Genetic analysis of the Complexin trans-clamping model for cross-linking SNARE complexes in vivo

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Genetic analysis of the Complexin trans-clamping model for cross-linking SNARE complexes in vivo

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Contributed by James E. Rothman, May 29, 2014 (sent for review April 1, 2014)

Complexin (Cpx) is a SNARE-binding protein that regulates neurotransmission by clamping spontaneous synaptic vesicle fusion in the absence of Ca²⁺ influx while promoting evoked release in response to an action potential. Previous studies indicated Cpx may cross-link multiple SNARE complexes via a trans interaction to function as a fusion clamp. During Ca²⁺ influx, Cpx is predicted to undergo a conformational switch and collapse onto a single SNARE complex in a cis-binding mode to activate vesicle release. To test this model in vivo, we performed structure–function studies of the Cpx protein in Drosophila. Using genetic rescue approaches with cpx mutants that disrupt SNARE cross-linking, we find that manipulations that are predicted to block formation of the trans SNARE array disrupt the clamping function of Cpx. Unexpectedly, these same mutants rescue action potential-triggered release, indicating trans–SNARE cross-linking by Cpx is not a prerequisite for triggering evoked fusion. In contrast, mutations that impair Cpx-mediated cis–SNARE interactions that are necessary for transition from an open to closed conformation fail to rescue evoked release defects in cpx mutants, although they clamp spontaneous release normally. Our in vivo genetic manipulations support several predictions made by the Cpx cross-linking model, but unexpected results suggest additional mechanisms are likely to exist that regulate Cpx’s effects on SNARE-mediated fusion. Our findings also indicate that the inhibitory and activating functions of Cpx are genetically separable, and can be mapped to distinct molecular mechanisms that differentially regulate the SNARE fusion machinery.

Significance

Synaptic vesicle fusion at synapses is the primary mechanism by which neurons communicate. A highly conserved membrane fusion machine known as the SNARE complex mediates this process. In addition, neuronal SNARE-binding regulatory proteins have evolved to control the kinetics and speed of SNARE assembly at synapses. One such SNARE-binding protein, Complexin, has been found to inhibit synaptic vesicle fusion in the absence of an action potential and activate SNARE-mediated release during stimulation. Here we examine molecular models for how Complexin can mediate these unique effects on the SNARE fusion machine using genetic rescue experiments in Drosophila. We find that alternate SNARE-binding mechanisms by Complexin are likely to contribute to distinct inhibitory and activating functions in vivo.


The authors declare no conflict of interest.

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mutations in the Cpx accessory helix that enhance its inhibitory activity (24), have suggested a structural basis by which Cpx might regulate these dual activities (25–27). Crystallization of the Cpx-bound truncated SNARE complex revealed that the N-terminal accessory helix domain of Cpx extends away from its central helix domain at a 45° angle to form a trans interaction with a second SNARE complex, binding within the open t-SNARE pocket of the partially zippered SNAREs (trans Cpx/SNARE or zigzag array). This finding suggested a structural basis by which Cpx clamps vesicles in a fusion capable state (26). In response to Ca\textsuperscript{2+}, the trans Cpx/SNARE array is predicted to collapse, with the Cpx helix undergoing a conformational switch to associate with the fully zippered cis–SNARE complex, providing a switch mechanism by which Cpx might promote release (Fig. 1B) (25). However, the in vivo relevance of such a mechanism in neurotransmitter release is unknown. Here, we undertook a genetic approach to test the trans Cpx/SNARE array and switch-release model of Cpx using the Drosophila melanogaster (Dm) neuromuscular junction (NMJ) as a model synapse.

**Results**

*Drosophila* has a single Cpx homolog that is enriched in presynaptic nerve terminals. Electrophysiological analysis at NMJs in cpx null mutants revealed dramatically enhanced spontaneous release and reduced evoked release compared with controls (16), consistent with Cpx’s in vitro properties (14, 15, 26). Based on the crystal structure of the Cpx/SNARE array, we designed a series of mutations that were previously shown to modulate Cpx function as a vesicle clamp in in vitro cell–cell fusion assays (Fig. 1A and B). A key molecular determinant of Cpx’s ability to bridge two SNARE complexes in vitro is the presence of hydrophobic residues in the accessory helix that bind to a second partially zippered t-SNARE complex to form the trans Cpx/SNARE array. Hydrophobic mutations in this region (termed superclamp (SC)) increased the ability of mammalian (m) Cpx to promote clamping in in vitro cell–cell “flipped” fusion assays, whereas charged residue substitutions within this region (termed nonclamp (NC)) reduced clamping (26). Furthermore, mutations that disrupt the continuity of the Cpx helix (termed helixbreaker (HB)) abolished clamping by Cpx in this assay (26).

To determine if a similar trans Cpx/SNARE array interaction might occur in *Drosophila*, we compared the accessory helix of *Drosophila* Cpx (DmCpx) to that of mCpx. The DmCpx accessory helix contains hydrophobic residues (A35, I46, and A49) that are predicted to orient and align similarly to the hydrophobic residues found in mCpx (Fig. 1C). We found that WT DmCpx clamps cell–cell fusion in vitro similar to WT mCpx (Fig. 1D). WT DmCpx = 7.1 ± 1.6% (n = 3) vs. WT mCpx = 5.0 ± 1.4% (n = 4); P > 0.05, suggesting a trans Cpx/SNARE array interface may be conserved in *Drosophila*.

In addition to clamping release to prevent spontaneous fusion, Cpx also promotes Syt-dependent vesicle fusion (16, 17, 19–22). Ca\textsuperscript{2+}-dependent triggering of release has been suggested to require a conformational switch in Cpx from an open (Cpx extends away from the SNARE surface at a ~45°) to a closed (Cpx lies on the surface of a postfusion SNARE complex) state (Fig. 1B) (26). This switch is mediated by hydrogen bond and salt bridge interactions of residues in VAMP2 (D64, D65, D68) with residues within the Cpx central helix (R48, Y52) (25, 28). The in vitro relevance of this interaction was tested previously using mutations within VAMP2 (25). Here, we designed an equivalent Cpx mutant (R48D/E, Y52A, termed switchbreaker (SB)) that is predicted to reduce Cpx’s ability to switch from an open to a closed conformation, and examined both the clamping and stimulating properties of SB mCpx using in vitro cell–cell fusion assays. Despite mutations in its central helix, SB mCpx maintained its ability to clamp in in vitro cell–cell fusion similar to WT mCpx (Fig. 1E). [SB mCpx = 7.6 ± 0.8% (n = 3) vs. WT mCpx = 5.0 ± 0.7% (n = 4); P > 0.05]. In contrast, activation of cell–cell fusion with SB mCpx was significantly reduced following addition of Ca\textsuperscript{2+} and Syt (Fig. 1F) [SB mCpx = 1.5 ± 0.4% fold increase (n = 3) vs. WT mCpx = 3.2 ± 0.5 fold increase (n = 4); P < 0.05]. These data indicate that interactions involving mCpx residues R48 and Y52 with zippering or fully assembled SNARES may be important to trigger release, but are not required for Cpx to clamp fusion.

To examine the in vivo relevance of the Cpx trans array clamping/switch model, we generated transgenic *Drosophila* strains expressing a series of mCpx mutants that are predicted to disrupt these activities. First, we tested the requirement of the interaction between the accessory domain of Cpx and the half-zippered t-SNARE complex using the SC and NC mCpx mutants. Using in vitro experiments, these mutants exhibited enhanced and reduced ability, respectively, to bind and clamp compared with wild-type Cpx.
A second aspect of the trans Cpx/SNARE array clamping model is that the Cpx helix forms a rigid bridge between two SNARE complexes (26). To test whether this rigidity is required in vivo, we expressed mCpx mutants with three glycine residues between the central helix and the accessory helix (HB) to perturb the continuous α-helical structure. In addition, we sought to express Cpx separately as a split transgenic protein, thereby directly preventing cross-linking of two SNARE complexes. One piece encoded the central SNARE binding domain (termed mCpx 51–134), whereas the second piece contained only the Cpx N-terminal fragment (1–50). However, the N-terminal fragment was unstable and not expressed properly in vivo (Fig. S1B). The Cpx C-terminal fragment was expressed, and was able to support aspects of neurotransmission (see below). Finally, we assayed whether a SB mCpx mutant designed to reduce the ability of mCpx to switch from an open to closed conformation (Fig. 1B) (25) could support synaptic transmission in vivo. A summary of these transgenic lines is shown in Fig. 1A and Table S1.

The WT and mutant mCpx transgenes were placed in the cpx null background and expressed under control of the GAL4-UAS system. We used the phiC31-attP recombination system to insert all mCpx transgenes into the same integration site on the third chromosome, eliminating variability in transgene expression. The mCpx transgenes were tagged with an N-terminal myc epitope to facilitate detection of the transgenic proteins by Western and immunocytochemical experiments. Western analysis demonstrated that all mutants, with one exception, were expressed at similar levels to WT mCpx I (Fig. S1A). The C-terminal mCpx 51–134 fragment was expressed at slightly lower levels compared with WT mCpx. All of the mutant mCpx transgenic proteins localized normally to presynaptic terminals at Drosophila NMJs (Fig. S1B), indicating these alterations do not disrupt Cpx trafficking.

We first examined the clamping properties of WT and mutant mCpxs by analyzing spontaneous release (minis) in cpx null and rescued animals (Fig. 2). cpx mutants exhibit a dramatic enhancement in spontaneous release frequency (Fig. 2A). Expression of WT mCpx presynaptically in cpx null animals significantly reduced the elevated spontaneous release rate in cpx mutants [cpx = 73.8 ± 3.6 Hz (n = 9) vs. WT mCpx rescue = 14.6 ± 1.1 Hz (n = 18); P < 0.001], although it remained elevated compared with WT control lines [control = 2.6 ± 0.1 Hz (n = 9) vs. WT mCpx rescue = 14.6 ± 1.1 Hz (n = 18); P < 0.01]. We next tested the relevance of the accessory helix of Cpx to associate with the prefusion t-SNARE complex (26) (Fig. 1A and B). Mutations that enhanced Cpx/t-SNARE binding (SC mCpx) have been previously shown to increase the ability of the protein to inhibit fusion in vitro (26). We found that animals expressing SC mCpx more effectively rescued the cpx mini phenotype compared with WT mCpx [SC mCpx = 5.6 ± 0.6 Hz (n = 15) vs. WT mCpx rescue = 14.6 ± 1.1 Hz (n = 18); P < 0.05] (Fig. 2). In contrast, mCpx mutants that disrupted the accessory helix interaction with t-SNAREs (NC mCpx) displayed mini frequencies that were only slightly elevated compared with WT mCpx rescued lines [NC mCpx = 19.1 ± 1.1 Hz (n = 17) vs. WT mCpx rescue = 14.6 ± 1.1 Hz (n = 18); P > 0.05] (Fig. 2); this was surprising because in vitro cell–cell fusion assays demonstrated a strong reduction in the clamping properties of NC mutants (26).

To exclude the possibility that NC mCpx does not alter association of Cpx with Drosophila t-SNAREs as expected, we performed isothermal titration calorimetry (ITC) experiments using blocked prefusion, partially assembled Drosophila SNAREs, following the strategy used in previous studies (26). The partially assembled Drosophila SNARE complex (pDmSNARE) was performed with the SNARE motifs from Drosophila syntaxin (residues 194–265), Drosophila SNAP25 (residues 18–89 and 149–211), and the N-terminal SNARE motif from Drosophila VAMP (residues 48–79). The interaction of pDmSNARE with the Cpx central helix was blocked using truncated mCpx (residues 48–134). mCpx 48–134 binds tightly to pDmSNARE with an affinity constant 667 ± 90 nM (Fig. S2), which is similar to its binding affinity with partially assembled mammalian SNARE complex (26). This tight binding reflects saturation of the central helix binding sites of pDmSNARE with mCpx 48–134 when mCpx 48–134 is added in molar excess. Thus, with blocked pDmSNARE, only the interaction between the mCpx accessory helix and unzipped t-SNARE would be measured. WT mCpx, NC mCpx (A30E A31E L41E A44E), and a mCpx containing only two mutations in the accessory helix, NC 2x mCpx (L41E, A44E), were titrated into the blocked pDmSNARE mixture. The binding affinity, KD, of the mCpx accessory helix to blocked pDmSNARE gradually weakened with mutations in the hydrophobic residues (Fig. S3 and Table S2); KD = 11 ± 1 µM for WT mCpx, 45 ± 8 µM for NC 2x mCpx, and undetectable for the quadruple mutant, equivalent to the NC mCpx mutant used in these studies. This finding demonstrated that NC mCpx indeed disrupted association of the Cpx accessory helix with prefusion Drosophila SNAREs in vitro. Because the disrupted association between NC mCpx with t-SNAREs was confirmed in ITC experiments, the ability of NC mCpx to function only slightly less efficiently than WT mCpx

Fig. 2. Mini frequency of elav-GAL4 transgenic rescued animals using WT or mutant mCpxs in the cpxres mutant background. (A) Sample traces of spontaneous release events from muscle 6 of control, cpxres, and rescue lines expressing WT mCpx, SC mCpx, NC mCpx, SB mCpx, HB mCpx, or mCpx 51–134. (B) Summary of mean mini frequency (hertz ± SEM) for each line. Numbers in parentheses (n) represent individual NMJ recordings from indicated genotypes. Horizontal lines indicate statistical comparisons determined using ANOVA with post hoc Tukey analysis.
in rescuing spontaneous release in vivo suggests that the association of the Cpx accessory helix with a t-SNARE may not be absolutely required for the clamping function, or this interaction is largely maintained in vivo but not in vitro (Discussion).

Previous in vitro studies indicated the Cpx helix forms a rigid bridge between two SNARE complexes (26). To test whether this rigidity is required in vivo, we expressed the HB mCpx mutant containing three glycine residues between the central and accessory helices. Expression of HB mCpx completely failed to rescue the cpx mini phenotype [WT mCpx rescue = 14.6 ± 1.1 Hz (n = 18) vs. HB mCpx = 80.0 ± 2.7 Hz (n = 9); P < 0.001] (Fig. 2). This result is consistent with in vitro cell–cell fusion assays, where perturbations of the α-helix reduced Cpx clamping function (26). We next tested the clamping functionality of the mCpx truncation mutant (mCpx 51–134) completely lacking the accessory helix. mCpx 51–134 failed to rescue the cpx mini phenotype [WT mCpx rescue = 14.6 ± 1.1 Hz (n = 18) vs. mCpx 51–134 rescue = 85.1 ± 2.6 Hz (n = 12); P < 0.001], consistent with a requirement for the Cpx accessory helix in clamping (Fig. 2). Taken together, we conclude that (i) the N-terminal domain of Cpx containing the N-terminal unstructured region and accessory helix domain (Fig. 1A) is critical for clamping, because mCpx 51–134 failed to rescue enhanced spontaneous release in vivo; and (ii) Cpx requires a continuous helix spanning its accessory and central domains, because disruption of this bridge impairs Cpx’s ability to function as a clamp.

In addition to its role as a fusion clamp, Cpx also promotes Ca\(^{2+}\)-triggered release in both Drosophila and mammals (16, 18, 21, 29, 30). cpx null mutants exhibited reduced evoked release, measured as evoked junctional potentials (EJPs) in both low and high Ca\(^{2+}\) concentrations (16) (Fig. 3). [control] = 34.2 ± 6.0 mV (n = 4) vs. cpx null = 20.0 ± 0.8 mV (n = 4) at [Ca\(^{2+}\)] = 1 mM; P < 0.001. To investigate whether the formation of a trans Cpx/SNARE array is required for Cpx’s activating function in fusion, we measured EJPs for the mutant mCpx rescues. In contrast to the differential abilities of trans Cpx/SNARE array mutants to rescue the clamping function of Cpx, all of the mutants showed rescue of the impaired evoked release, similar to WT mCpx [SC mCpx rescue = 36.1 ± 0.4 mV (n = 5) and NC mCpx rescue = 32.89 ± 0.9 mV (n = 10); vs. WT mCpx rescue = 34.0 ± 0.5 mV (n = 5); P > 0.05 for SC mCpx vs. WT mCpx rescues and P > 0.05 for NC mCpx vs. WT mCpx rescues] (Fig. 3). In addition, the HB mCpx and mCpx 51–134 mutants rescued evoked release despite their inability to rescue the cpx mini phenotype [HB mCpx rescue = 35.2 ± 1.1 mV (n = 4) and mCpx 51–134 rescue = 35.24 ± 0.8 mV (n = 6); vs. WT mCpx rescue = 34.0 ± 0.5 mV (n = 5); P > 0.05 for HB mCpx vs. WT mCpx; and P > 0.05 for mCpx 51–134 vs. WT mCpx]. These results indicate the activating function of Cpx can occur in the absence of a trans Cpx/SNARE array with cross-linked SNAREs in vivo.

In vitro experiments supported a Cpx switch mechanism that promotes release in response to Ca\(^{2+}\) (25). Our in vitro cell–cell fusion assays demonstrated that the SB mCpx mutant reduced cell fusion similar to WT mCpx, but exhibited attenuated stimulated fusion compared with WT mCpx (Fig. 1E and F). To test this model in vivo, we expressed the SB mCpx mutant in cpx null mutants. Expression of SB mCpx was unable to rescue evoked responses in the cpx mutant compared with WT rescue [SB mCpx = 22.3 ± 1.8 mV (n = 5) vs. WT mCpx rescue = 34.0 ± 0.5 mV (n = 5); P < 0.001] (Fig. 3). Using ITC in vitro binding assays, we measured the thermodynamic parameters of WT mCpx and SB mCpx binding to Drosophila cis SNARE complexes (Fig. 4 A and B and Table 1). The cis DmSNARE is a fully assembled complex that was formed with Drosophila Syntaxin (residues 194–265), SNAP25 (residues 18–89 and 149–211), and VAMP (residues 1–115). The K_D of binding between mCpx and cis

![Fig. 3.](image)

**Fig. 3.** Evoked release properties of WT mCpx and individual mutant mCpx rescues. (A) Averaged traces of EJPs from control, cpx\(^{-/-}\), and rescued strains expressing indicated mutant mCpxs. Recordings were performed at various Ca\(^{2+}\) concentrations (0.15, 0.2, 0.4, and 1 mM). (B) Summary of mean EJP amplitude (millivolts ± SEM) plotted at the indicated Ca\(^{2+}\) concentrations. Numbers in parentheses (n) represent individual muscle recordings at the indicated [Ca\(^{2+}\)]; data were collected from at least three independent larvae for each genotype.

![Fig. 4.](image)

**Fig. 4.** SB mCpx exhibits impaired binding to postfusion, cis-DmSNAREs. (A) ~65 μM WT mCpx was titrated into a mixture of ~5.3 μM DmSNARE complexes. (B) ~140 μM SB mCpx was titrated into ~8 μM DmSNAREs. (A and B, Upper) Raw data in power vs. time during the injection after subtracting from the baseline. (Lower) Integrated heat of each injection normalized by the moles of injectant vs. the molar ratio between Cpx and SNARE in the sample cell. The solid lines represent the best fit to the black squares obtained from a nonlinear least-squares fit assuming a simple one-site chemical reaction. The results gave the thermodynamic parameters for each binding reaction, which are listed in Table 1.
Table 1. Thermodynamic parameters of various mCpx binding to postfusion, cis-DmSNARE complexes

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<th>$K_B$, nM</th>
<th>$\Delta H$, kcal·mol$^{-1}$</th>
<th>$\Delta S$, cal·mol$^{-1}$·°C$^{-1}$</th>
<th>$\Delta G$, kcal·mol$^{-1}$</th>
<th>$\Delta G$, $k_B T$</th>
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<td>WT mCpx/postfusion DmSNARE</td>
<td>0.97 ± 0.03</td>
<td>33 ± 2</td>
<td>-27.2 ± 0.1</td>
<td>-57.6 ± 0.5</td>
<td>-10.1 ± 0.1</td>
<td>17.2 ± 0.1</td>
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<tr>
<td>SB mCpx/postfusion DmSNARE</td>
<td>1.01 ± 0.02</td>
<td>1104 ± 95</td>
<td>-7.7 ± 0.2</td>
<td>1.1 ± 0.7</td>
<td>-8.1 ± 0.1</td>
<td>13.7 ± 0.1</td>
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DmSNAREs is 33 ± 2 nM, similar to the affinity constant of mCpx with mammalian cis SNAREs (25). Compared with WT mCpx, the SB mCpx mutant displayed a weaker affinity ($-1.1$ ± 0.1 μM). Additionally, the binding enthalpy of SB mCpx with cis DmSNAREs was weaker compared with WT mCpx by $\sim -20$ kcal·mol$^{-1}$ (SB mCpx: $\Delta H = -7.7$ ± 0.2 kcal·mol$^{-1}$ vs. WT mCpx: $\Delta H = -27.2$ ± 0.1; Table 1). These differences are similar to those previously reported using the VAMP2 SB mutant (D64A, D65A, and D68A) designed to disrupt hydrogen bond and salt bridge interactions with the Cpx central helix (R48 and Y52). Despite the impaired association of SB mCpx with fully assembled SNARE complexes and the inability to rescue evoked release, SB mCpx was able to rescue mini-synapses similarly to WT mCpx [SB mCpx rescue = 16.8 ± 1.3 Hz (n = 11) vs. WT mCpx rescue = 14.6 ± 1.1 Hz (n = 18); P $>$ 0.05] (Fig. 2). These data indicate the central helix is sufficient to support evoked release, whereas the accessory helix is needed to maintain its clamp function. In summary, our findings suggest that Cpx promotes Ca$^{2+}$-dependent vesicle fusion by mechanisms that are independent of accessory domain interactions, and instead require residues within the central helix of Cpx. The independent effects on spontaneous vs. evoked release in both the SB and trans interaction-abolishing mutants indicate the Cpx clamping and promoting functions are genetically separable, consistent with prior studies (17, 19, 20, 31–33).

**Discussion**

To characterize the mechanisms by which Cpx regulates synaptic vesicle fusion, we performed an in vivo structure-function study by expressing WT and mutant Cpx transgenes in cpx null mutants. Unexpectedly, Cpx mutants that disrupt the formation of a trans Cpx/SNARE array, as confirmed by in vitro binding experiments, were capable of promoting action potential-triggered release. However, these same mutants failed to rescue the clamping defect in cpx, indicating differential effects on Cpx’s two primary roles in exocytosis. In contrast, mutants that altered Cpx interactions with the fully zipping SNARE complex through cis rather than trans interactions, failed to promote evoked vesicle release, but clamped spontaneous fusion normally. These findings demonstrate that the clamping and promoting mechanism of Cpx are genetically separable, and may be regulated by distinct mechanisms at the level of SNARE interactions.

Consistent with previous in vitro experiments (26), mutants that disrupted the ability of Cpx to form a rigid bridge between two SNARE complexes failed to support a clamping function at the synapse in vivo (see HB mCpx rescues in Fig. 2). The Cpx N terminus (1–48) was absolutely required to clamp spontaneous fusion in vivo (mCpx 51–134; Fig. 2), indicating Cpx may form a cross-linked SNARE structure in vivo. Surprisingly however, NC Cpx mutants that disrupted the interaction between Cpx accessory domain and the t-SNAREs of a second SNARE complex were able to largely rescue the elevated spontaneous fusion rate found in cpx null mutants (Fig. 2). This observation was not consistent with the cross-linked SNARE model given that NC mCpx exhibited reduced clamping activity in previous cell–cell fusion assays (26), and that ITC experiments demonstrated that NC mCpx does not associate with either mammalian or Drosophila SNAREs in vitro (Fig. S3 and Table S2). The NC mCpx mutant analysis raises the question of whether trans interactions are essential for clamping in vivo. It is possible that association of the Cpx N terminus with a second prefusion SNARE complex may be more difficult to perturb in vivo than in vitro. For example, additional factors might stabilize this interaction, or secondary residues flanking the primary association site in the t-SNARE complex may contribute to the Cpx/t-SNARE association in vivo. The inability of the HB mCpx and truncated mCpx 51–134 to rescue the elevated mini rate indicates a rigid N-terminal extension away from the central SNARE-binding domain is important for Cpx-mediated vesicle clamping. However, we cannot rule out that these mutants may also disrupt a distinct in vivo Cpx–SNARE interaction beyond the predicted trans Cpx/SNARE array. Indeed, there is evidence that mutations within the N-terminal domain of Cpx may alter release by blocking cis–SNARE zipper formation (34). Unlike NC mCpx mutants, we observed a strong effect of the SC mCpx mutants, which enhanced the clamping function of Cpx in vivo, and enhanced formation of trans interactions in vitro (26).

In contrast to the effects of Cpx cross-linking mutants on their clamping properties, these same mutations were capable of rescuing action potential-triggered synaptic vesicle fusion. Indeed, even an N-terminal truncation mutant completely lacking the Cpx accessory helix was capable of restoring evoked vesicle release in vivo (Fig. 3). Although we cannot exclude the possibility that these mutants exert subtle effects on vesicle pool sizes, or vesicle release kinetics and synchronicity (19, 21, 31, 35), our findings indicate a trans Cpx/SNARE array is not absolutely required for vesicle release following an action potential.

The SB mutant that alters Cpx interactions with the fully zipping SNARE complex in cis, rather than with a second SNARE complex in trans, failed to promote evoked vesicle release efficiently (Fig. 3). Why does this SB mCpx mutant fail to rescue evoked release? The crystal structure of wild-type Cpx with the postfusion SNARE complex shows that R48 and Y52 interact with D64, D65, and D68 in the C terminus of VAMP2 (28). ITC measurements show that the SB mutations in Cpx result in a loss of $\sim -20$ kcal·mol$^{-1}$ in binding enthalpy to the postfusion SNARE complex (Table 1 and Fig. 4), which is similar to the enthalpy loss caused by the D64A, D65A, and D68A mutations in VAMP2 (25), indicating similar defects to those found in the SB mCpx mutants. FRET studies demonstrated that Cpx remains in the open state (Cpx extends away from postfusion SNARE surface at $-45^\circ$) when D64, D65, and D68 are mutated (25). Hence, the R48, Y52 mutation of Cpx is likely to abolish the transition of Cpx from an open to closed state as the molecular driving force of this transition is impaired. Given the N-terminal domain of Cpx (1–50) is not required for evoked release (Fig. 3), it is also possible that a conformational transition of the Cpx central helix from an open to closed state is sufficient for evoked release. Interestingly, the SB mCpx mutant clamps spontaneous release normally (Fig. 2); this is the first Cpx mutant that selectively alters the ability of Cpx to promote evoked vesicle fusion, while leaving the clamping function intact.

In summary, these results indicate that the clamping and activating functions of Cpx are genetically separable, and are regulated through distinct SNARE interaction mechanisms. This conclusion is consistent with additional studies examining the contribution of the Cpx C terminus in regulating synaptic vesicle release (17, 31–33, 36). What mechanism is ultimately used to separate Cpx’s role in spontaneous vs. evoked release is still unclear, and may involve a complex interplay with the SNARE complex and other SNARE-associated proteins, including Syt (37, 38). These distinct roles may also be manifest through...
effects of Cpx on molecularly distinct pools of vesicles (39), or on specific active zones dedicated to evoked vs. spontaneous release (40). Given that Cpx mutants that interrupt the trans Cpx/SNARE array support evoked release, it is unlikely that a Cpx-mediated cross-linking of SNARE complexes is required during Ca\textsuperscript{2+}-triggered release. As such, the SB Cpx mutant may impede the transition of the Cpx central helix from an open to closed conformation with a single zipping SNARE complex. Within Cpx, therefore, the central \(\alpha\)-helix is the primary domain that associates with SNARE complexes (28), and is absolutely required for all Cpx function (17, 20, 23). The N-terminal accessory domain is necessary for clamping functions, as demonstrated in this study and others (23, 30, 41). The nonhelical N-terminal domain of Cpx is required for promotion of evoked release at some synapses (18, 30), whereas the C terminus functions to regulate both clamping and priming through its ability to target Cpx to membranes (17, 32, 33, 36, 42). How these distinct domains work in concert to regulate the overall mode of synaptic release is an important question, and likely to be critical for distinct plasticity mechanisms that alter release through changes in Cpx function (17, 20, 23). The N-terminal accessory domain is therefore, the central

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**Materials and Methods**

**Protein Constructs, Expression, and Purification.** Recombinant proteins were expressed and purified using standard bacterial expression systems. See SI Materials and Methods for details.

**Isothermal Titration Calorimetry Analysis.** ITC experiments were performed as previously described (26). See SI Materials and Methods for details.

**Cell–Cell Fusion Assays.** Cell–cell fusion assays were performed as previously described (14, 24). See SI Materials and Methods for details.

**Drosophila Genetics.** Drosophila melanogaster were cultured on standard medium at 25 °C. Drosophila transgenic lines were generated using standard methods. Briefly, WT and mutant mcPxs were transgenes were recombined into Cpx\textsuperscript{null} mutant (16) and expressed using neuronal C155 elav-Gal4 driver. See SI Materials and Methods for details.

**Electrophysiology.** Muscle fiber 6 (segment A3) of dissected third instar larvae was used for all sharp electrode potential recordings as previously described (16). See SI Materials and Methods for details.

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