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Behavioral/Systems/Cognitive

DLG97/SAP97 Is Developmentally Upregulated and Is Required for Complex Adult Behaviors and Synapse Morphology and Function

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The synaptic membrane-associated guanylate kinase (MAGUK) scaffolding protein family is thought to play key roles in synapse assembly and synaptic plasticity. Evidence supporting these roles in vivo is scarce, as a consequence of gene redundancy in mammals. The genome of Drosophila contains only one MAGUK gene, discs large (dlg), from which two major proteins originate: DLGA [PSD95 (postsynaptic density 95)-like] and DLG97 [SAP97 (synapse-associated protein)-like]. These differ only by the inclusion in DLG97 of an L27 domain, important for the formation of supramolecular assemblies. Known dlg mutations affect both forms and are lethal at larval stages attributable to tumoral overgrowth of epithelia. We generated independent null mutations for each, dlgA and dlgS97. These allowed unveiling of a shift in expression during the development of the nervous system: predominant expression of DLGA in the embryo, balanced expression of both during larval stages, and almost exclusive DLG97 expression in the adult brain. Loss of embryonic DLG97 does not alter the development of the nervous system. At larval stages, DLGA and DLG97 fulfill both unique and partially redundant functions in the neuromuscular junction. Contrary to dlg and dlgA mutants, dlgS97 mutants are viable to adulthood, but they exhibit marked alterations in complex behaviors such as phototaxis, circadian activity, and courtship, whereas simpler behaviors like locomotion and odor and light perception are spared. We propose that the increased repertoire of associations of a synaptic scaffold protein given by an additional domain of protein–protein interaction underlies its ability to integrate molecular networks required for complex functions in adult synapses.

Key words: scaffold proteins; synapses; Drosophila; DLG; behavior; MAGUK; SAP97

Introduction

Synaptic transmission relies on the proper spatial organization of protein complexes, which are shaped by scaffolding proteins bearing multiple protein interaction domains. The membrane-associated guanylate kinase (MAGUK) family of scaffolding proteins and in particular the synapse-associated protein (SAP) subfamily, is extensively expressed in the brain and links synaptic proteins to signal transduction cascades, the cytoskeleton, and the endocytic machinery (Fanning and Anderson, 1999; Garner et al., 2000a,b; Sheng and Lee, 2001; Tepass et al., 2001).

In vertebrates, SAPs postsynaptic density 95 (PSD95)/SAP90, SAP102/neuroendocrine-Discs large (NEDLG), SAP97/human DLG (hDLG), and PSD93/Chapsyn-110 are thought to play key roles in synapse assembly and plasticity (Rumbaugh et al., 2003; Funke et al., 2005; Regalado et al., 2006); in vivo evidence for these roles has been scarce, likely because of functional redundancy. Although studies in cultured neurons demonstrate a role for SAPs in protein clustering and dendritic spine formation, PSD95 (Migaud et al., 1998) or PSD93 (McGee et al., 2001) knock-out mice lack obvious alterations in synaptic structure and function. Nevertheless, behavioral analysis of these mutants reveals learning and memory defects. SAP97 mutant mice are not viable because of profound developmental defects. However, the synaptic function of cultured SAP97 mutant neurons is normal (Caruana and Bernstein, 2001; Klocker et al., 2002). Drosophila contains a single SAP gene, dlg, with functions in epithelial development (Woods et al., 1996), asymmetric cell di-
vision (Oshiro et al., 2000), and the development and function of the larval neuromuscular junction (NMJ) (Lahey et al., 1994; Budnik et al., 1996; Tejedor et al., 1997; Thomas et al., 1997). In dlg mutants, all gene products are severely decreased, which leads to early pupal lethality and thus precludes their analysis beyond this stage.

The dlg locus generates multiple products through different transcription start sites and mRNA splicing (Mendoza et al., 2003). The two main products are dlgA (PSD95-like) and dlgS97 (SAP97-like) transcripts. Unlike DLGA, DLGS97 contains an extended N-terminal region bearing a L27 domain. L27 domains form tetrameric complexes with other L27 domain-containing proteins, providing a platform for supramolecular assemblies (Doerks et al., 2000; Feng et al., 2004; Petrosky et al., 2005). Although DLGA is broadly expressed in epithelia, somatic muscles, and nervous system (Woods and Bryant, 1991), DLGS97 is exclusive to the nervous system and the NMJ (Mendoza et al., 2003).

To investigate the function of DLGA and DLGS97 in vivo, we generated form-specific mutations. We found that during nervous system development there is a shift in dlg variant usage: DLGA during embryonic development, coexistence of DLGA and DLGS97 in the larvae, and predominant DLGS97 expression in the adult. Contrary to dlgA mutants, dlgS97 flies are viable, but complex behaviors, such as phototaxis, circadian rhythms, and courtship are disrupted. At the larval NMJ, isoform-specific mutations resulted in functional and structural abnormalities, but some phenotypes observed in dlg mutants were not detected, suggesting reciprocal compensation. These results highlight specific functions of two closely related SAPs that may arise from the ability of DLGS97 to form supramolecular complexes through its L27 domain.

Materials and Methods

Fly strains and genetics

The following strains were used: the UAS strains UAS-dlgA-EGFP and UAS-EGFP-dlgS97, the pan-neural Gal4 activator strain elav-Gal4 (Bloomington Stock Center, Bloomington, IN), the P-element insertion line NP7225 (referred as dlgS97NP7225 here; National Institute of Genetics, Shizuoka, Japan) and eyS003 (Bloomington Stock Center), the transposase-bearing strain D2-3Dr/TM2 (provided by A. Garcia Bellido, Universidad Autónoma de Madrid, Spain), and the phototransduction mutant inaD (Pak, 1979). All crosses were performed at 25°C, but once the progeny of UAS/Gal4 crosses reached the wandering third instar larval stage they were shifted to 29°C to maximize expression of transgenes for studies in adult stages.

Transposition. Because dlg is necessary for spermatogenesis (U. Thomas, unpublished observations), a gene region with a duplication of the dlg locus in the Y chromosome, Dp(1;2) v 75d (Bloomington Stock Center) was incorporated to the D2-3Dr/TM2 strain and males were crossed with dlgS97NP7225 females or dlgAeyS003 to mobilize the P-element. A total of 320 excision lines was generated and analyzed for DLGS97 expression in Western blots, 10 lethal lines with tumorous larvae were also analyzed for no complementation with dlgS97 and for expression of DLG. For rescue experiments, the dlgS97 mutant was recombined with the elav-Gal4 insertion.

Immunohistochemistry

Embryos and body wall muscle preparations were stained as described previously (Thomas et al., 1997; Mendoza et al., 2003). Primary antibodies used were rabbit polyclonal anti-DLGS97 (1:500–1:2000) (Mendoza et al., 2003), rat anti-Scribble (Scrib) (1:1000) (Y. F. Fuentes-Medel, S. Marfatia, and V. Budnik, unpublished observation), rabbit anti-glutamate receptor III (GluRIII) (1:200) (Marrus et al., 2004), and Cy3-conjugated anti-HRP (1:200; Jackson ImmunoResearch, West Grove, PA). The following mouse monoclonal antibodies used were from Developmental Studies Hybridoma Bank (University of Iowa, Iowa City, IA): anti-Fasciclin II (FasII) (1:14; 1:2) and anti-DLGS97 (4F3; 1:500). HRP- or fluorescent-coupled secondary antibodies were from Jackson ImmunoResearch or Invitrogen (Eugene, OR). After immunocytochemical procedures, samples were mounted in 70% glycerol in PBS or Vectashield mounting medium (Vector Laboratories, Burlingame, CA). Images were captured using a digital camera (Nikon Coolpix E500; Nikon, Tokyo, Japan) coupled to a Nikon E400 microscope, or a confocal microscope (LSM 510 Pascal; Carl Zeiss MicrolImaging, Oberkochen, Germany). Quantification of confocal images was performed using Volocity 4.0 imaging software (Improvement, Lexington, MA) measuring the density of the fluorescence and normalizing by the average density of the control.

Western blots

Embryos were homogenized in homogenization buffer (50 mM Tris-Cl, pH 7.5, 150 mM NaCl) and centrifuged for 10 min at 800 × g, and the pellet was resuspended in RIPA buffer (0.15 M NaCl, 1% NP-40, 0.5% sodium deoxycholate, 0.1% SDS, 1 mM EDTA, and 0.2% Tris-Cl, pH 7.5) supplemented with a protease inhibitor mixture (Boehringer, Mannheim, Germany). Larval brains were dissected in cold calcium-free dissection buffer and homogenized in RIPA buffer supplemented with protease inhibitor mixture. Adult heads were homogenized directly in RIPA buffer. Proteins were separated in 10% acrylamide SDS-PAGE, transferred to nitrocellulose membranes, and incubated with rabbit anti-DLGS97 (1:3000) (Mendoza et al., 2003), mouse anti-DLGS97 (4F3; 1:1500), or mouse anti-β-tubulin (12G10; 1:1000; Developmental Studies Hybridoma Bank, University of Iowa, Iowa City, IA) antibodies. Quantification of signal intensity in Western blots was performed using Quantity One software (Bio-Rad, Hercules, CA).

Genomic PCR

PCR was performed on genomic DNA obtained from single flies homogenized in DNA buffer (10 mM Tris-Cl, pH 8.2, 1 mM EDTA, 25 mM NaCl) with 200 mg/ml freshly added proteinase K. Primers used for genomic PCR to map P-element excision-derived deletions were as follows: for dlgs975–38, 5′-GCCACACCAAGGCAAAATAA and 5′-ATCCGTCTCTCGGA CGTGTTCTCA; for dlgs975, 5′-CGCTTGAGGCAGCGTAGAG and 5′-GCTCTCGG CTGTTCTTGT; and for dlga40–2, 5′-ATAATACATCATATTGCGTCTCT and 5′-CCACAGAACACACTGAAAATG.

Electron microscopy and bouton morphometry

Body wall muscles were prepared for transmission electron microscopy, and boutons were serially sectioned and subjected to morphological analysis as described by Lahey et al. (1994). Briefly, electron micrographs taken at 11,500× magnification were used to identify bouton midlines (section of largest diameter within a serially sectioned bouton) where the perimeter of subsynaptic reticulum (SSR) was traced using Photoshop CS2. SSR parameters (length and thickness, as well as bouton midline area, were measured using NIH Image software; for each midline, the total length of the lines drawn (length of SSR) and the length of the cross sections (for the detail, see supplemental Fig. S6, available at www.jneurosci.org as supplemental material) were measured. For measurements of synaptic length, 28 synapses from 3 control samples, 50 synapses from 6 dlga40–2 samples, 45 synapses from 10 dlga75–1 samples, and 47 synapses from 6 dlgs975 samples were measured using ImageJ. Measurements of SSR and synaptic bouton area, five wt, seven dlga75–1, eight dlga40–2, and six dlgs975 bouton midlines were analyzed. For measurements of internal vesicle diameter, EM pictures were scanned at high resolution. Overall, 19 wt boutons, 22 dlga75–1 boutons, 23 dlga40–2 boutons, and 21 dlgs975 boutons were analyzed. For each bouton in the above genotypes, the internal diameter of at least 20 vesicles was measured.

Electrophysiology

Electrophysiological recordings were done as previously described by Ashley et al. (2005). For each muscle recorded, the resting membrane potential, input resistance, and specific capacitance were measured.
Seven samples for the mutant dlg$^{X-2}$ were analyzed. Behavioral tests
Climbing assay. Climbing assays were performed using 3-d-old adults in multiple batches of 30–60 flies. The ability to climb against gravity was measured by a countercurrent distribution (Benzer, 1967) and scored as by Xu et al. (2006).

Olfactory assay. Olfactory avoidance responses were measured as described by Anholt et al. (1996) using 1% benzaldehyde as the repellent odor in groups of five individuals not separated by genre.

Phototaxis assays. Phototaxis assays were performed as described by Benzer (1967) with modifications. Approximately 100 5-d-old males were placed in glass test tubes (14 cm long) horizontally for at least 1 h in an artificially light illuminated room before they were transferred to complete darkness for at least 5 min. A clean tube was then connected to the one containing the flies, and a halogen light (15 W), as the only light source, was turned on at the end of the empty tube. Flies were allowed to move to the illuminated tube for 1 min, and then the tube was replaced for a new tube. This procedure repeated four times. The number of flies in each tube was determined.

Courtship behavior assay. Four- to seven-day-old flies kept isolated shortly after hatching were used for the courtship assay. Virgin females of the white Oregon strain were gently introduced into the courtship chamber unanesthetized. The time over which the male was engaged in courtship behavior (orientation toward the female, licking female genitals, wing extension, female following, wing vibration, and attempts to copulate) was measured for 10 min. Males that did not show any courtship behavior during the experiment were discarded from the quantification. The courtship index was calculated as the amount of time spent courting during the 10 min of the assay divided by 10. Statistical analysis was performed using the Wilcoxon–Mann–Whitney test for unpaired data. Control males were of the strain yw;UAS-EGFP-dlgS$^{97}$.

Rhythmicity assays. Locomotor activity was monitored using an automated setup (Trikinetics, Waltham, MA). Experiments were repeated three times, each time including 28–32 individuals. For the average locomotor activity histograms, the activity of each genotype was averaged across 3 d (days 2–4 of a light/dark (LD) cycle). For each individual fly, the activity of each 30 min bin was normalized to the fly total activity during that particular day, averaged over successive days, and an average of the daily averages was obtained. The power fast Fourier transform (FFT) (a measure of the strength of the rhythm) was calculated (Clocklab; Actimetrics, Wilmette, IL). Statistical analysis included ANOVA and pairwise comparisons against the control (original P-element insertion; dlgS$^{97}$/NP7225 or elav-Gal4, dlgS$^{97}$/H11005/H11002 for the rescue experiments) using Dunnett’s multiple-comparisons post hoc test.

Electroretinograms. Flies, 10 d of age or younger posteclosion, were dark-adapted for at least 5 min, and then exposed to a 1 s pulse of white light (400–700 nm), log $I/I_{0} = −4$ for the first light stimulus and log $I/I_{0} = −2$ for the second light stimulus; $I_{0} = 6600$ lux. Electroretinogram (ERG) recordings were conducted at room temperature using two glass microelectrodes filled with 1 M NaCl. The recording electrode was placed on the surface of the fly eye, while the ground electrode was inserted into the thorax of the fly. White light stimulation was a xenon arc lamp (Lambda LS 175W; Sutter Instruments, Novato, CA) passed through a 400–700 nm bandpass filter. Signals were sampled at 1 kHz using a Digidata 1322A digitizer (Molecular Devices, Sunnyvale, CA) and filtered using a boxcar smoothing filter (Clampfit; Molecular Devices, Sunnyvale, CA) (5–11 points depending on noise level).

Results
Generation of specific dlgA and dlgS$^{97}$ mutants
Previous studies show that several transcripts are generated from the dlg locus, which would translate into peptides ranging from 27 to 130 kDa (Mendoza et al., 2003) (flybase record). However, only two proteins of high molecular weight predominate, DLGA and DLGS$^{97}$, which result from the use of two different transcriptional start sites (Mendoza et al., 2003) separated by 18 kb (Fig. 1 A, B). To generate specific mutants for the two isoforms, we mobilized P-element insertions (NP7225 and EY5003), located 959 bp upstream from the first translated exon of dlgS$^{97}$ or 10 bp from the first translated exon of dlgA, respectively (Fig. 1 A). This strategy allowed us to isolate specific excision-induced dlgS$^{97}$ and dlgA mutants. From the mobilization of the P-element EY5003, we isolated the excision dlgA$^{60,2}$, which completely eliminated DLGPDZ staining in epithelia, leaving DLGS$^{97}$/NMJ undiminished, as determined by Western blots of larval body wall muscles and imaginal discs (Fig. 1 E) (data not shown). As expected from the tumor suppression function ascribed to dlg in epithelia (Woods et al., 1996), these larvae have tumorous imaginal discs and enlarged brain, and they die in the third-instar larval stage, similar to dlg mutant alleles.

From the mobilization of the P-element NP7225, we isolated two excision strains, dlgS$^{97}$ and dlgS$^{97}$, in which DLGS$^{97}$/NMJ immunoreactivity was eliminated (Fig. 1 A, C). Both dlgS$^{97}$ alleles retained DLGA expression as revealed by immunocytochemistry (Fig. 1 D) and Western blot assays (Fig. 1 E) using either a monoclonal antibody against the PSD-95/DLG/zona occludens-1 (2 PDZ-2) (anti-DLGPDZ, 4F5) (Parnas et al., 2001) or a polyclonal antibody against the PDZ1 and two domains of DLG (Thomas et al., 1997). dlgS$^{97}$ has a 3.2 kb deletion that includes exon 1 and most of exon 2 (Fig. 1 A). dlgS$^{97}$ has an 8 kb deletion, which removes exons 1–3 and a portion of exon 4 (Fig. 1 A). In both
Figure 2. Progressive replacement of DLGA for DLGS97 during development. A, Representative Western blots of homogenized tissue of embryo (all stages, approximate MW, 130 kDa), larval body wall (body wall, approximate MW, 116 and 97 kDa), larval brain (approximate MW, 130 kDa), and adult head (approximate MW, 130 kDa). All blots were tested in parallel with the same concentration of antibody (1:3000, affinity-purified DKGpdz, and 1:1500 DKG97N). The load was as follows: 30 μg for embryos, and the equivalent to one larval body wall, six larval brains, and one head per lane. The line at left in each blot points the position of the 116 kDa molecular weight standard. B, Quantification of total DLG label of at least three independent Western blot assays tested with anti-DLGpdz, the bars represent averages ± SEM of the percentage of the signal in dls97 mutants compared with the signal of the control strain dls97p145, at different developmental stages. Body HMW, Larval body wall high molecular weight band (116 kDa); body LMW, larval body wall low molecular weight band (97 kDa). *p < 0.05; **p < 0.01. C, DLG proteins in adult brain. Confocal images (composite of 17 slices) of WT (top panel) and dls97 mutant (bottom panel) adult brain labeled with DKGpdz or DKG97N antibodies and the merged image showing the complete overlapping of the labeling patterns and the strong decrease in intensity of the labeling to DKGpdz. Note that DKGpdz antibody labels both DLGA and DLGS97 proteins. In embryos, despite the complete lack of DLGS97, there is a significant decrease in DKGpdz immunoreactivity (Figs. 1B, 2A, B), suggesting that DLGA is the main dls product expressed in the embryonic nervous system and somatic muscle. At the wild-type (WT) larval body wall, two characteristic bands are revealed by anti-DKGpdz antibodies [a 116 kDa, high molecular weight (HMW) band also recognized by DKG97N antibody and a 97 kDa, low molecular weight (LMW) band]. In dls97 mutants, the HMW band show a 70% reduction in DKGpdz immunoreactivity levels, but no reduction in the LMW band is observed (Fig. 2A, B). This, together with the elimination of the LMW band in dlgA mutants (Fig. 1E), confirms that the LMW band corresponds exclusively to DLGA. DKGpdz immunoreactivity is reduced by 70% in the larval and 90% in the adult CNS (Fig. 2A, B), which indicates that DLGS97 is the predominant variant in both the adult and the larval brain. Thus, the expression of dls isoforms is developmentally regulated, with the DLGS97 isofom becoming increasingly dominant in the adult brain and the DLGA isoform being preponderant during embryonic development.

dlg protein products are expressed in the adult brain, particularly in the visual centers (lobula plate, medulla, and lamina), the mushroom bodies, and the antennal lobes (Rogero et al., 1997; Ruiz-Canada et al., 2002). However, the lack of an adult viable null mutant has precluded the analysis of their function in adult brain function.

Our Western blot studies demonstrated that DLGS97 predominates in the adult brain (Fig. 2A, B). To determine whether there is differential localization of the two main dls products, we labeled the brain structures with the available DLG antibodies. No difference in the brain structures labeled by DKGpdz and DKG97N antibodies was detected (Fig. 2C). In dls97 mutants, there is a strong decrease in the immunoreactivity to DKGpdz, consistent with the results obtained by the Western blot analysis; a very low level of DKGpdz reactivity is detectable only in the lamina, mushroom bodies, and antennal lobes, the regions in which total DLG is higher in the WT (Fig. 2C). Thus, in dls97 mutants, the remaining DLG (<10% by Western blots) is distributed in a pattern similar to the WT. Thus, dls97 mutants constitute an excellent tool to investigate the role of the main synaptic MAGUK expressed in the Drosophila adult brain.

Behavioral consequences of the loss of DLGS97
To explore the function of the adult brain in the absence of DLGS97, we first centered our analysis in simple behaviors such as locomotion, odor, and light perception. To evaluate locomotion, we measured the ability of flies to climb against gravity (Benzer, 1967; Xu et al., 2006). No significant difference between dls97 alleles and controls is observed (Fig. 3A, left panel). To assess odor perception, we performed an "olfactory avoidance assay" (Anholt et al., 1996). Again, no differences in avoidance responses between dls97 mutants and controls are observed (Fig. 3A, right panel).

The function of the visual system in the mutants was examined by testing the natural ability of the flies to go toward light in a "phototaxis assay" (Benzer, 1967). Whereas ~30% of control flies remained in the dark in the first minute, this number was more than doubled (to ~70%) in dls97^-10^ and dls97^-7^ mutants.
Mann–Whitney test in expression of DLGS97, but only partially rescued by the expression of DLGA. dlgS97 mutants have phototaxis defects that are not statistically different from controls. Each point corresponds to the average of three independent experiments. Bars ± SEM represent the average of 9 – 21 (climbing score) and 11 – 19 (odor detection) independent experiments. B. Phototaxis assay showing the percentage of flies remaining in the dark. Left, Comparison between controls, dlgS97 mutants, and inaD mutants showing that dlgS97 mutants have phototaxis defects that are not statistically different from inaD mutants and different from controls. Each point corresponds to the average of three independent experiments ± SEM. Right, The stimulus was a 1s pulse of white light (400 – 700 nm), log \( I_0 = -4 \) for the first light stimulus and \( \log I_0 = -2 \) for the second light stimulus; \( I_0 = 6600 \) lux, at the time indicated beneath the recordings. Note the lack of differences between wild type and mutants. C. Courtship index of individual control and dlgS97 flies showing that courtship behavior is defective in the mutant, and that this phenotype can be rescued by neuronal DLGS97 but not by DLGA expression. The horizontal lines represent the median of each group. Levels of significance were determined by a two-tail Student’s t-test in A and B and by a Wilcoxon–Mann–Whitney test in D (*p < 0.05 and **p < 0.01).

**Figure 3.** Behavioral analysis and ERG recordings of dlgS97 mutants. A, Climbing and benzaldehyde odor avoidance assay, showing no significant differences between mutants and controls. B, Phototaxis assay showing the percentage of flies remaining in the dark. C, ERGs from wild-type, dlgS97, and dlgS97 flies. The stimulus was a 1 s pulse of white light (400 – 700 nm), log \( I_0 = -4 \) for the first light stimulus and \( \log I_0 = -2 \) for the second light stimulus; \( I_0 = 6600 \) lux, at the time indicated beneath the recordings. Note the lack of differences between wild type and mutants. D, Courtship index of individual control and dlgS97 flies showing that courtship behavior is defective in the mutant, and that this phenotype can be rescued by neuronal DLGS97 but not by DLGA expression. The horizontal lines represent the median of each group. Levels of significance were determined by a two-tail Student’s t-test in A and B and by a Wilcoxon–Mann–Whitney test in D (*p < 0.05 and **p < 0.01).
DLGA and DLGS97 are differentially used at larval NMJs in a context-specific manner

The results presented above indicate a marked difference in the expression pattern and functional requirements for DLGA and DLGS97 in the embryonic versus the adult nervous system. Thus, although DLGS97 is not required for basic behaviors, more complex processes such as phototaxis, courtship, and circadian rhythms require DLGS97 for proper behavioral display. Furthermore, courtship behavior appears to have a unique requirement for the DLGS97 isoform, because mutant defects are not rescued by expressing the dlga transgene. These isoform- and developmental-specific requirements led us to ask whether DLGA and DLGS97 were also differentially required at intermediate, larval stages, and in particular in the NMJ, where the two variants coexist, and most of the studies about the role of dlg products have been conducted. This was addressed by examining the influence of the selective mutations in dlga or dlgs97 in the structure and function of this glutamatergic synapse.

Previous studies, using dlg mutations that severely decrease both DLGA and DLGS97, have demonstrated that DLG proteins have fundamental functions in the development and morphological plasticity of the larval NMJ as well as in synaptic function (Ataman et al., 2006). Although DLGPDZ immunoreactivity (recognizing both DLGA and DLGS97) is completely eliminated in epithelial cells of dlga<sup>A0.2</sup> mutant larvae (data not shown), PDZ staining at the NMJ is not significantly reduced (Fig. 5), and DLG<sup>SG7N</sup> immunoreactivity is upregulated in this mutant in ~50% (Fig. 5). In contrast, in dlgs97 mutants, where NMJs completely lack DLG<sup>SG7N</sup> immunoreactivity, only a partial (20%) decrease in DLGPDZ immunoreactivity is observed (Fig. 5B, first panel). Together, these observations suggest that (1) both DLGS97 and DLGA coexist in the WT NMJ at approximately the same level of expression, (2) when DLGA is eliminated, DLGS97 is upregulated to WT levels of total DLG (DLGA plus DLGS97) (Fig. 5B), and (3) when DLGS97 is eliminated, there is an upregulation of DLGA but this upregulation does not completely reach WT levels because total DLG<sup>PDZ</sup> immunoreactivity is still decreased by 20% (Fig. 5B)

We studied the expression of FasII and Scrib, two synaptic proteins whose localization depends on dlg (Thomas et al., 1997; Mathew et al., 2002). Selective mutations in either dlgs97 or dlga causes abnormal localization of FasII around synaptic boutons, although this phenotype is not as strong as that observed in the dlgs97<sup>BX2</sup> allele (Thomas et al., 1997), which affects both the DLGA and DLGS97 isoforms (Fig. 5; supplemental Fig. S3, available at www.jneurosci.org as supplemental material). Thus, both dlgs97 and dlga appear to be required for normal FasII localization at the NMJ.

Scrib is a scaffolding protein of the LAP (LRR and PDZ) family, which like DLG and FasII is localized at both presynaptic and postsynaptic sites at the NMJ, and which interacts with DLG.
through GUK-holder (Mathew et al., 2002). Elimination of either DLGS97 or DLGA alone has little impact on Scrib localization (Fig. 5A), suggesting that in this case either isoform can completely compensate for the lack of the other.

DLG isoform-specific function was also tested by examining the structure and function of the NMJ in both dlgS97 and dlgA mutants. Active zones at the larval NMJ are composed of two structural elements, the T-bars, which regulate the efficiency or the synchrony of evoked neurotransmitter release (Kittel et al., 2006), and the presynaptic density (PRD), a region of the presynaptic membrane with increased electron density, exactly apposed to the postsynaptic density (PSD), and thought to be the site for synaptic vesicle fusion (Prokop, 2006) (Fig. 6A,D). Mutations in dlg lead to an increase in the number of T-bars (Lahey et al., 1994). We found that, in both dlgS97 and dlgA mutants, there is a significant increase in the length of the PRD (Fig. 6D,G,F). Interestingly, this phenotype is of the same magnitude as in dlgX1-2 mutants, suggesting that both isoforms collaborate in the regulation of active zone structure, and that neither is sufficient for this regulation.

Another notable phenotype in dlg mutants is the presence of a highly reduced SSR (Lahey et al., 1994). The SSR is a complex membrane structure that expands gradually during larval development and is thought to play a variety of roles, including postsynaptic protein localization, and local translation (Ataman et al., 2006). Notably, no changes in SSR structure when normalized to bouton size are observed in either mutant (Fig. 6G, middle panel), suggesting that either dlg isoform is sufficient for normal SSR development. Intriguingly, however, analysis of the SSR thickness revealed that, although a reduction in SSR thickness is observed in dlgX1-2 mutants, no such difference was observed in dlgA40.2 and dlgS97 mutants (Fig. 6B,C,E,G). Furthermore, SSR thickness is significantly increased in dlgS97 mutants (Fig. 6E,G, right panel). Thus, DLGA and DLGS97 can compensate, or even overcompensate in the case of dlgS97, for each other in the regulation of SSR length and thickness.

Because we detected both form-specific as well as redundant functions for the two DLG variants, we next studied the NMJ postsynaptic density (PSD), and thought to be the site for synaptic vesicle fusion (Prokop, 2006) (Fig. 6A,D). Mutations in dlg lead to an increase in the number of T-bars (Lahey et al., 1994). We found that, in both dlgS97 and dlgA mutants, there is a significant increase in the length of the PRD (Fig. 6D,G,F). Interestingly, this phenotype is of the same magnitude as in dlgX1-2 mutants, suggesting that both isoforms collaborate in the regulation of active zone structure, and that neither is sufficient for this regulation.

Another notable phenotype in dlg mutants is the presence of a highly reduced SSR (Lahey et al., 1994). The SSR is a complex membrane structure that expands gradually during larval development and is thought to play a variety of roles, including postsynaptic protein localization, and local translation (Ataman et al., 2006). Notably, no changes in SSR structure when normalized to bouton size are observed in either mutant (Fig. 6G, middle panel), suggesting that either dlg isoform is sufficient for normal SSR development. Intriguingly, however, analysis of the SSR thickness revealed that, although a reduction in SSR thickness is observed in dlgX1-2 mutants, no such difference was observed in dlgA40.2 and dlgS97 mutants (Fig. 6B,C,E,G). Furthermore, SSR thickness is significantly increased in dlgS97 mutants (Fig. 6E,G, right panel). Thus, DLGA and DLGS97 can compensate, or even overcompensate in the case of dlgS97, for each other in the regulation of SSR length and thickness.

Because we detected both form-specific as well as redundant functions for the two DLG variants, we next studied the NMJ synaptic transmission in dlgA and dlgS97 mutants. This was examined by measuring the amplitude and frequency of spontaneous miniature excitatory junctional potentials (mEJPs), and evoked responses (EJPs) on motor-nerve stimulation. We compared synaptic transmission of the most severe allele dlgX1-2 with dlgA and dlgS97 null mutants. dlgX1-2 has a significant decrease in evoked responses, and a similar decrease is observed in the dlgA mutant. However, responses are indistinguishable from wild type in the dlgS97 mutant allele (Fig. 7B,F). In contrast, a significant increase in the amplitude of mEJPs is observed in dlgX1-2 and dlgS97 but not in dlgA mutants (Fig. 7A,C) without change in frequency in all mutant lines (Fig. 7D). Overall, quantal content is depressed in all mutant combinations (Fig. 7G), suggesting synaptic transmission defects in all the genotypes. The increased amplitude of the mEJPs may be attributable to an increase of the size of the vesicles as it was described for dlgX1-2 mutants (Karanainthi et al., 2002) or to an increase in the density or size of the glutamate receptor clusters. To differentiate between these alternatives, we evaluated the sizes of the synaptic vesicles and the density and size of glutamate receptor clusters. To differentiate between these alternatives, we evaluated the sizes of the synaptic vesicles and the density and size of glutamate receptor clusters. The size of vesicles in CS (internal diameter, 21.72 ± 2.1 nm; average ± SD) shows differences with all the mutants; dlgX1-2 mutant (29.2 ± 1.99 nm), dlgA40.2 (26.4 ± 3.67 nm), and dlgS97 (27.03 ± 2.82 nm) mutants; p < 0.001 for all mutants. These vesicle sizes are in agreement with those reported in the literature for internal diameters (Karanainthi et al., 2002). However, the density and size of glutamate receptor clusters is increased only in dlgS97 mutants (p < 0.05) and not in dlgX1-2 or dlgA40.2 mutants (supplemental Fig. S4, available at www.jneurosci.org as supplemental material).

These results show that, although DLGA and DLGS97 have some redundant functions at the NMJ, normal synaptic transmission requires specific functions of each form.

**Discussion**

The study of the expression and function of the main *Drosophila* synaptic MAGUKs reported here brings about four significant conclusions. (1) The expression of dlg products in the nervous
one cannot completely compensate for the absence of the other; (3) a single isoform is required, and thus the absence of the other has no noticeable effects. These findings demonstrate the complexity and versatility of MAGUK family members, and highlight the notion that specific MAGUKs can perform different nonoverlapping functions when present in the same cell, and even in the same cellular compartment.

In mammals, the four SAP genes are either partially redundant, or mutations in single genes result in early lethality, which has hampered assessing the significance of this diversity for synapses and behavior in vivo. Our ability to individually eliminate SAPs in the intact organism provides a powerful tool to begin to understand this diversity. Based on our findings, it is tempting to speculate that, although DLGA has a preponderant function in establishing the nervous system and ensuring proper organization of synaptic connections, DLGS97 might be most relevant in modulating the function of complex neuronal networks. Nevertheless, our studies at the larval NMJ also emphasize the fact that there is relevant overlap in the function of both isoforms when operating in the same cell.

The significant differences in the roles of DLGA and DLGS97 correlate with a single molecular change, the presence of an extended L27-containing N-terminal sequence in DLGS97. It is of high interest to understand the mechanisms linking this discrete molecular difference to the function of the entire system.

Although the in vivo function of the L27 domain of DLGS97/SAP97 in neurons is not fully understood, it has been implicated in AMPA receptor trafficking (Nakagawa et al., 2004), in the synaptic localization of Dlin-7 (Bachmann et al., 2004), in activity-dependent redistribution of AMPA receptors to spines (Mauceri et al., 2004), and in postsynaptic clustering (Chetkovich et al., 2002). L27 domains are found in proteins of the MAGUK family and in proteins of the LIN-7 family and have been widely implicated in the homo-oligomerization and hetero-oligomerization of these scaffolding proteins (Marfatia et al., 2000; Nakagawa et al., 2004; Petrosky et al., 2005). The L27 domain of DLGS97 could coordinate the function of many multiprotein complexes, consisting of a scaffolding protein and all its binding partners. In vertebrates, SAP97 associates through its L27 domain of DLGS97/SAP97 in neurons is supported by the presence of CASK (CAKI) and LIN-7 (dLIN-7) homologues and the interaction between CAKI and the L27 of DLGS97 (Lee et al., 2002). CAKI is expressed in a pattern similar to DLG in adults and caki mutants, like dlgs97

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Figure 6. Ultrastructure of synaptic boutons in dlgs mutants. A–C and E show TEM micrographs of type Ib boutons at muscle 6 or 7 (abdominal segment 3) of third-instar (A) wild-type, (B) dlgs10, (C) dlgs410 and (E) dlgs97 larvae. b, Bouton. The arrow in A points to an active zone. D, F, High-magnification views of a representative active zone in wild-type (B) and dlgs97 mutants (F). The arrowheads indicate the outer limits of the active zone. G: Morphometric analysis of synaptic boutons showing synaptic length (left panel), normalized SSR length (middle panel), and SSR thickness (right panel). Note that active zones are increased in length in dlg, dlgs97, and dlgs4 mutants, but normalized SSR length is decreased only in dlgs97. Scale bar: A–C, 1.2 μm; D, 0.3 μm. For a comparison of dlgs97 with dlgs97128 mutant allele in other parameters, see supplemental Table 2 (available at www.jneurosci.org as supplemental material).
mutants, are viable. These mutants show locomotor speed defects (Martin and Ollo, 1996) and abnormal optomotor behavior (Zordan et al., 2005), although no other behaviors have been examined. CAKI has also been suggested to be involved in the regulation of the autonomous activity of CaMKII regulating its activation and deactivation and shown to be important for the male habituation behavior during mating (Lu et al., 2003). In vertebrates, SAP97/CASK/VELI complex has been implicated in the transport of glutamate receptors (Wu et al., 2002) as well as in the recruitment of SAP97 to the membrane (Lee et al., 2002). Thus, DLGS97 is likely to form supramolecular complexes, in which the specific function of lower order complexes is harmonized and perhaps synchronized. The observation that DLGS97 appears to play a role in behaviors that require multiple sensory and motor pathways makes the speculation that DLGS97 control the coordination of complexes involved in the regulation of CaMKII activity and/or the delivery of receptors at the synapse highly attractive (for a cartoon on the type of protein complexes likely to be established by DLGS97 and DLGA, see supplemental Fig. S5, available at www.jneurosci.org as supplemental material).

Another feature DLGS97 proteins have is their ability to regulate the switch-like characteristics of MAGUKs. The GUK and SH3 domains of PSD95 and SAP97 can establish intramolecular interactions rendering the proteins in an open (available for partner binding) or closed configuration (McGee and Bredt, 1999; Shin et al., 2000). Notably, the N-terminal extension of SAP97 can inhibit these intramolecular interactions (Wu et al., 2000). Thus, L27 domain-containing proteins have an additional level of regulation able to regulate MAGUK interactions with binding partners.

Remarkably, a recent report shows that the mammalian MAGUKs PSD95 and SAP97 are expressed in the CNS as alternative splice forms containing or lacking an L27 domain. Furthermore, these studies suggest that only the L27 domain-bearing forms are sensitive to activity associated to the CaMKII activity (Schluter et al., 2006), supporting a role of the L27 domain in activity-induced synaptic modification.

A significant finding in this work is the versatility of SAP proteins within the same cell. Although eliminating either of the two isoforms did not prevent normal localization of Scrib, FasII localization was altered in both dlgA and dlgS97 mutants, although the total amount of DLG was only decreased at most by 20%. These observations are intriguing, given that FasII and Scrib interact with DLG domains present in both isoforms (Thomas et al., 1997; Mathew et al., 2002). This suggests that form-specific characteristics or the interaction or balance between the two proteins are important for proper FasII localization. Similar codependence/independence between isoforms was found at the ultrastructural level. Although both isoforms appeared to be required for the regulation of active zones, bouton and synaptic vesicle size, either of them had functions in SSR development.

Figure 7. Electrophysiological analysis of dlg mutants. A, B, Voltage recordings of muscle 6 in wild-type and dlg mutants, showing representative traces of mEJP (A), and evoked responses (EJP) (B). Calibration: A, 6.5 mV, 1.7 s; B, 10 mV, 125 ms. C, D, F, G, Histograms showing the average ± SEM of mEJP amplitude (C), mEJP frequency (D), EJP amplitude (F), and quantal content (G). E, mEJP amplitude cumulative distribution. Average ± SEM of the resting membrane potential (in millivolts) and input resistance (in kilohms · square centimeter) was 62.14 ± 0.96 and 6.35 ± 0.61 for C5, 63.38 ± 0.6 and 6.2 ± 0.53 for dlgA, 63.45 ± 0.66 and 6.11 ± 0.58 for dlgA, and 63.33 ± 0.41 and 6.39 ± 0.61 for dlgS97, respectively; no significant differences between genotypes were detected. Statistical analysis for the frequency, EJP amplitudes, and quantal contents was conducted using Student’s t test (**p < 0.01; ***p < 0.001). Statistical analysis for the mEJP amplitude cumulative curves was conducted using a Kolmogorov–Smirnov test.
The detected abnormalities in synaptic architecture were also accompanied by functional alterations. The mEJP amplitude change of \( \text{dlg}^{X^2} \) was phenocopied when DLSG97 was eliminated, whereas the absence of DLGA did not increase the amplitude of the mEJPs. The increase of mEJPs amplitude was correlated with an increase in the size of the vesicles (significant for all genotypes) and an increase in the labeling intensity and size of the GluR clusters only in \( \text{dlg}^{97} \) mutants. Thus, the increased mEJP amplitude in \( \text{dlg}^{97} \) mutants correlates with presynaptic and postsynaptic defects. However, the decrease in EJP amplitude depended only on DLGA. Overall, both mutants had a decrease in quantal content, indicating that both isoforms are required for effective neurotransmission. Such SAP-specific functions between PSD95 and SAP97 have been suggested in neuronal culture studies (Tiffany et al., 2000; Cai et al., 2006).

We found a striking shift in isoform usage during development, with DLSG97 becoming increasingly preponderant at more mature stages. These results, added to the previously described DLSG97 exclusive expression in excitable tissues, suggest that this shift underscores a fundamental and unique requirement of the L27 domain in neurons. A similar developmental shift is observed in mammalian neuronal cultures, in which PSD95 and PSD93 (proteins that bear L27 domains as splice variants) play most relevant roles in mature neurons, whereas SAP102 (lacking L27 domain) is essential in immature neurons (Elías et al., 2006). Thus, although SAPs devoid of L27 domain might have roles in protein clustering in a broad number of polarized cells, L27-bearing SAPs might couple the basic clustering machinery to multiple cellular processes. Our isolation of isoform-specific mutants in the absence of SAP redundancy constitutes the first step to address this possibility.

We highlight the correlation between the acquisition of a single domain of protein–protein interaction and the ability of DLSG97 to engage in processes required for complex functions of the adult brain. Although the mechanisms mediating between both levels need to be unraveled and are probably multiple, this example appears relevant to understand the elaboration of increasingly complex structures and functions with a limited set of molecular tools.

References


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