The discrepancy between presenilin subcellular localization and γ-secretase processing of amyloid precursor protein

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We investigated the relationship between PS1 and γ-secretase processing of amyloid precursor protein (APP) in primary cultures of neurons. Increasing the amount of APP at the cell surface or towards endosomes did not significantly affect PS1-dependent γ-secretase cleavage, although little PS1 is present in those subcellular compartments. In contrast, almost no γ-secretase processing was observed when holo-APP or APP-C99, a direct substrate for γ-secretase, were specifically retained in the endoplasmic reticulum (ER) by a double lysine retention motif. Nevertheless, APP-C99-dilysine (KK) colocalized with PS1 in the ER. In contrast, APP-C99 did not colocalize with PS1, but was efficiently processed by PS1-dependent γ-secretase. APP-C99 resides in a compartment that is negative for ER, intermediate compartment, and Golgi marker proteins. We conclude that γ-secretase cleavage of APP-C99 occurs in a specialized subcellular compartment where little or no PS1 is detected. This suggests that at least one other factor than PS1, located downstream of the ER, is required for the γ-cleavage of APP-C99. In agreement, we found that intracellular γ-secretase processing of APP-C99-KK both at the γ40 and the γ42 site could be restored partially after brefeldin A treatment. Our data confirm the “spatial paradox” and raise several questions regarding the PS1 is γ-secretase hypothesis.

Introduction

Amyloid precursor protein (APP)* and presenilins (PSs) are key proteins in the pathogenesis of Alzheimer’s disease (Selkoe, 1999). PSs are multimembrane-spanning domain proteins, essentially located in the ER, the intermediate compartment, and the cis-Golgi region (Walter et al., 1996; Culvenor et al., 1997; Annaert et al., 1999; Kim et al., 2000). Some evidence for the presence of minute amounts of PS at the cell surface has been provided (Ray et al., 1999).

APP is a type I transmembrane protein processed by secretases, resulting in the generation of various fragments, most notoriously the amyloid peptide (Aβ). Aggregation of this peptide is considered to be a central event in the process leading to Alzheimer’s disease (Selkoe, 1999). The β-secretase BACE (β-site amyloid cleaving enzyme) has been identified recently. It is an aspartyl protease cleaving APP at the NH2 terminus of the amyloid peptide sequence (Vassar et al., 1999). The α-secretase cleaves in the Aβ sequence itself, precluding further Aβ production. Several members of the ADAM family (a disintegrin and metalloprotease), i.e., TACE, MDC9, and ADAM10, have been implied in α-secretase processing of APP (Buxbaum et al., 1998; Koike et al., 1999; Lammich et al., 1999). Finally, presenilin 1 (PS1)-dependent γ-secretase cleavage of APP releases the COOH terminus of the amyloid peptide (De Strooper et al., 1998). PS-dependent γ-secretase activities are also involved in the processing of other integral membrane proteins like Notch and APLP-1 (De Strooper et al., 1999; Naruse et al., 1998;
Song et al., 1999; Struhl and Greenwald, 1999). This γ-secretase cleavage is a novel type of proteolytic processing, occurring in the hydrophobic environment of the cell membrane. In the case of Notch, the cleavage results in the release of its intracellular domain that regulates gene transcription in a process that has been called “regulated intramembrane proteolysis” (Annaert and De Strooper, 1999; Brown et al., 2000).

Several lines of evidence have led to the hypothesis that PS is the γ-secretase. First, γ-secretase cleavage of APP and Notch is inactivated partially in PS1-deficient cells and completely in PS1/PS2 double-deficient cells (De Strooper et al., 1998, 1999; Song et al., 1999; Struhl and Greenwald, 1999; Herreman et al., 2000; Zhang et al., 2000). Moreover, mutagenesis of one or two aspartyl residues located in transmembrane domain 6 or 7 results in dominant negative–like effects on γ-secretase cleavage, suggesting that these aspartates contribute to the active site of PS (Wolfe et al., 1999). Some similarities with the preptin peptidases has been taken as further evidence that the PS are proteases (Steiner et al., 2000). However, the strongest argument in favor for this idea comes from the observation that several compounds that inhibit γ-secretase bind specifically to PS (Esler et al., 2000; Li et al., 2000; Seiffert et al., 2000). Nevertheless, direct proof that the PS can hydrolyze peptide bounds is still lacking.

Remarkably, both Notch and APP apparently first need proteolytical trimming of their extracellular domain by TACE and α-/β-secretase, respectively, to become a substrate for PS/γ-secretase (De Strooper et al., 1998; Brou et al., 2000; Mumm et al., 2000; Struhl and Adachi, 2000). These proteases are located downstream in the biosynthetic pathway and therefore both Notch and APP first have to leave the ER to become a substrate for PS/γ-secretase. Despite significant advances in our understanding of γ-secretase processing, it remains unclear how APP, after its cleavage by α- or β-secretase, becomes exposed to PS. Moreover, αβ appears to be produced mainly in the endosomal compartment (Koo and Squazzo, 1994; Hartmann et al., 1997), whereas PS is abundantly present in the ER and intermediate compartment (Walter et al., 1996; Culvenor et al., 1997; Annaert et al., 1999; Kim et al., 2000). This problem can be summarized as “the spatial paradox” (Annaert and De Strooper, 1999) and we now tackle this problem further by analyzing the processing of a series of APP-trafficking mutants in primary cortical neurons derived from PS1+/+ or PS1−/− mice. We analyzed the consequences of restricting APP trafficking to certain subcellular compartments for the generation of total αβ and αβ42. Constructs tested: (a) APP with deleted cytosolic tail (APP-Δct); (b) APP with a double lysine ER retention motif in its cytoplasmic tail (APP-KK); (c) APP with a cytoplasmic tail from the LDL receptor (APP-LDL); (d) APP truncated at the β-secretase cleavage site (APP-C99); and (e) APP-C99 with a double lysine (KK) motif. The APP-Δct is poorly reinternalized and stays for longer times at the cell surface (Tienari et al., 1996). The KK motif acts an ER-retrieval signal (Jackson et al., 1993; Gaynor et al., 1994) and therefore APP-KK colocalizes abundantly with endogenous PS1 (Peraus et al., 1997; Annaert et al., 1999). The APP-LDL recycles between the endosomal system and the cell surface (Annaert et al., 1999). APP-C99 is a direct substrate for γ-secretase and after addition of the KK ER retention motif (APP-C99-KK) we anticipated creating an excellent substrate for PS1/γ-secretase. Overall, our data confirm the spatial paradox in the PS-γ-secretase hypothesis and provide evidence that the transfer of APP-C99 in a compartment downstream of the ER is needed in addition to processed PS1 to obtain γ-secretase activity in primary cultures of neurons.

Figure 1. APP-trafficking mutants. APP is schematically represented (APP-WT). The different relevant proteolytic fragments are indicated at the top. The ectodomain is detected by pAb207, the amyloid peptide region 1–16 is detected by pAb B7, region 1–5 by mAb D6, region 17–24 is detected by mAb 4G8, and the last 20 amino acids of the COOH-terminal cytoplasmic tail are detected by pAb B11/4 and pAb 6687. α-, β-, and γ-secretase cleavage sites are indicated in the APP-C99 construct, a supplementary Asp and Ala residue (DA) has been added to obtain cleavage by the signal peptidase at the β-secretase site (see Lichtenhaller et al., 1999). For further details see Materials and methods.

Results

Different APP-trafficking mutants (Fig. 1) were expressed in primary cortical neurons derived from PS1+/+ and PS1−/− littermate embryos. Metabolically labeled full-length APP and secretase-cleaved APP fragments were immunoprecipitated and analyzed by phosphorimaging as described in Materials and methods. For all constructs, protein expression levels are very similar in PS1+/+ and in PS1−/− cells (Fig. 2 A). Both full-length wild-type and APP-LDL chimera run as a doublet (Fig. 2 A) of ~120 kD, corresponding to mature- and immature-glycosylated APP. The majority for both the APP-KK and APP-Δct recombinant proteins is, however, the immature protein. This is expected for APP-KK, as the d lysine motif actively retains the protein in pre-Golgi compartments. The stronger immature APP-Δct band could reflect the rapid processing of the mature form by α-secretase at the cell surface (Tienari et al., 1997). Next, we analyzed proteolytical fragments derived from the different APP mutants. Secretion of the soluble ectodomain after α-
or β-secretase cleavage generated from the different trafficking mutants was not significantly altered by PS1 deficiency, although the APP-Δct, for instance, produced roughly twice as many APPs (Fig. 2). β-Cleaved COOH-terminal stubs (APP-CTF) derived from APP-WT accumulated strongly in PS1−/− neurons (Fig. 2 B), confirming previous data (De Strooper et al., 1998). Interestingly, the same relative accumulation was observed for APP-CTF derived from the APP-LDL chimera. Also, total Aβ secretion was severely decreased in PS1−/− neurons transduced for APP-WT and
APP-LDL (Fig. 2 B). Although the secretion of Aβ42 derived from APP-LDL is reduced by 80% in PS1+/+ neurons, in line with previous observations (Koo and Squazzo, 1994; Perez et al., 1999), the additional relative decrease caused by PS1−/− deficiency remained unaltered when compared with APP-WT (Fig. 2, B and C). Together, these data suggest that in the case of the APP-LDL chimera, the enhanced recycling in the endosomal limb does not directly influence PS1-dependent γ-secretase processing.

The reduction of β-cleaved APP-CTF in the APP-Δct-transduced wild-type neurons is accompanied by an 80% decrease in secretion of total Aβ and Aβ42 (Fig. 2, A and C). Moreover, no relative accumulation of β-cleaved APP-CTF in PS1−/− neurons was observed. All this can be explained by a predominant α-secretase cleavage of APP-Δct at or near the plasma membrane, as reflected by the increased secretion of APPs cleaved at the α-secretase site and the concomitant fivefold increase in p3 secretion (Fig. 3). Interestingly, secretion of p3 is dramatically inhibited in the absence of PS1 (Fig. 3, bottom), indicating that α-stubs generated near or at the cell surface are still substrates for PS1-dependent γ-secretase processing. Therefore, the data on APP-Δct and APP-LDL clearly demonstrate that PS1 is needed for normal γ-secretase processing in the late Golgi region, at the cell surface, and in the endosomal compartments.

In contrast to other mutants, the levels of APPs and of the COOH-terminal β-stubs generated from APP-KK are very low, confirming the low α- and β-secretase activity in the ER (Fig. 2, A and B). Accordingly, the total Aβ (Fig. 2 B) and Aβ42 (Fig. 2 C) secretion was also strongly reduced by 90%. However, when overexpressed in PS1−/− neurons, secretion of Aβ peptides was inhibited to the same extent as observed for peptides derived from APP-WT (Fig. 2, B and C).

To circumvent the need for "preactivation" of APP-KK by α- or β-secretase, we generated APP-C99-KK, corresponding to APP truncated at the β-secretase site (Lichtenthaler et al., 1999) and containing the KK-ER retention motif. When expressed in neurons, APP-C99-KK migrated with the same apparent molecular weight (10 kD) as the β-stub coming from APP-WT or the APP-C99 without KK motif (Fig. 4 A; Lichtenthaler et al., 1999). APP-C99, like APP-WT, can be processed by α-secretase as reflected by the generation of α-APPCTF (Fig. 4 A). APP-C99-KK, in contrast, is either not processed or processed very little by α- or β-secretase, confirming the specific retention of APP-C99-KK in the ER and cis-Golgi region. In line with the prediction that APP-C99 does not require α- or β-secretase cleavage to become a substrate for γ-secretase, an estimated sevenfold increase in total Aβ secretion (Fig. 4 A) is observed. This effect is also observed with Aβ42, as detected by ELISA (Fig. 4 B). The γ-secretase cleavage of APP-C99 is strongly inhibited in the absence of PS1 (Fig. 4 C). Most surprisingly, however, was the observation that APP-C99-KK, which was also expected to be a substrate for PS1-γ-secretase because it is retained in the ER, turned out to yield little if any Aβ peptides (Fig. 4, A and B). It is unlikely that the KK motif directly interfered with the recognition of C99 by the γ-secretase complex, since the cytoplasmic tail of APP can be removed without affecting γ-secretase cleavage (Fig. 3). Moreover, C99KK becomes a substrate for γ-secretase under conditions specified below. Alternatively, the low Aβ secretion from neurons expressing APP-C99-KK might be explained by intracellular retention of newly formed Aβ peptides. Again, this could be ruled out, as no increased amounts of Aβ could be immunoprecipitated from cell extracts (result not shown, but see Fig. 7 below).

Using confocal scanning microscopy, we confirmed that APP-C99-KK was effectively retained in the ER, as demonstrated by its colocalization with the ER marker protein BIP (Fig. 5, A–C), and to a more limited extent with the intermediate compartment marker ERGIC-53 (Fig. 5, D–F, and to a more limited extent with the intermediate compartment marker ERGIC-53 (Fig. 5, D–F). Importantly, APP-C99-KK colocalized abundantly with PS1 (Fig. 5, D–F), indicating that the simple presence of PS1 is not sufficient for γ-secretase processing to occur. In this respect, it is important to note that we have demonstrated previously that PS1 in the ER is already processed towards NH2- and COOH-terminal fragments (Annaert et al., 1999). We next investigated the subcellular localization of APP-C99 in primary cortical neurons. APP-C99 is clearly not distributed in the ER (Fig. 6, A–C), as deduced from the complete lack of colocalization with BIP. Similarly, little if any colocalization was observed with ERGIC-53 marking the intermediate compartment (arrowheads in Fig. 6, D–F, including horizontal section [arrow]). Most surprisingly, however, was the observation that APP-C99 immunoreactivity also essentially did not distribute into the Golgi apparatus as demonstrated by GM130 staining (Fig. 6, G–I). Finally, and despite APP-C99 being a good γ-secretase substrate (Fig. 4), this fragment does not colocalize with PS1 (arrowheads and vertical section in Fig. 6, J–L). This is in clear contrast to the colocalization of PS1 with the inactive γ-secretase substrate APP-C99-KK (see also Fig. 5).

![Figure 3](https://example.com/figure3.png)

**Figure 3.** Secretion of p3 in PS1+/+ and −/− neurons expressing APP-Δct. Neurons were transduced and metabolically labeled as above. Cell extracts (top) and culture media (bottom) were immunoprecipitated using pAb207 (holo-APP) or mAb4G8 (αAPPs and Aβ/p3). The intermediate band running between Aβ and p3 in cells transduced with APP-WT corresponds to the truncated Aβ generated by β-secretase cleavage at the Glu11 position (Creemers et al., 2000).
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To test the hypothesis that a component of a more downstream subcellular compartment is needed to process APP-C99-KK in the ER, we treated neurons expressing APP-C99 or APP-C99-KK with brefeldin A (BFA), a drug that causes a rapid redistribution of the Golgi apparatus into the ER (Lippincott-Schwartz et al., 1989). This treatment resulted in a drastic reduction in APP-C99–derived Aβ secretion, whereas no difference was observed in the case of APP-C99-KK (Fig. 7 A). However, addition of BFA resulted in a strong increase in intracellular Aβ generated from APP-C99-KK, towards levels indistinguishable from those obtained in BFA-treated APP-C99–transduced cells. This suggests that some unknown factors required for γ-secretase activity are redistributed from the Golgi region to the ER, which appears to be sufficient to partially restore Aβ production from APP-C99-KK. It has been suggested that Aβ generated in the endoplasmic reticulum consists mainly of Aβ ending at residue 42 (Chyung et al., 1997; Cook et al., 1997; Hartmann et al., 1997; Wild-Bode et al., 1997). Remarkably, although we detect little intracellular Aβ under our experimental conditions (Fig. 7, A and B), treatment with BFA induces the generation of Aβ peptides, ending at residue 40 as well as at residue 42 (Fig. 7 B).

Discussion

Previous studies (Koo and Squazzo, 1994; Hartmann et al., 1997; Tienari et al., 1997) have shown that Aβ can be generated at the cell surface and in the endosomes of neurons, where little, if any, PS1 is present (Annaert et al., 1999). The first aim of the current study was to investigate to what extent γ-secretase activity in these subcellular compartments depends indeed on PS1. To this end we expressed APP-Δct and APP-LDL, two previously characterized trafficking mutants of APP (Peraus et al., 1997; Tienari et al., 1997; Annaert et al., 1999), in neurons. APP-Δct lacks the endocytosis signals in the cytoplasmic domain of APP and is therefore only slowly internalized. Compared with APP-WT, APP-Δct is processed mainly by an α-secretase activity at the cell surface (Sisodia, 1992; Tienari et al., 1997; Annaert et al., 1999). This results in the replacement of Aβ production by a roughly equal production of p3, the product of consecutive α- and γ-secretase activity (Figs. 2 and 3), confirming that the APP-Δct construct indeed behaves as predicted. Therefore, p3 production from this substrate reflects mainly γ-secretase cleavage of the α-APPCTF at the cell surface. Expression of this construct in PS1-deficient neurons resulted in a strong decrease of p3, demonstrating that γ-secretase cleavage at the cell surface depends on PS1 (Fig. 3). Since αAPPs secretion is not affected in the absence of PS1 (Fig. 3), we rule out the possibility that the decreased p3 production is caused by decreased α-secretase activity in these PS1-deficient cells.

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somes (Koo and Squazzo, 1994; Peraus et al., 1997; Perez et al., 1999). Again, in the absence of PS1, Aβ generation from APP-LDL strongly decreased, demonstrating that γ-secretase processing of APP in the endosomes depends on PS1. It should be noted that we have not been able to detect any endogenous PS1 immunoreactivity at the cell surface or in the endosomes of the neuronal cells used in the current study (Annaert et al., 1999).

We next investigated whether we could increase γ-secretase processing of APP in the ER and the intermediate compartment, which contain the bulk of PS1 immunoreactivity in these neurons. Although several authors have provided evidence that the ER is a production site of this peptide, in particular Aβ42 (Chyung et al., 1997; Cook et al., 1997; Hartmann et al., 1997; Wild-Bode et al., 1997), we and others have not been able to confirm these observations (Annaert et al., 1999; Iwata et al., 2001; Maltese et al., 2001). As shown in Fig. 2, a severe decrease in both Aβ40 and Aβ42 secretion is observed when APP is retained in the ER by means of the double lysine retention motif (APP-KK). Since the retention of APP in the ER implies that cleavage by α- and β-secretase (residing in the TGN, cell surface, and endosomes) becomes strongly compromised, and since proteolytic trimming of the APP ectodomain is a prerequisite for further γ-secretase processing (Struhl and Adachi, 2000), it seems logical that the APP-KK mutation results in a strongly decreased γ-secretase cleavage and inhibition of Aβ generation. It is by consequence difficult to interpret the data obtained with APP-KK in regard to γ-secretase sensitivity. Therefore, we generated the APP-C99 construct, which is a direct substrate for γ-secretase (Lichtenthal et al., 1999), and added to it the double lysine ER retention motif. As shown in Fig. 5, this construct is indeed retained in the ER, where it codistributes abundantly with PS1. Although we expected increased Aβ production, no significant amount of Aβ could be precipitated from the wild-type neurons (Fig. 4; Iwata et al., 2001; Maltese et al., 2001). This result was even more significant, as neurons expressing APP-C99 secreted about seven times more total Aβ, or specifically Aβ42, than those expressing APP-WT. The possibility that the Aβ generated from APP-C99-KK is retained in the cells was ruled out, since no significant accumulation of cells associated Aβ could be demonstrated (Fig. 7 A, lane 9, and B, lanes 2 and 5). The possibility that the KK motif directly interfered with γ-secretase cleavage was ruled out by two observations. First, it is clear from the results with APP-C99 that the cytoplasmic domain of APP is not involved in the processing of APP by γ-secretase. Second, treatment of the cell cultures with BFA could restore the processing of C99-KK, clearly demonstrating that the inhibitory effect of the KK mutations is a trans, and not a cis phenomenon (Fig. 7). It should be pointed out here that PS1 in the ER is already proteolytically processed by the “presenilinase” and present as PS1-CTF and PS1-NTF (Annaert et al., 1999), thus in the putative active conformation. It follows from these data that the simple colocalization of a substrate (APP-C99-KK) with its putative protease (PS1) is not sufficient for proteolytic cleavage.

We conclude that Aβ production, including Aβ42, can not occur directly in the ER and requires at least one factor.
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derived from a post-ER compartment. This conclusion is corroborated by two important pieces of evidence from the current work. First, APP-C99, which is a good substrate for γ-secretase, is mainly localized in a PS1-, BIP-, and ERGIC53-negative subcellular compartment (Fig. 6). Although the characterization of this compartment requires further experimentation, this result suggests that at least the proteolytic cleavage of the APP-C99 substrate occurs in a non-ER compartment. The second, more important argument comes from the experiments using BFA. BFA is a drug that causes the redistribution of post-ER compartments into the ER (Lippincott-Schwartz et al., 1989). Treatment with this drug was sufficient to restore partially γ-secretase processing of APP-C99-KK proving that at least one non-ER component is needed to activate γ-secretase in the ER (Fig. 7). BFA treatment results in γ-secretase processing of APP at position Aβ42, something which could possibly be anticipated based on current knowledge (Chyung et al., 1997; Cook et al., 1997; Hartmann et al., 1997; Wild-Bode et al., 1997). Surprisingly, however, cleavage at position Aβ40 is also observed (Fig. 7 B), which is believed to occur mainly in the late compartments of the secretary and in the endosomal limbs of the subcellular trafficking pathways (Koo and Squazzo, 1994; Hartmann et al., 1997; Tienari et al., 1997).

Summarizing, our data indicate that efficient γ-secretase cleavage of APP can occur in compartments that contain little, if any, PS1, and that no or little γ-secretase activity is observed in compartments where abundant (maturated) PS1 is residing. This is a surprising result since most of the data currently available imply that PS1 is closely involved in γ-secretase type enzymatic activity (De Strooper et al., 1998, 1999; Steiner et al., 1999, 2000; Struhl and Greenwald, 1999; Wolfe et al., 1999; Esler et al., 2000; Herreman et al., 2000; Li et al., 2000; Zhang et al., 2000). The spatial paradox between PS1 localization and γ-secretase activity can be explained by two hypotheses: (a) the minute amounts of PS1 in post–cis-Golgi compartments are the active enzymes. This implies that in addition to activation by presenilinase, additional proteins from these compartments are needed to make PS1 enzymatically active; and (b) PS1 is actually not the γ-secretase but acts, probably in concert with other proteins in the ER and intermediate compartment, to dispatch APP or γ-secretase to the subcellular compartment where cleavage will occur. In this hypothesis, BFA treatment results in the relocalization of the catalytic subunit(s) of γ-secretase to the ER.

In support for the first hypothesis, evidence for the presence of minute amounts of PS1 in other compartments than

Figure 6. APP-C99 does not colocalize with PS1 and is essentially present in a BIP, ERGIC-53, and GM130 negative compartment. SFV-APP-C99 transduced hippocampal neurons were fixed and the subcellular localization of APP-C99 (A and G with pAb 6687; D and J with mAb 3D6) was compared with established marker proteins of the ER (BIP in B), the intermediate compartment (ERGIC-53 in E), the Golgi apparatus (GM130 in H), and finally with PS1 (K). C, F, I, and L show merged pictures. For D–F and J–L, the arrows point to the position of the corresponding vertical sections. Immunodetection was done as in Fig. 6. APP-C99 immunoreactivity was mainly concentrated in discrete spots that did not colocalize with the ER (C for BIP and arrowheads in L for PS1), and the Golgi region (merged panel I). Occasionally minor colocalization with ERGIC-53 could be observed (arrowheads in D–F). Bar, 10 μm.
that at least one other component of a non-ER compartment is needed to obtain activated PS1. This component is not the elusive protease called “presenilinase” responsible for PS maturation, and most probably not nicastrin, since this protein is present in the ER (Yu et al., 2000).

The second hypothesis, that PS1 is needed for the correct trafficking of γ-secretase and its substrates, finds some theoretical support in the analogy with the sterol regulatory element–binding protein (SREBP)–SCAP cleavage–activating protein (SCAP) complex and the regulation of the proteolytical cleavage of SREBP (Brown et al., 2000). SCAP is, like PS1, an ER resident, multi-transmembrane domain–containing protein and regulates the trafficking of the membrane-bound transcription factor SREBP to post-ER compartments. Upon cholesterol depletion, SREBP travels to the cis-Golgi, where a site 1 protease cleaves SREBP in its luminal domain. The remaining NH2-terminal, membrane-bound fragment then becomes a substrate for a site 2 protease that cleaves in the transmembrane domain of SREBP (Rawson et al., 1997; Nohturfft et al., 1999). The coupling of vesicular protein transport and proteolysis provides a stringent control on the activation of the system and it could be envisaged that PS1, like SCAP, provides a similar control on APP (and Notch) processing. However, it should be pointed out that in case of SREBP processing, SCAP regulates its luminal cleavage and that the site 2 intramembranous cleavage occurs by default. In case of PS1, its role is limited to the regulation of the intramembraneous γ-secretase cleavage (De Strooper et al., 1998).

In conclusion, our data indicate a complex relationship between APP trafficking and its processing by γ-secretase. Moreover, they directly question the exact role of PS1 in γ-secretase processing and demonstrate that at least one cofactor (in the first hypothesis) or the protease (in the second hypothesis) is located in a compartment downstream of the ER. In the future, reconstitution of γ-secretase processing of APP, by mixing extracts of purified ER fractions and post-ER compartments, should allow us to further define at a molecular level this highly intriguing proteolytic system.

Materials and methods

Neuronal cell culture

Primary cultures of mixed cortical neurons derived from wild-type and PS1 knock-out littermates were generated as described previously (De Strooper et al., 1998). In brief, total brain of 14-d-old embryos was dissected in HBSS medium (GIBCO BRL), trypsinized, and plated on dishes (Nunc) pre-coated with poly-L-lysine (Sigma-Aldrich). Cultures were maintained in neurobasal medium (GIBCO BRL) with B27 supplement (GIBCO BRL) and 5 µM cytosine arabinoside to prevent glial cell proliferation.

Semliki forest virus (SFV) constructs

The following modifications were made to the cDNA coding for human APP695 (Fig. 1): (a) deletion of the last 43 amino acids of the cytoplasmic tail (APP-ΔCt) as described in Tiernan et al. (1996); (b) addition of a di-lysine motif (QM mutated to KK; APP-KK) by site-directed mutagenesis (Stratagene); (c) exchange of its cytoplasmic domain with that of the LDL receptor (APP-LDL); (d) full deletion of the APP ectodomain until the Asp1 amino acid of the signal peptide (APP-DA) as cloned by site-directed mutagenesis (Stratagene) between the last amino acid of the signal sequence (Ala) and the first of the AB region (Lichtenhainer et al., 1999) (APP-C99). Site-directed mutagenesis was used to add the di-lysine motif (APP-C99-KK). Recombinant SFV containing the APP mutants were generated as described previously (De Strooper et al., 1995).
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The presence of a glial feeder layer (Goslin and Banker, 1991; De Strooper and Yarin, 2002) promotes the differentiation of NT2N cells. BioRad MRC1024 confocal microscope and Adobe Photoshop® were used (Fig. 1). Rabbit pAb B7 recognizes the first 17 amino acids of Aβ, B11 the last 20 amino acids of the APP COOH-terminal domain (De Strooper et al., 1995), goat pAb 207 the APP ectodomain (provided by Dr. M. Savage, Cephalon, Inc., West Chester, PA), mAb 4G8 (Senetek) amino acids 17 to 24 of Aβ, and mAb W0-2 the NH2-terminal region of Aβ (provided by Dr. Tobias Hartmann and Konrad Beyreuther, University of Heidelberg, Heidelberg, Germany) (Ito et al., 1996). Antibodies FCA40 and FCA42 specifically precipitate Aβ peptides ending at residue 40 (at) or at 42 (at) and were provided by Dr. F. Checher (Institut de Pharmacologie Moléculaire et Cellulaire, Valbonne, France) (Barelli et al., 1997).

Quantification of the Aβ42 peptide by ELISA

Levels of Aβ42 in conditioned media and cell lysates were quantified by a sandwich ELISA test (De Strooper et al., 1998), as published about protocols (Vanderstichele et al., 2000). In brief, samples were dried by speed vacuum (Savant), resuspended in 300 μl of sample diluent, and incubated on 96-well ELISA plates precoated with mAb 3D6 against Aβ. After washing, samples were incubated with a biotin-labeled anti-Aβ42 antibody mAb 21F12 that only recognizes the final two amino acids of the Aβ sequence, followed by streptavidine-HRP. After adding the HRP substrate, samples were measured spectrophotometrically using a Victor2 (Wallac) with a 450-nm filter. The Aβ42 concentration in the samples was calculated based on the Aβ42 standards sigmoid curve equation, and using Prism 3.0 (GraphPad Software).

Confocal microscopy

Hippocampal neurons grow on poly-l-lysine–coated glass coverslips in the presence of a glial feeder layer (Goslin and Banker, 1991; De Strooper et al., 1995) were transfected with SV40-APP-C99 or -C99K4. 4 h after transfection, cycloheximide (100 μg/ml) was added to block further protein synthesis. After 6 h, neurons were fixed in 120 mM phosphate buffer containing 4% paraformaldehyde (pH 7.3) and 4% sucrose, permeabilized in ice-cold methanol and acetone, and immunostained (Annaert et al., 1997). Characterization of new polyclonal antibodies specific for 40 and 42 amino acid long amyloid β peptides: their use to examine the cell biology of presenilins and the immunohistochemistry of sporadic Alzheimer’s disease and cerebral amyloid angiopathy cases. Mol. Med. 3: 695–707.

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