Mutations in Synaptojanin Disrupt Synaptic Vesicle Recycling

Todd W. Harris,* Erika Hartwig,§ H. Robert Horvitz,‡ and Erik M. Jorgensen*

*Department of Biology, University of Utah, Salt Lake City, Utah 84112-0840; and ‡Department of Biology, Massachusetts Institute of Technology, Cambridge, Massachusetts 02139

Abstract. Synaptojanin is a polyphosphoinositide phosphatase that is found at synapses and binds to proteins implicated in endocytosis. For these reasons, it has been proposed that synaptojanin is involved in the recycling of synaptic vesicles. Here, we demonstrate that the unc-26 gene encodes the Caenorhabditis elegans ortholog of synaptojanin. unc-26 mutants exhibit defects in vesicle trafficking in several tissues, but most defects are found at synaptic termini. Specifically, we observed defects in the budding of synaptic vesicles from the plasma membrane, in the uncoating of vesicles after fission, in the recovery of vesicles from endosomes, and in the tethering of vesicles to the cytoskeleton. Thus, these results confirm studies of the mouse synaptojanin 1 mutants, which exhibit defects in the uncoating of synaptic vesicles (Cremona, O., G. Di Paolo, M. R. Wenk, A. Luthi, W. T. Kim, K. Takei, L. Daniell, Y. Nemoto, S. B. Shears, R. A. Flavell, D. A. McCormick, and P. De Camilli. 1999. Cell. 99:179–188), and further demonstrate that synaptojanin facilitates multiple steps of synaptic vesicle recycling.

Key words: Caenorhabditis elegans • synaptic transmission • endocytosis • unc-26 • polyphosphoinositide phosphatase

Introduction

Depolarization of neurons causes synaptic vesicles to fuse with the plasma membrane and to release their cargo of neurotransmitter into the synaptic cleft. During periods of high neuronal activity, synaptic vesicles must fuse with the plasma membrane at high rates. Sustained rates of vesicle fusion in turn are facilitated by an efficient mechanism of synaptic vesicle recycling (De Camilli and Takei, 1996). The recycling pathway recovers vesicle membrane and proteins from the plasma membrane, and returns them to the reserve pool of synaptic vesicles for subsequent rounds of release.

Synaptic vesicle recovery from the plasma membrane can be divided into four steps: clathrin coat assembly, budding, fission, and uncoating (Cremona and De Camilli, 1997). During the initial step, synaptic vesicle proteins are assembled together in the plasma membrane and marked for recycling (Miller and Heuser, 1984; Jorgensen et al., 1995; Nonet et al., 1999). The process is likely to be mediated by the clathrin adaptor complex, which subsequently recruits clathrin to the area of membrane to be recycled. In the budding step, clathrin assembles into a curved array and the membrane invaginates. In the fission step, dynamin monomers assemble into a collar around the neck of the vesicle and sever the vesicle from the plasma membrane. In the uncoating step, the clathrin and clathrin adaptor protein coat is disassembled. Vesicle uncoating must occur before vesicles can fuse to other membranes.

The phosphoinositide (PI)³ phosphatase synaptojanin has been proposed to function within the synaptic vesicle recycling pathway. Synaptojanin is defined by three domains (McPherson et al., 1994, 1996): a polyphosphoinositide phosphatase domain similar to the yeast Sac1 protein (Chung et al., 1997; Guo et al., 1999), a PI 5-phosphatase domain, and a proline-rich domain. Three attributes of synaptojanin suggest a role in synaptic vesicle recycling: its location, its protein interactions, and its lipid substrate specificity.

First, the location of synaptojanin is consistent with a role for the protein in the endocytosis of synaptic vesicles. Synaptojanin is highly enriched in the brain and is located at nerve terminals, and it is associated with synaptic vesicles and coated endocytic intermediates (McPherson et al., 1994; Haffner et al., 1997). Moreover, the distribution of synaptojanin is coincident with that of other endocytic

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A d d r e s s correspondence to Erik M. Jorgensen, Department of Biology, University of Utah, 257 South 1400 East, Salt Lake City, UT 84112-0840. Tel.: 801 585-3517. Fax: 801 581-4668. E-mail: jorgensen@biology.utah.edu

Abbreviations used in this paper: Ce-synaptojanin, Caenorhabditis elegans synaptojanin; EST, expressed sequence tag; GABA, γ-aminobutyric acid; GFP, green fluorescent protein; ORF, open reading frame; PI, phosphoinositide.
proteins, such as amphiphysin and dynamin (McPherson et al., 1994, 1996).

Second, synaptojanin binds a complex of proteins implicated in endocytosis. Synaptojanin binds to amphiphysin and endophilin directly (McPherson et al., 1996; Micheva et al., 1997). A amphiphysin also binds to both the GTPase dynamin and the α subunit of the A P2 clathrin adaptor complex (D avid et al., 1996; G rabs et al., 1997). M oreover, synaptojanin, dynamin, and amphiphysin can be isolated in a complex with the clathrin adaptor A P2. A similar complex can be isolated lacking amphiphysin, but including endophilin (Micheva et al., 1997; Slepnev et al., 1998). Injection of the SH 3 domains of amphiphysin (into lampprey terminals) or of endophilin (into a reconstructed in vitro assay) blocks endocytosis via a dominant-negative disruption of protein interactions central to the complex (Shupliakov et al., 1997; Wigge et al., 1997; Simpson et al., 1999), illustrating the importance of these complexes in synaptic vesicle recycling.

Third, proteins implicated in endocytosis have been shown to bind to the lipid substrates of synaptojanin. Synaptojanin is a polyphosphoinositide phosphatase, capable of selectively cleaving the 3-, 4-, and 5-phosphates from PI(3)P, PI(4)P, PI(3,5)P₂, PI(4,5)P₂, and PI(3,4,5)P₃ (McPherson et al., 1996; Chung et al., 1997; W oscholski et al., 1997; Guo et al., 1999). The Sac1 domain of synaptojanin acts as a 3-, 4-, and 5-polyphosphoinositide phospha-

Material and Methods

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Strains and Alleles

Strains used in this study were maintained using standard techniques (Brenner, 1974). The wild type was N2 Bristol. The following mutations were used in this study: LG IV, unc-26(e250; e314; e345; e629; e446; e568; e1048; e3196; m2; n1307; n1308n1307; ox1; s1710; unc-22(s7); dpy-4(e1166d)). M ost strains are available from the C. elegans Genetics Center.

Molecular Characterization of C. elegans Synaptojanin

A BLASTP Genbank database search using full-length rat synaptojanin revealed four C. elegans expressed sequence tags (ESTs): yk32c3, yk27c9, yk3c31, and yk16a11, belonging to the overlapping EST group CELK 00306. Primers were designed against the sequence of the ESTs and used to amplify a 2-kb genomic region from wild-type DNA. This fragment was used to probe 70,000 plaques from a phage C. elegans genomic DNA library. We isolated three genomic clones that extended ~5 kb past the end of cosmid J 813. A 10-kb HindII fragment extending into the gap was subcloned from one of these clones, and the sequence of the nonoverlap-

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data were compared with reconstructions of wild-type ventral nerve cords (328 sections) derived from two worms.

**Vesicle Depletion.** The average number of synaptic vesicles per synapse was determined in the cholinergic neurons VA and VB, and in the γ-aminobutyric acid (GABA) neuron VD. These neurons were identified by their dorsal/ventral positioning within the ventral nerve cord, and by their polarization: VA and VB neurons synapse on other neurons and muscle, whereas VD is directed solely to muscle (White et al., 1976). Synapses were defined to be any axon profile containing a morphologically defined electron-dense presynaptic specialization, including lateral sections until the number of synaptic vesicles in the profile dropped below the total average number of synaptic vesicles in all sections (wild-type  9 synaptic vesicles; unc-26(e1710)  5 synaptic vesicles), and no fewer than two lateral sections on each side.

**Endocytic Pits and Coated Vesicles.** The presence of endocytic pits in VA, VB, and VD neurons was quantified. To avoid counting ripples in the membrane as endocytic pits, we scored invaginations as an endocytic pit only if they were present in a single section and did not continue into lateral sections. The distribution of these pits relative to active zones was quantified by measuring their distance to the nearest active zone in sections, where each section represents 33 nm. Pits found within sections containing an active zone were pooled into the  33-nm distance bin. The average number of pits at this distance was calculated by dividing the number of pits by the total number of sections at this distance. The average number of pits at any given distance in lateral sections was calculated by dividing the number of pits scored by twice the number of sections at that distance, to account for the double representation of each distance on either side of the synapse. Coated vesicles were scored and their distribution quantified using the same methodology as that outlined for endocytic structures.

**Endosomal Compartments.** The presence of recognizable endosomal structures in VA, VB, and VD neurons was noted. A novel endosomal structure was defined as an amorphous vesicle 50 nm that extended two or more lateral sections.

**Results**

**Cloning of C. elegans Synaptojanin**

C. elegans synaptojanin (Ce-synaptojanin) was cloned using a homology-based approach. BLAST searches using the rat synaptojanin sequence revealed a set of overlapping ESTs encoding predicted proteins highly similar to the vertebrate protein. This EST group hybridized to YAC Y 67H2 on linkage group IV. However, only a small 3' portion of the consensus sequence was contained on cosmids covered by the YAC, indicating that most of the synaptojanin gene resided within the cosmid gap between cosmids JCB and W02A 2 (Fig. 1 A). We isolated phage clones that extended into the gap, but these clones lacked the 5' end of the gene. The remaining 5' end of the ORF was determined by sequencing full-length cDNAs. The sequence of the 5' end of the cDNA was used to amplify the genomic DNA from which the complete gene sequence was determined.

An analysis of the cDNA revealed that the locus is a nematode ortholog of synaptojanin. The longest predicted Ce-synaptojanin protein is 1199 amino acids and contains the three defining domains of synaptojanin: an amino-terminal Sac1-like polyphosphoinositide phosphatase domain, a PI 5-phosphatase domain, and a COOH-terminal proline-rich domain (Fig. 2). The predicted protein is 43% identical to the rat protein, showing the highest degree of identity in the Sac1 (46%) and 5-phosphatase (43%) domains. Although there are four predicted inositol 5-phosphatases and at least four Sac1 domain-containing proteins encoded in the C. elegans genome (data not shown), Ce-synaptojanin is the only predicted ORF containing the three canonical domains of synaptojanin.

Ce-synaptojanin cDNAs defined three splice variants. 2 of 12 cDNAs represented the longest isoform and this splice variant most closely resembles the vertebrate protein (Fig. 1 B, UNC-26A). UNC-26A differs from the most abundant variant (Fig. 1 B, UNC-26B, 9 of 12 cDNA s) only by the presence of a single exon insertion encoding six amino acids within the phosphatase domain (Fig. 2). Finally, a single cDNA was isolated that encodes a truncated protein, containing only the Sac1 domain, and lacking the phosphatase and proline-rich domains (Fig. 1 B, UNC-26C). Conversely, in vertebrates, splice variants lacking the Sac1 domain, but retaining the 5-phosphatase and proline-rich domains have been identified. These variants retain full 5-phosphatase activity (Woscholski et al., 1998). In yeast, Sac1 domain-containing proteins are expressed alone from the SA C1 gene or together with a 5-phosphatase domain in the INP5 gene products (Guo et al., 1999). These observations suggest that the Sac1 and 5-phosphatase domains possess distinct and separable functions.

We demonstrated that synaptojanin is encoded by the unc-26 gene by analyzing mutations of the locus. Because unc-26 genetically maps within a 0.67-map unit interval spanning the physical region containing Ce-synaptojanin (Fig. 1 A), it was a strong candidate gene for this ORF. We
determined the sequences of the synaptojanin gene from 13 unc-26 alleles, and all 13 alleles contained mutations in this ORF (Table I). The linear order of the unc-26 mutations within the gene corresponds to their previously determined (Charest et al., 1990) intragenic map positions (Fig. 1C), demonstrating that unc-26 encodes Ce-synaptojanin. Further proof is provided by an unstable allele; the duplication associated with the unc-26(n1307) allele is restored to both wild-type size on genomic Southern blots and wild-type sequence in the revertant allele unc-26(n1308n1307) (data not shown). The best candidate for a null allele is unc-26(s1710), a five-nucleotide deletion that results in a protein truncated within the NH$_2$-terminal Sac1 domain.

**Neurotransmission Defects**

Behavioral and pharmacological analyses indicate that unc-26 mutants possess a presynaptic disruption of cholinergic and GABA neurotransmission. First, unc-26 mutants resemble mutants lacking the biosynthetic enzyme for acetylcholine encoded by the cha-1 gene. Mutations in cha-1 (and unc-26) result in characteristic locomotory defects: animals are small, move backwards with a jerky motion,

**Table I. Sequence of unc-26 Alleles**

<table>
<thead>
<tr>
<th>Allele</th>
<th>Mutagen</th>
<th>Wild-type</th>
<th>Mutant</th>
<th>Amino acid change</th>
<th>Domain</th>
<th>Phenotypic strength</th>
</tr>
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<td>e176</td>
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<td>Aat</td>
<td>D722N</td>
<td>Phosphatase</td>
<td>Strong</td>
</tr>
<tr>
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<td>tGg</td>
<td>tAg</td>
<td>W903stop</td>
<td>Phosphatase</td>
<td>Strong</td>
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<tr>
<td>e314</td>
<td>EMS</td>
<td>gGa</td>
<td>gAa</td>
<td>G662E</td>
<td>Phosphatase</td>
<td>Weak</td>
</tr>
<tr>
<td>e345</td>
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<td>415-bp deletion, frameshift at aa183-280</td>
<td>In-frame deletion of aa183-280</td>
<td>Sac1</td>
<td>Strong</td>
</tr>
<tr>
<td>e429</td>
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<td>Gat</td>
<td>Aat</td>
<td>D825N</td>
<td>Phosphatase</td>
<td>Weak</td>
</tr>
<tr>
<td>e446 (1st site)</td>
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<td>Gag</td>
<td>Tag</td>
<td>E623stop</td>
<td>Phosphatase</td>
<td>Strong</td>
</tr>
<tr>
<td>e446 (2nd site)</td>
<td>EMS</td>
<td>aGa</td>
<td>aGa</td>
<td>R709T</td>
<td>Phosphatase</td>
<td>Strong</td>
</tr>
<tr>
<td>e568</td>
<td>EMS</td>
<td>Gga</td>
<td>Tag</td>
<td>R709stop</td>
<td>Phosphatase</td>
<td>Moderate</td>
</tr>
<tr>
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<td>Aaa</td>
<td>G721R</td>
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<td>Strong</td>
</tr>
<tr>
<td>e1196</td>
<td>ICR</td>
<td>gat</td>
<td>gAa</td>
<td>Frameshift at 732, stop at 733</td>
<td>Phosphatase</td>
<td>Strong</td>
</tr>
<tr>
<td>m2</td>
<td>ICR</td>
<td>tgG</td>
<td>tgA</td>
<td>W796stop</td>
<td>Phosphatase</td>
<td>Strong</td>
</tr>
<tr>
<td>n1307</td>
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<td>~650-bp tandem duplication in 1st intron</td>
<td>Frameshift at 309, stop at 328</td>
<td>Sac1</td>
<td>Strong</td>
</tr>
<tr>
<td>ox1</td>
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<td>tgG</td>
<td>tgA</td>
<td>W802stop</td>
<td>Phosphatase</td>
<td>Strong</td>
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<tr>
<td>s1710</td>
<td>mut-4 mutator</td>
<td>gAT GCG ttc</td>
<td>gtt caa aac</td>
<td>Frameshift at 309, stop at 328</td>
<td>Sac1</td>
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</tr>
</tbody>
</table>
we determined if synaptic vesicle proteins were transported intermediates. To distinguish between these possibilities, synaptic vesicle precursors or Golgi complex trafficking of vesicles, it was unclear if these vesicles were examined. Although some cell bodies exhibited an accumulation was observed in the wild type (11 cell bodies exhibited an accumulation of vesicles (Fig. 4 A); no accumulation was observed in the ventral and dorsal nerve cords. These puncta correspond to pools of vesicles at synapses (Jorgensen et al., 1995; Nonet, 1999). In a wild-type (left) and an unc-26(s1710) adult hermaphrodite (right). The ventral nerve cord was reconstructed from serial electron micrographs. GABA neurons were identified based on their position within the cord, and because they form synaptic connections exclusively to muscle. Cholinergic neurons were identified based on their position in the cord and because they form synaptic connections to neurons and muscle (White et al., 1976). SV, Synaptic vesicle; AZ, active zone. B, The average number of synaptic vesicles per reconstructed synapse was decreased in unc-26 mutants. Number SV per synapse: ACh, wild-type = 173 ± 25 SV, n = 32 synapses; unc-26(s1710) = 72 ± 5 SV, n = 61 synapses. GABA, wild-type = 242 ± 28 SV, n = 14 synapses; unc-26(s1710) = 78 ± 10 SV, n = 23 synapses. Pooled, wild-type = 194 ± 19 SV, n = 46 synapses; unc-26(s1710) = 74 ± 4 SV, n = 85 synapses.

Figure 3. Mutations in the unc-26 gene cause a depletion of synaptic vesicles at neuromuscular synapses. A, Representative electron micrographs of acetylcholine and GABA neuromuscular junctions in a wild-type (left) and an unc-26(s1710) adult hermaphrodite (right). The ventral nerve cord was reconstructed from serial electron micrographs. GABA neurons were identified based on their position in the cord and because they form synaptic connections exclusively to muscle. Cholinergic neurons were identified based on their position in the cord and because they form synaptic connections to neurons and muscle (White et al., 1976). SV, Synaptic vesicle; AZ, active zone. B, The average number of synaptic vesicles per reconstructed synapse was decreased in unc-26 mutants. Number SV per synapse: ACh, wild-type = 173 ± 25 SV, n = 32 synapses; unc-26(s1710) = 72 ± 5 SV, n = 61 synapses. GABA, wild-type = 242 ± 28 SV, n = 14 synapses; unc-26(s1710) = 78 ± 10 SV, n = 23 synapses. Pooled, wild-type = 194 ± 19 SV, n = 46 synapses; unc-26(s1710) = 74 ± 4 SV, n = 85 synapses.

and frequently coil (Rand and Russell, 1984; Alfonso et al., 1994). Second, unc-26 mutants are strongly resistant to inhibitors of acetylcholinesterase, indicative of a decrease in acetylcholine release (Rand and Russell, 1984; Nguyen et al., 1995; M iller et al., 1996; Y ook, C., and E. M. Jorgensen, personal communication). Third, unc-26 mutants display abnormalities associated with the loss of GABA neurotransmission. For example, mutations that eliminate GABA synthesis disrupt the enteric muscle contractions of the defecation cycle (McIntire et al., 1993; Jin et al., 1999) and unc-26 mutants have reduced numbers of enteric muscle contractions (Miller et al., 1996). Taken together, these data indicate defects in both cholinergic and GABA function in unc-26 mutants.

Although these abnormalities suggest a defect in synaptic function, they could also arise through defects in development of the nervous system. We examined the architecture of the GABA nervous system in unc-26 mutants using an unc-47-GFP reporter construct that expresses GFP in all 26 GABA neurons (McIntire et al., 1997). In the null allele unc-26(s1710), all 26 cell bodies were properly positioned and the axonal architecture appeared normal (wild-type, n = 4 animals; unc-26(s1710), n = 5 animals; data not shown). These results suggest that the nervous system develops normally, and that the locomotory defects are likely to be caused by aberrant function of the nervous system, possibly by defects in the endocytosis of synaptic vesicles.

Synaptic Vesicle Distribution Defects

To determine if there were defects in the recycling of synaptic vesicles in unc-26 mutants, we reconstructed serial electron micrographs of the ventral nerve cord of wild-type and unc-26(s1710) animals. unc-26(s1710) animals exhibited two defects in the distribution of synaptic vesicles at synapses. First, the total number of synaptic vesicles at synapses was depleted relative to the wild type. Second, the remaining vesicles exhibited linear arrangements and were dissociated from the active zone.

Qualitatively, unc-26 mutants exhibited a depletion of vesicles at synapses relative to the wild type (Fig. 3 A). Quantification of vesicles at synapses in the cholinergic and GABA-releasing motor neurons demonstrated that the number of vesicles per synapse in unc-26(s1710) animals (74 ± 4.8 vesicles/synapse, n = 85 synapses) was reduced to 38% of the number of synaptic vesicles in the wild type (194 ± 19.6 vesicles/synapse, n = 46 synapses; Fig. 3 B). This decrease suggested that unc-26 mutants are defective in synaptic vesicle endocytosis, or alternatively, in the transport of vesicles from the cell body (Jorgensen et al., 1995).

To test for defects in vesicle transport from the cell body, we looked for the presence of vesicles in motor neuron cell bodies in the null mutant unc-26(s1710). At the ultrastructural level, 10 of 24 mutant cell bodies examined exhibited an accumulation of vesicles (Fig. 4 A); no accumulation was observed in the wild type (11 cell bodies examined). Although some cell bodies exhibited an accumulation of vesicles, it was unclear if these vesicles were synaptic vesicle precursors or Golgi complex trafficking intermediates. To distinguish between these possibilities, we determined if synaptic vesicle proteins were transported to sites of release. Specifically, we examined the distribution of the synaptic vesicle protein synaptobrevin in unc-26(s1710) animals. Wild-type worms expressing synaptobrevin tagged with GFP exhibited punctate staining along the ventral and dorsal nerve cords. These puncta correspond to pools of vesicles at synapses (Jorgensen et al., 1995; Nonet, 1999). In unc-26 mutants, a similar level of synaptobrevin-GFP fluorescence was observed at synapses along the nerve cords (Fig. 4 B and C), indicating that most synaptic vesicle precursors are appropriately delivered to synapses. In blind tests, we detected a slight increase in the fluorescence of some, but not all, motor neu-
ron cell bodies (see Materials and Methods). These data suggest that in some cells, synaptic vesicle precursors are not transported as efficiently in the synaptojanin mutant. However, in most cells, transport of synaptic vesicle proteins was normal, therefore the depletion of synaptic vesicles at the synapse was likely to be caused by a defect in endocytosis.

**Endocytosis Defects**

To ascertain whether there was a defect in the recovery of synaptic vesicle components from the plasma membrane, we further characterized the distribution of synaptobrevin-GFP in unc-26(s1710) mutants. In wild-type animals, fusion of synaptic vesicles at the active zone delivers synaptobrevin to the plasma membrane. Synaptobrevin is recovered from the membrane by endocytosis and regenerated synaptic vesicles are clustered at the active zone, preserving a punctate staining of synaptic varicosities (Fig. 4, B and C). In mutants that have defects in synaptic vesicle endocytosis, such as in synaptotagmin and AP180 mutants, synaptobrevin-GFP is diffusely distributed in the plasma membrane of axons (Jorgensen et al., 1995; Nonet et al., 1999). unc-26 mutants exhibited a similarly diffuse staining pattern of synaptobrevin-GFP along the nerve cords (Fig. 4, B and C), indicating that at least this synaptic vesicle protein is not efficiently recovered from the plasma membrane, and suggesting that synaptic vesicle membrane remains in the plasma membrane longer in unc-26 mutants.

Our ultrastructural analysis of neuromuscular junctions confirmed that unc-26 mutants are defective in synaptic vesicle recycling by revealing an accumulation of endocytic pits in the plasma membrane. These endocytic pits had faint collars at the neck of the budding vesicle; such collars are likely to be dynamin polymers, which are known to form rings visible by EM (Takei et al., 1995). The endocytic pits fell into two morphological classes: those coated by matrices resembling clathrin cages, and those lacking a coat (Fig. 5 A). The presence of two distinct types of endocytic pits suggests that multiple recycling pathways may exist at *C. elegans* neuromuscular junctions. Most of these pits were found within 100 nm of active zones (Fig. 5 B), and therefore, these structures are likely to be intermediates in the synaptic vesicle recycling pathway. Noncoated pits were often found immediately adjacent to active zones (Fig. 5 C). Such intermediate endocytic structures were not found at any synapses in the wild-type (wild-type, n = 328 sections; unc-26(s1710), n = 433 sections). The presence of these endocytic pits indicated a vesicle membrane recycling defect in unc-26 mutants, suggesting that the recycling pathway is slowed, allowing for the accumulation of short-lived endocytic intermediates. However, the number of these structures could not account for the depletion of mature vesicles at synapses. Thus, the loss of vesicles was likely to be due to
delays at a previous step, such as in clathrin recruitment or vesicle budding.

Synaptojanin mutants also accumulated coated vesicles. These vesicles were not attached to the membrane, yet still retained their clathrin coat (Figs. 6 A and 7 A). Some of these vesicles were likely to be recycling synaptic vesicles, because of their close association with synapses (Fig. 6 B). unc-26(s1710) animals contained an almost tenfold increase in the number of coated vesicles over the wild-type (Fig. 6 C, left). Although our serial reconstruction focused on the neuromuscular junction-rich ventral nerve cord, coated vesicles were found in a number of different cell types, but were seen predominantly in neurons, at both synapses, and in cell bodies (Fig. 6 C, right). Coated vesicles found in cell bodies were usually near Golgi stacks (Fig. 6 D). These vesicles were likely to have been trans-Golgi complex trafficking intermediates, since some could still be seen attached to Golgi stacks. The presence of coated vesicles at both the Golgi complex and the synapse in unc-26 mutants suggest similarities between uncoating mechanisms acting on A P1 and A P2 clathrin complexes. A defect at the Golgi complex is not altogether surprising, since the synaptojanin-related INP5 proteins in yeast and the OCRL protein in animals have been implicated in Golgi complex function (Olivos-Glander et al., 1995; Suchy et al., 1995; Bensen et al., 2000). The accumulation of coated vesicles in diverse tissues indicated that, in the absence of synaptojanin, the uncoating process is blocked or delayed for synaptic vesicle endocytosis, as well as for other trafficking events.

Mutations in synaptojanin also caused an increase in endosome-like compartments (Fig. 7, A and B). Endosomes predominantly accumulated in regions with active zones; the presence of endosomes fell as distance from the active zone increased (data not shown). Because endosomes were often seen adjacent to morphologically identified active zones (Fig. 7 A), these structures may represent sorting compartments in synaptic vesicle biogenesis. These defects suggest a role for synaptojanin at the endosome analogous to its role at the plasma membrane. Alternatively, they may reflect an indirect effect of disrupted trafficking from the plasma membrane.

**Cytoskeletal Defects**

After synaptic vesicles are regenerated from endosomes or the plasma membrane, they must be clustered at the synapse to provide a reserve pool of vesicles for future neurotransmission events. One possible mechanism for this clustering is via interactions with the synaptic cyto-
skeleton (Fernandez-Chacon and Sudhof, 1999). In unc-26(s1710) mutants, we observed an abnormal organization of the reserve pool, suggesting that vesicle interactions with the cytoskeleton are altered in the mutant. In the wild-type, vesicles cluster in a sphere around the active zone (Fig. 8A). In unc-26(s1710) animals, fewer vesicles were seen closely associated with the active zone. Instead, most vesicles were distant from the active zone, and arranged in a linear string-of-pearls configuration (Fig. 8B). This linear arrangement suggested that vesicles were attached along a single cytoskeletal filament or lamella. A collapse in cytoskeletal architecture in the unc-26 mutant is consistent with observations implicating synaptojanin and PI metabolism in maintenance of the actin cytoskeleton (Sakisaka et al., 1997; Raucher et al., 2000). Surprisingly, these cytoskeletal defects did not affect the architecture of the nervous system in the adult animal (data not shown; see Materials and Methods).

**Discussion**

We cloned the single Ce-synaptojanin gene, and demonstrated that it corresponds to the mutationally defined gene, unc-26. We observed defects indicating that synaptojanin functions in general trafficking events in all tissues: coated vesicles accumulated in muscles, neurons, and the hypodermis. Moreover, noncoated vesicle trafficking intermediates accumulated to high levels in some cell bodies, suggesting defects in general vesicle trafficking. However, two observations suggested that although syn-
aptojanin may function in general vesicle trafficking, the process most sensitive to synaptojanin function is vesicle trafficking at the synapse. First, the most obvious defect of unc-26 animals was their uncoordination; specifically, they exhibited phenotypes typical of defects in synaptic transmission. Second, mutants in general endocytic machinery, such as mutations in the medium subunit of the A P2 complex (B. aum, P., and G. G arriga, personal communication), cause severe morphological defects and the mutants have reduced viability. By contrast, unc-26 mutants were relatively healthy with respect to body shape, brood size, and growth rate. These observations indicated that the phenotypes of unc-26 mutants are largely attributable to a defect in synaptic function and not general vesicle trafficking.

Our analysis of the unc-26 mutant revealed defects in multiple steps of synaptic vesicle recycling. Specifically, we observed defects in the recruitment of endocytic machinery, the fission of vesicles from the plasma membrane, the uncoating of vesicles after fission from the membrane, the recovery of vesicles from endosomes, and the tethering of synaptic vesicles to the cytoskeleton in the reserve pool. In contrast to the pleiotropic defects observed at the synapses of unc-26 mutants, mouse synaptojanin 1 mutants exhibited only an accumulation of coated vesicles at nerve terminals (Cremona et al., 1999). Why do unc-26 mutants exhibit a larger variety of defects than the mouse mutant? One explanation is that functional redundancy in the mouse rescues some phenotypes. unc-26 represents the only synaptojanin-like molecule encoded by the C. elegans genome, whereas the mouse genome encodes at least one other synaptojanin-like molecule (Kvotchev and Sudhof, 1998). This gene may provide functional redundancy with synaptojanin 1; however, such redundancy can only be partial since synaptojanin 1 mutants are inviable.

How might the known catalytic properties of synaptojanin explain the pleiotropic defects we observed in the synaptic vesicle recycling pathway? Synaptojanin may alter the structural properties of the membrane, or alter the binding properties of the membrane. First, synaptojanin may affect the structural properties of the membrane. During vesicle formation, tight curvature of the membrane at the neck of the bud must be achieved. The phosphatase activity of synaptojanin may facilitate membrane curvature by removing negative charges from the inner membrane surface, thereby relieving the inhibition of lipid-packing caused by repulsion between charged lipids. This model is similar to a mechanism proposed for endophilin, a lysophosphatidic acid acyl transferase. Specifically, endophilin converts inverted cone-shaped lipids to cone-shaped lipids, which favors the negative membrane curvature required for bud formation (Schmidt et al., 1999).

Alternatively, there are a number of proteins implicated in endocytosis that bind polyphosphoinositides. Specifically, synaptotagmin, which is implicated in the recruitment of the clathrin adaptor complex to the plasma membrane (Zhang et al., 1994; Jorgensen et al., 1995), dynamin, which is required for fission of the vesicles (Schmid et al., 1998), and the clathrin adaptor complex, which coats the vesicle (Cremona and De Camilli, 1997), all bind PIs (Schiavo et al., 1996; Zheng et al., 1996; Hao et al., 1997; Jost et al., 1998; Gaidarov and Keen, 1999). Since endocytosis is stalled at each of these steps in the synaptojanin mutant, it is conceivable that cleavage of phosphates from phospholipids is required to release these proteins from the membrane, which allows the next step in the endocytic pathway to proceed.

Finally, the defects we observed in unc-26 mutants are not consistent with a block at any one of these steps, but are most consistent with an overall kinetic slowing in the synaptic vesicle recycling pathway. Support for this hypothesis is provided first by the variety of defects seen along multiple steps of the pathway, and second, by the continued presence of vesicles, the end product of endocytosis, at synapses. Synaptojanin, therefore, is not essential for synaptic vesicle recycling per se, but more likely accel-

Figure 7. Endosome-like compartments accumulated in unc-26.
A, Electron micrograph of a synapse in the VB cholinergic motor neuron of an unc-26(s1710) adult hermaphrodite. Endosomes were defined as 50 nm or larger membrane-bound structures extending two or more lateral sections. AZ, Active zone. B, Quantification of endosome-like structures in unc-26(s1710) adult hermaphrodites.
erates the progress of intermediates along multiple steps of the synaptic vesicle recycling pathway.

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