR subunits alone (control) or together with PS1, PS2, or SERCA2b cRNA. The inset shows the same data on a semilogarithmic scale. (B–D) Data from, respectively, control, PS2, and SERCA2b oocytes, fitted by biexponential decays (superimposed red traces). (E) Table listing fast (T1) and slow (T2) time constants of double-exponential fits to the Ca\(^{2+}\) decay data.](https://example.com/figure3)
Ca\textsuperscript{2+} influx through open nicotinic channels. The decay rate of the fluorescence signals after termination of the voltage pulse was then used to quantify the rate of Ca\textsuperscript{2+} sequestration from the cytosol. For video footage of Ca\textsuperscript{2+} entry and subsequent clearance from the cytosol in this system please see Video 1 (available at http://www.jcb.org/cgi/content/full/jcb.200706171/DC1).

Fig. 3A shows mean traces of Oregon Green fluorescence, illustrating differences in the decay rate of the Ca\textsuperscript{2+} signal in control, PS1-, PS2- and SERCA2b-expressing oocytes. The decay presumably reflects a summation of several factors (e.g., diffusion of Ca\textsuperscript{2+} ions into the interior of the oocyte, mitochondrial uptake, and extrusion across the plasma membrane) in addition to sequestration into the ER by SERCA pumps. Consistent with this, decay kinetics were best fit by double-exponential processes (Fig. 2, B–D), with time constants of a few hundred milliseconds and a few seconds (Fig. 2E). Sequestration by SERCA pumps is expected to be reflected primarily in the slower component (τ2) and, in agreement with this interpretation, τ2 was accelerated almost twofold in SERCA2b-overexpressing oocytes as compared with control cells.

The acceleration of Ca\textsuperscript{2+} sequestration was even greater in oocytes expressing PS2 than in those overexpressing SERCA2b, and a small acceleration was also evident with overexpression of PS1 (Fig. 3E). These results confirm our finding that PS2 plays a more important role in regulating ER store Ca\textsuperscript{2+} refilling than does PS1 (Fig. 1), and they point to regulatory roles in both mammalian cells and X. laevis oocytes.

**Pharmacological inhibition of SERCA prevents presenilin-mediated acceleration of cytosolic Ca\textsuperscript{2+} sequestration**

Overexpression of either PS1, 2, or SERCA resulted in an accelerated sequestration of the cytosolic Ca\textsuperscript{2+} after a controlled Ca\textsuperscript{2+} influx across the plasma membrane, with PS2 having the most robust effect (Fig. 3). To prove that overexpression of presenilin was accelerating Ca\textsuperscript{2+} clearance from the cytosol by increasing SERCA activity, we measured Ca\textsuperscript{2+} clearance in the presence of thapsigargin, a specific inhibitor of SERCA. If our hypothesis was true, then presenilin should no longer accelerate clearance of Ca\textsuperscript{2+} from the cytosol in the presence of thapsigargin, compared with control oocytes also in the presence of thapsigargin. We incubated control and PS2-expressing oocytes in 30 μM thapsigargin in the bathing solution for 30 min. After a 30-min incubation, we applied a 300-ms hyperpolarization pulse, as before, to allow a controlled influx of Ca\textsuperscript{2+} across the plasma membrane into the cytosol and then tracked the clearance of this Ca\textsuperscript{2+} into the intracellular stores. In both control and PS2-expressing oocytes, thapsigargin reduced the speed of the Ca\textsuperscript{2+} fluorescence decay, with PS2-expressing oocytes showing the strongest effect, which is consistent with impairment of PS2 modulation of SERCA activity (Fig. 4, A and B). Double-exponential curve fitting revealed that both control and PS2-expressing oocytes having markedly faster τ2 values compared with control oocytes in the absence of thapsigargin (Fig. 4C).

**PS1 familial AD (FAD) mutation M146V accelerates cytosolic Ca\textsuperscript{2+} sequestration**

Mutations in the presenilins have been associated with enhanced IP\textsubscript{3}-mediated Ca\textsuperscript{2+} release from oocytes (Leisssring et al., 1999a,b) and a variety of mammalian cell types (Smith et al., 2002). We have showed that wild-type presenilins accelerate Ca\textsuperscript{2+} sequestration from the cytosol in a thapsigargin-sensitive pathway and that overexpression of SERCA phenocopies this. We expressed the presenilin FAD mutant PS1M146V in X. laevis oocytes.
SERCA2b and PS1/PS2 are colocalized and interact

Although both PS1 and PS2 have been localized to ER in several cell types (Walter et al., 1996) and SERCA is an ER Ca\(^{2+}\) pump, it is not known if they colocalize within specific regions of the ER. To address this question, we used confocal dual-label imaging of wild-type fibroblasts using a polyclonal antiserum against SERCA2b and a polyclonal antiserum against either PS1 or PS2 and found that SERCA2b and PS2 do colocalize, whereas colocalization between SERCA2b and PS1 was present but not as prevalent (Fig. 7 A).

To biochemically determine whether presenilins physically associate with SERCA2b, we conducted immunoprecipitation experiments. Fibroblast cell lysates were immunoprecipitated with either a PS1- or PS2-specific antibody or an irrelevant control antibody (anti-p35). The resultant pellets were fractionated on a 4–12% Bis/Tris gel and immunoblotted for SERCA2b. Both PS1 and PS2 were found to specifically bind to SERCA2b, whereas SERCA2b did not coprecipitate with the control antibody (Fig. 7 B). Conversely, immunoprecipitating with an anti-SERCA2b antibody followed by immunoblotting for PS1 or PS2 was not feasible because the weights of the IgG heavy and light chains (\(<55\) and 25 kD) are the same as of presenilin holoprotein (\(<55\) kD) or carboxy fragment (\(<22\) kD), and although using different species of polyclonal antibodies revealed bands at the correct weights, we could not absolutely determine whether they were presenilin or cross-reactivity with intraspecies IgG chains.

SERCA activity regulates A\(_{\beta}\) production

Our data indicate that presenilins are required for normal SERCA function and physiological maintenance of cellular calcium homeostasis. Moreover, given that presenilins are integral for the production of A\(_{\beta}\), we investigated whether SERCA function influenced A\(_{\beta}\) production. To address this issue, we used pharmacological and gain-of-function and loss-of-function genetic approaches. First, we considered the consequences of overexpressing SERCA2b in CHO cells stably expressing APP. After 48 h, we found that higher SERCA2b levels caused a marked increase in A\(_{\beta}\)40 production (Fig. 8 A). Conversely, reducing SERCA2b via siRNA-mediated knockdown caused a significant decrease in both A\(_{\beta}\)40 and A\(_{\beta}\)42 levels (Fig. 8 B). Pharmacological inhibition of SERCA2b with thapsigargin rapidly reduced A\(_{\beta}\)40 and A\(_{\beta}\)42 production (Fig. 8, C and D), which is in agreement with SERCA2b knockdown. The sum of these findings indicates that SERCA pump activity impacts A\(_{\beta}\) production.

Discussion

Cellular Ca\(^{2+}\) dyshomeostasis has been consistently observed in numerous experimental systems harboring presenilin mutations, including X. laevis oocytes, transfected cell lines, genetically altered mice, and human fibroblasts from FAD patients (LaFerla, 2002). These pathological disruptions in Ca\(^{2+}\) signaling suggest that the presenilins may play a physiological role in cellular Ca\(^{2+}\) regulation, although this has not been firmly established or characterized. In this paper, we examined the role of wild-type presenilins

Figure 5. PS1 FAD mutation M146V accelerates cytosolic Ca\(^{2+}\) sequestration. (A) Traces show Ca\(^{2+}\)-dependent fluorescence changes ($\Delta F/F_o$) after 300-ms hyperpolarizing pulses to induce Ca\(^{2+}\) entry through nAChR expressed in the plasma membrane obtained from control and PS1 M146V expressing oocytes. (B) Table listing fast ($T_1$) and slow ($T_2$) time constants of double-exponential fits to the Ca\(^{2+}\) decay data.

SERCA2b overexpression increases IP\(_3\) mediated calcium release

We previously showed that overexpression of either PS1 or PS2 leads to an increase in IP\(_3\)-mediated Ca\(^{2+}\) release in X. laevis oocytes (Leissring et al., 1999a,b), but it was unclear whether this arose through increased activation or conductance of IP\(_3\) receptor/channels or from enhanced store filling. To discriminate between these possibilities, we examined whether enhanced SERCA pump activity could replicate the increased IP\(_3\) response. We monitored Ca\(^{2+}\) liberation by linescan confocal microscopy in response to photorelease of IP\(_3\) from a caged precursor evoked by UV flashes of varying duration as previously described (Leissring et al., 1999a,b). Similar to the effects of presenilin overexpression, mean Ca\(^{2+}\) responses evoked by high IP\(_3\) were enhanced by \(<50\%\) (Fig. 6 D), and the decay of IP\(_3\)-evoked Ca\(^{2+}\) transients was accelerated (Figs. 6, B and C). These findings show that an increase in SERCA pump activity mimics the phenotype previously seen with presenilin overexpression.
Ca\textsuperscript{2+} leak channels in the ER (Tu et al., 2006) and are an integral part of intracellular Ca\textsuperscript{2+} homeostasis via passive leak from the ER stores. The prospect of presenilins forming ER leak channels is, however, at odds with the observation that overexpression of presenilins leads to enhanced IP\textsubscript{3}-mediated Ca\textsuperscript{2+} release (Leissring et al., 1999a, b; Smith et al., 2002). Wild-type presenilin should increase passive leak from the ER stores, resulting in diminished IP\textsubscript{3}-mediated Ca\textsuperscript{2+} release, whereas the opposite actually occurs, with FAD-linked presenilin mutations augmenting IP\textsubscript{3}-mediated Ca\textsuperscript{2+} release even further (Leissring et al., 1999a, b). This paradox suggests that presenilins also have an impact on Ca\textsuperscript{2+} homeostasis through other means, which should be sufficient to explain how wild-type presenilin overexpression enhances IP\textsubscript{3}-mediated responses, whereas presenilin knockout cells have reduced IP\textsubscript{3}-mediated responses (Leissring et al., 2002). Presenilin regulating SERCA function is consistent with both of these observations, as we have shown in both mammalian cell lines and X. laevis oocyte expression systems, with overexpression of SERCA resulting in enhanced IP\textsubscript{3}-mediated Ca\textsuperscript{2+} release mimicking the phenotype seen with overexpression of presenilin (Fig. 5). Combining this with our data, it appears that presenilins contribute to both the active filling of the ER stores and the passive emptying and helps explain why mutations in these proteins have such widespread effects on global Ca\textsuperscript{2+} signaling.

**Figure 6.** Overexpression of SERCA2b phenocopies the enhanced IP\textsubscript{3}-evoked signals and accelerated Ca\textsuperscript{2+} decay observed with presenilin overexpression. (A) Representative linescan images showing Ca\textsuperscript{2+} signals evoked by photolysis flashes of 10-, 40-, 70-, and 100-ms durations. In each panel, distance along the scan line is depicted vertically, time runs from left to right, and increasing fluorescence ratio (increasing Ca\textsuperscript{2+}) corresponds to increasingly “warm” colors. Note the enhanced response in the oocyte overexpressing SERCA2b. (B and C) B and C show, respectively, Ca\textsuperscript{2+}-dependent fluorescence signals evoked by photoreleased IP\textsubscript{3} in a control oocyte and an oocyte expressing SERCA2b. Each panel, superimposed traces show responses (fluorescence ratio change averaged across the scan line) evoked by UV light flash durations in 10-ms increments between 10 and 110 ms. (D) Mean peak Ca\textsuperscript{2+} concentration plotted as a function of flash duration (linearly proportional to IP\textsubscript{3}) in control oocytes (n = 6) and in oocytes expressing SERCA2b (n = 5) from at least six recordings from multiple oocytes. Error bars show SEM.

on Ca\textsuperscript{2+} regulation in a mammalian cell system by using genetic knockout models and also in X. laevis oocytes through protein overexpression. Our results indicate that the presenilins regulate the activity of the SERCA pump and are necessary for its proper functioning. Indeed, siRNA knockdown of SERCA leads to a phenotype resembling presenilin-null cells (Fig. 1 A vs. Fig. 2 F), including elevated basal Ca\textsuperscript{2+} levels (also seen in Zhang et al. [2006]) and diminished thapsigargin-mediated Ca\textsuperscript{2+} release. Altered cytosolic Ca\textsuperscript{2+} levels probably arise because of changes in other Ca\textsuperscript{2+} influx pathways as a result of SERCA down-regulation, as it is unlikely that SERCA directly controls basal cytosolic Ca\textsuperscript{2+}. However, both of these phenotypes in presenilin-null cells are rescued by overexpression of presenilin (Fig. 2 A). Although interpretation of our functional data in cell lines is dependent on Ca\textsuperscript{2+} rises evoked by thapsigargin, which has pitfalls associated with it, the data obtained in oocytes confirm presenilin as a positive modulator of SERCA function. Overexpression of presenilins accelerates the clearance of a known quantity of Ca\textsuperscript{2+} from the cytosol with similar dynamics to SERCA overexpression. Crucially, accelerated Ca\textsuperscript{2+} clearance with presenilin overexpression is prevented by pharmacological inhibition of SERCA, providing direct functional evidence for an interaction between presenilin and SERCA. Supporting a physiological role for the presenilins, a recent study suggested that they can form Ca\textsuperscript{2+} leak channels in the ER (Tu et al., 2006) and are an integral part of intracellular Ca\textsuperscript{2+} homeostasis via passive leak from the ER stores. The prospect of presenilins forming ER leak channels is, however, at odds with the observation that overexpression of presenilins leads to enhanced IP\textsubscript{3}-mediated Ca\textsuperscript{2+} release (Leissring et al., 1999a, b; Smith et al., 2002). Wild-type presenilin should increase passive leak from the ER stores, resulting in diminished IP\textsubscript{3}-mediated Ca\textsuperscript{2+} release, whereas the opposite actually occurs, with FAD-linked presenilin mutations augmenting IP\textsubscript{3}-mediated Ca\textsuperscript{2+} release even further (Leissring et al., 1999a, b). This paradox suggests that presenilins also have an impact on Ca\textsuperscript{2+} homeostasis through other means, which should be sufficient to explain how wild-type presenilin overexpression enhances IP\textsubscript{3}-mediated responses, whereas presenilin knockout cells have reduced IP\textsubscript{3}-mediated responses (Leissring et al., 2002). Presenilin regulating SERCA function is consistent with both of these observations, as we have shown in both mammalian cell lines and X. laevis oocyte expression systems, with overexpression of SERCA resulting in enhanced IP\textsubscript{3}-mediated Ca\textsuperscript{2+} release mimicking the phenotype seen with overexpression of presenilin (Fig. 5). Combining this with our data, it appears that presenilins contribute to both the active filling of the ER stores and the passive emptying and helps explain why mutations in these proteins have such widespread effects on global Ca\textsuperscript{2+} signaling.
As both presenilin and SERCA have activities that can be modulated by several proteins as well as by one another, this presents an interesting question: if presenilins regulate SERCA function, then can SERCA also regulate γ-secretase activity? Several studies have illustrated how modulating Ca²⁺ influx can modulate production of the Aβ peptide (Querfurth and Selkoe, 1994; Pierrot et al., 2004), as well as increasing intracellular store release (Querfurth et al., 1997). Indeed, any regimen that affects intracellular Ca²⁺ will invariably alter the activity of SERCA, as it is itself modulated by cytosolic and ER Ca²⁺ concentration as models have shown (Yano et al., 2004). In this paper, we demonstrate through both pharmacological and genetic means that modulation of SERCA2b function results in altered Aβ production with decreased SERCA function leading to decreased Aβ and increased SERCA function leading to increased Aβ. Therefore, it seems possible that SERCA activity plays a modulatory role in γ-secretase function or at least in APP processing leading to further generation of the Aβ peptide. Curiously, it has been reported that either stimulation (Pierrot et al., 2004) or inhibition (Yoo et al., 2000) of capacitative Ca²⁺ entrance (CCE) leads to increased production of Aβ.42. Our results show that thapsigargin treatment, which depletes ER stores, diminishes...
Aβ production, yet depletion of ER stores leads to increased Ca\textsuperscript{2+} influx via CCE. This suggests that depleting ER stores of Ca\textsuperscript{2+} has a stronger effect on preventing Aβ production than CCE activation has on inhibiting it.

Numerous proteins, such as calsenilin, ryanodine receptor, and calmyrin (for review see Chen and Schubert, 2002), have been shown to interact with and bind the presenilins as well as the known components of the γ-secretase complex (nicastrin, PEN2, and Aph1), making the presenilins part of a very large multiprotein complex with multiple functions. Our results suggest that the interaction between SERCA and presenilin is an additional, but very important, interaction that serves to regulate sequestration of calcium into the ER stores, making presenilin a key component of cellular calcium homeostasis. A puzzling aspect is how mutations in the presenilins that modulate γ-secretase activity could cause the increases in intracellular Ca\textsuperscript{2+} signaling reported (Leissring et al., 1999a,b). Conversely, inhibitors of γ-secretase, which bind to the active site of presenilin in the γ-secretase complex, completely diminish ER Ca\textsuperscript{2+} release (Leissring et al., 2002; Kasri et al., 2006). Mutations in presenilin have been reported to disrupt the formation of ER leak channels, thereby preventing passive Ca\textsuperscript{2+} leak, which then leads to store overfilling (Tu et al., 2006) and, hence, exaggerated IP\textsubscript{3}-mediated release. Whether these same mutations also affect presenilins’ modulation of SERCA function remains to be seen, but many of these FAD-linked mutations are associated with an increase, or at least change, in γ-secretase activity, making the prospect plausible. Indeed, we have shown here that the FAD-linked PS1 mutation M146V does show enhanced clearance of cytosolic Ca\textsuperscript{2+} compared with wild-type PS1. The requirement of SERCA activity to have presenilins present may provide problems for drugs that inhibit the actions of the γ-secretase complex to therapeutically reduce Aβ levels in AD. Such drugs have already been shown to abolish ER Ca\textsuperscript{2+} release in cell cultures (Leissring et al., 2002; Kasri et al., 2006) but their chronic in vivo use has yet to be documented. Certainly, reducing or abolishing ER Ca\textsuperscript{2+} release in neurons will have massive implications on memory and behavior, which suggests that BACE may be a more prudent drug target to reduce Aβ in AD.

Materials and methods

Cell culture and calcium imaging

MEFs (Bart de Strooper, Katholieke Universiteit Leuven, Leuven, Netherlands) and CHO cells were maintained with DME and 10% FBS. Calcium imaging was performed as previously described (Leissring et al., 2002). In brief, measurements of intracellular calcium were obtained using the InCyt Im2 Ration imaging system (Intracellular Imaging, Inc.) using excitation at 340 and 380 nm. cDNA transfection was achieved using the Nucleofection technique (Amaxa) as per the manufacturer’s instructions. 5 μg cDNA was used alongside 1 μg GFP cDNA to assess transfection efficiency and for selecting cells that had been successfully transfected for Ca\textsuperscript{2+} imaging. Typically, 70% transfection efficiency was seen.

RNA interference

A 20:1 stock solution of opti-MEM (Invitrogen) to Mirus TransIT-IT1 transfection reagent (Mirus Bio) was incubated at room temperature for 20 min. siRNAs were added and the solution was incubated for an additional 20 min at room temperature. This mixture was then added to cells, already in opti-MEM, to a final siRNA concentration of 25 nM of each partial sequence. The cells were then incubated in 5% CO\textsubscript{2} atmosphere at 37°C for 12 h. Subsequently, cells were rescued with DME containing 10% FBS for an additional 12 h in 5% CO\textsubscript{2} atmosphere at 37°C. Thereafter, cells were given the same siRNA treatment for an additional 12 h and rescued for the next 12 h with DME containing 10% FBS in 5% CO\textsubscript{2} atmosphere at 37°C. Cells were then lysed and the lysates were stored at −80°C for further immunoblotting analysis. SERCA2b siRNA was acquired as a smartpool containing the following partial sequences: GCCAAUAUUGCCUUUUA, CAAAGUUCUCCUGUG, GĂĂUAGUCUGUCA, and GAUAUAAGGUAUAC.

Oocyte calcium imaging and photolysis of caged IP\textsubscript{3}

Plasmids containing cDNA clones encoding for human PS1, PS2, SERCA2b, and the mouse muscle α, β, γ, and δ NACH subunits (S.F. Heinemann, Salk Institute, La Jolla, CA) were linearized and transcribed in vitro with SP\textsubscript{6} or T3 RNA polymerases as previously described (Leissring et al., 1999b). The RNA transcripts were extracted with phenol-chloroform, precipitated with ethanol, and suspended in RNase-free water at a concentration of 1 μg/μl.

Detailculated stage-VI oocytes from X. laevis were prepared as previously described (Demuro et al. 2005) and injected the next day with 46 nl of the appropriate cRNA mixtures. 3 d after cRNA injection and 1–4 h before Ca\textsuperscript{2+} imaging experiments, oocytes were injected with 23 nl of 2 mM of Oregon Green BAPTA-1 (Invitrogen) alone or together with 0.5 mM of caged Ins(1,4,5)P\textsubscript{3} (M-tero-inositol 1,4,5-trisphosphate Fura-1[2-nitrophenoxy]ethyl]ester; Invitrogen) for experiments involving IP\textsubscript{3}-mediated Ca\textsuperscript{2+} release.

For experiments imaging the clearance of Ca\textsuperscript{2+} after plasma membrane influx [Fig. 3], oocytes were voltage clamped using a conventional two-microelectrodes technique. The membrane potential was held at 0 mV during superfusion with ACh (100–300 nM) in Ringer’s solution and was briefly (300 ms) stepped to −150 mV to strongly increase the electrical driving force for Ca\textsuperscript{2+} influx. Oocytes were imaged at room temperature by wide-field fluorescence microscopy using an inverted microscope (IX 71; Olympus) equipped with a 60x oil-immersion objective, a 488-nm argon laser for fluorescence excitation, and a charge-coupled device camera (Cascade 128+; Roper Scientific) for imaging fluorescence emission (510–600 nm) at frame rates of up to 500 s\textsuperscript{−1}. Fluorescence signals were monitored from a 40 × 40-μm region within the animal hemisphere of the oocyte and are expressed as a ratio (ΔF/Fo) of the mean change in fluorescence (ΔF) relative to the resting fluorescence before stimulation (Fo) using MetaMorph software (MDS Analytical Technologies). Mean values of Fo were obtained by averaging over several frame before stimulation.

Experiments measuring Ca\textsuperscript{2+} liberation in response to photolysis of caged IP\textsubscript{3} [Fig. 4] were performed using a linescan confocal microscope (IX70 inverted microscope with a 40x oil-immersion fluor objective lens, using a 488-nm beam from a 100-mW argon laser [Callamaras and Parker, 1999]) to image fluorescence signals evoked by flashes of UV light (340–400 nm) from a mercury arc lamp, illuminating a disc of 100-μm diameter surrounding the 50-μm scan line in the animal hemisphere of the oocyte.

Protein immunoblotting

Protein extracts were prepared from cells using M-per (Thermo Fisher Scientific) extraction buffer and Complete Mini Protease Inhibitor Tablets (Roche). Protein concentrations were determined by the Bradford method. Equal amounts of protein (10 μg) were separated by SDS/PAGE on a 4–12% Bis/Tris gel (Invitrogen), transferred to PVDF membranes, blocked for 1 h in 5% vol/vol nonfat milk in Tris-buffered saline, pH 7.5, supplemented with 0.2% Tween 20, and incubated overnight at 4°C with primary antibody. Antibodies and dilutions used in this study include α-SERCA2b (1:20,000; F. Woytack, Katholieke Universiteit Leuven, Leuven, Netherlands), CIP20 (1:5,000; EMD), and α-Actin (1:10,000; Sigma-Aldrich). Membranes were washed five times and then incubated with HRP-conjugated secondary antibodies for 1 h at room temperature. Quantitative densitometric analyses were performed on digitized images of immunoblots with Scion Image 4.0 (Scion Corporation).

Aβ ELISA

MaxiSorp immunoplates (Thermo Fisher Scientific) were coated with BAN50 at a concentration of 5 μg/ml in 0.1 M NaCO\textsubscript{3} buffer, pH 9.6, and blocked with 1% Block Ace (Snow Brand Milk Products, Ltd.). Synthetic Aβ standards, internal controls, and samples were run at least in duplicate. After overnight incubation at 4°C, wells were probed with either HRP-conjugated BA27 (for Aβ1–40) or BC05 (for Aβ1–42) for 2–3 h at 37°C. 3,3’,2,5-tetramethylbenzidine was used as the chromogen, and the reaction
was stopped by 6% v/v phosphoric acid and read at 450 nm on a plate reader (Molecular Dynamics). Data are reported as mean per live cell + SEM, and statistical significance was evaluated using Student’s t-test.

Immunoprecipitation
50 μg MEF cell lysate was incubated with 40 μl of Protein A Sepharose beads (Sigma-Aldrich) for 1 h and centrifuged, and the supernatant was recovered. A further 40 μl of beads was added along with anti-PS1 (Cell Signaling Technology), FS2 (G. Thinkanar, University of Chicago, Chicago, IL), or p35 (Santa Cruz Biotechnology, Inc.) as a control (1:100), and the volume was made up to 1 ml with water and incubated overnight at 4°C overnight. After pelleting the beads, the supernatant was discarded and the beads were washed with STEN buffer (0.15 M NaCl, 0.05 M Tris HCl, 0.002 M EDTA, and 2% NP-40, pH 7.6) and then STEN containing 0.1% SDS. The beads were then pelleted and 4x loading buffer was added (Innvoigen). The samples were boiled for 10 min and spun down again, and the supernatant was run on a 4–12% Bis/Tris gel. SERCA2b was probed using aSERCA2b (1:20,000; F. Wuytack).

Confocal microscopy
Fluorescent immunolabeling followed a standard two-way technique (primary antibody followed by fluorescent secondary antibody). Free-floating sections were rinsed in TBS, pH 7.4, and then blocked (0.25% Triton X-100 and 5% normal goat serum in TBS) for 1 h. Sections were incubated in primary antibody overnight at 4°C, rinsed in PBS, and incubated for 1 h in either fluorescently labeled secondary antibody (Alexa 488, 1:200; Invitrogen). Confocal images were captured on a confocal system (Radiance 2100;Bio-Rad Laboratories). All double-labeled specimens were imaged using the x-strobing function to prevent nonspecific cross-excitation of fluorophores.

Statistics
Data are presented as mean ± 1 SEM, with n = number of cells examined. An unpaired Student’s t-test was used to determine statistical significance (P < 0.05).

Online supplemental material
Video 1 shows representative calcium clearance from oocyte cytosol after a 300ms influx through nACHR. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.200706171/DC1.

We thank Dr. Bart de Strooper for the PS knockout fibroblasts, Dr. Frank Wuytack for the generous gift of the anti-SERCA2b antibody, and Dr. Gopal Thinkanar for providing us with the anti-PS2 antibody. We are also grateful to Dr. Stephen F. Heinemann for providing the muscle nACHRs subunits cDNAs. This work was supported by the National Institutes of Health (grants AG17968, AG16573, and GM48071).

Submitted: 26 June 2007
Accepted: 28 May 2008

References