

Glycolipid Crosslinking Is Required for Cholera Toxin to Partition Into and Stabilize Ordered Domains

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ABSTRACT Current models of lipid rafts propose that lipid domains exist as nanoscale compositional fluctuations and these fluctuations can potentially be stabilized into larger domains, consequently better compartmentalizing cellular functions. However, the mechanisms governing stabilized raft assembly and function remain unclear. Here, we test the role of glycolipid crosslinking as a raft targeting and ordering mechanism using the well-studied raft marker cholera toxin B pentamer (CTxB) that binds up to five GM1 glycosphingolipids to enter host cells. We show that when applied to cell-derived giant plasma membrane vesicles, a variant of CTxB containing only a single functional GM1 binding site exhibits significantly reduced partitioning to the ordered phase compared to wild-type CTxB with five binding sites. Moreover, monovalent CTxB does not stabilize membrane domains, unlike wild-type CTxB. These results support the long-held hypothesis that CTxB stabilizes raft domains via a lipid crosslinking mechanism and establish a role for crosslinking in the partitioning of CTxB to ordered domains.

The plasma membrane is hypothesized to contain dynamic subdiffraction-sized coexisting liquid-ordered (l_o , raft) and liquid-disordered (l_d) phases (1). Although not readily apparent in intact cells, micron-sized l_o and l_d phases have been observed in isolated giant plasma membrane vesicles (GPMVs). It has been proposed that these micron-sized phase separations are related to the nanoscale organization of membranes (2). Thus, GPMVs can be used as a model system for understanding the origins of lipid-mediated membrane organization (2,3). Several proteins are known to associate with the l_o phase in GPMVs, suggesting they are selectively targeted to raftlike domains (4). However, mechanisms that control the partitioning of proteins to rafts remain incompletely understood.

Cholera toxin (CTx), an AB5 toxin, is a well-known lipid raft marker that has been used extensively to study the origins and functionality of lipid rafts (5). Its homopentameric B subunit (CTxB) recognizes and binds up to five molecules of its glycolipid receptor ganglioside GM1 (5). Previous studies have established that CTxB partitions into the l_o

phase, defining it as a raft marker (6–8). (Working definitions of terminologies used are in the [Supporting Material](#).) This preference of CTxB for the l_o phase is thought to arise in part from the intrinsic phase preference of GM1 itself (9). Moreover, binding of CTxB can drive the formation of both nanoscale and large-scale domains in cell-derived vesicles and model membranes that are close to a demixing point (6–8,10). Thus, CTxB not only functions as a raft marker but also as a domain inducer and raft stabilizer. It is widely assumed that these properties of CTxB depend on its ability to bind and cluster multiple GM1 molecules (6). However, this model remains to be formally tested. In this Letter, we test this hypothesis by comparing the behavior of wild-type forms of CTx and CTxB that can bind up to five GM1 molecules with corresponding monovalent variants (mCTx and mCTxB) that can bind only a single GM1 (11).

We first examined whether the ability of CTxB to bind multiple copies of its glycolipid receptor stabilizes micron-sized domains in GPMVs. To test this, we compared the effect of wild-type (WT) versus mCTxB binding on the miscibility transition temperature (T_{misc}) of GPMVs. T_{misc} is defined as the temperature at which 50% of the GPMVs contain coexisting l_o and l_d phases and provides a measure of the energetics of mixing behavior of the two phases (12,13). Treatment of GPMVs with WT CTxB has been

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previously reported to increase T_{misc} , indicating that rafts are stabilized in the presence of CTxB (7). Consistent with this, we found that GPMVs isolated from COS-7 cells and subsequently treated with WT CTxB exhibited an increased T_{misc} . This change in T_{misc} was dependent on the concentration of CTxB (Fig. 1). Similar results were obtained in a second cell line and when COS-7 cells were labeled with CTxB before GPMV isolation (Fig. S3 in the Supporting Material). In contrast, binding of mCTxB to the GPMVs did not change T_{misc} over the range of concentrations studied (Fig. 1). Thus, while WT CTxB binding stabilizes microscopic domains in the membrane, mCTxB is incapable of doing so.

We next compared the phase preference of WT and monovalent CTx and CTxB (refer to Supporting Materials and Methods and Fig. S4 for details). As expected (2), WT CTxB and CTx exhibited l_o phase preference (Fig. 2). In contrast, mCTx and mCTxB, which cannot cluster GM1, had reduced raft preference (Fig. 2). This difference in partitioning was not a consequence of the decreased avidity of binding of monovalent compared to the WT toxins (Fig. S4). Thus, preferential partitioning of CTx and CTxB into the l_o phase appears to be an emergent behavior dependent on its binding to multiple molecules of GM1.

To confirm if clustering is sufficient to drive raft partitioning and raft stabilization, we examined the effects of antibody crosslinking. Crosslinking of mCTxB increased the T_{misc} of the GPMVs (Fig. S5) and induced mCTxB to strongly partition into the l_o phase (Figs. S6 and S7), consistent with the role of clustering in enabling raft partitioning.

Our results have two major implications for our understanding of raft stabilization and partitioning mechanisms. First, they strongly suggest that the previously observed stabilization of microscopic phases by CTxB (6–8) indeed has its origins in the ability of CTxB to bind multiple molecules of GM1. While the impact of toxin binding

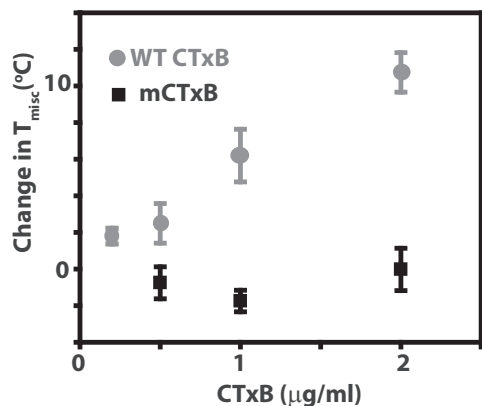


FIGURE 1 WT CTxB but not mCTxB increases T_{misc} of GPMVs isolated from COS-7 cells. See text for details. Data represent mean \pm SE ($N \geq 3$).

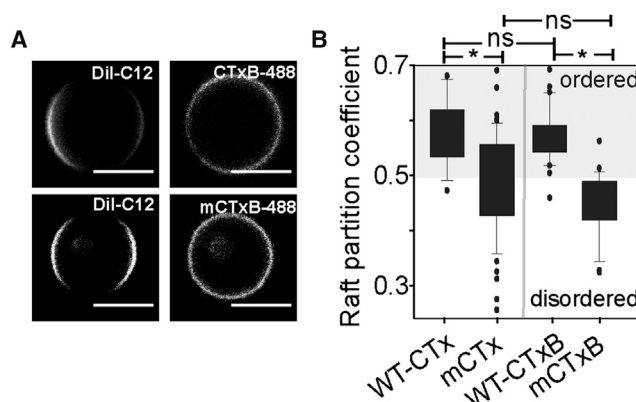


FIGURE 2 Monovalent and WT variants of CTx and CTxB exhibit different phase partitioning preferences in GPMVs derived from COS-7 cells. (A) Representative images of GPMVs labeled with WT or monovalent CTxB and the l_o phase marker Dil-C12. Scale bars, 5 μm . (B) Quantification of raft partition coefficients for WT and monovalent CTx and CTxB.

is observed at the micron scale in our experiments, this likely translates into differences in plasma membrane organization at the nanoscale under physiological conditions (refer to the Supporting Material for further discussion).

Second, we find that the mere binding of CTxB to GM1 is not sufficient to ensure its preference for partitioning into the l_o phase. One potential explanation for these findings is that clustering of GM1 induced by CTxB binding increases its l_o phase preference. This model stems from earlier experimental observations that CTxB binds initially to the disordered phase in GUVs and with increased time partitions into the l_o phase (14). Such a rationale is further supported by our current findings that an increase in clustering induced through antibody crosslinking of the toxin increases raft partitioning. However, additional factors could also potentially contribute to differences in the phase preference of WT and monovalent CTxB. For example, binding of CTxB to GM1 is cooperative (15,16), depends on the orientation of the GM1 headgroup (17–19), and is sensitive to the local density and clustering of GM1 (17,20). Another major factor that can impact the partitioning of CTxB is the structure of GM1's ceramide moiety (21). Thus, even though clustering of GM1 by CTxB stabilizes large-scale domains and is linked to CTxB's phase preference, properties of GM1 itself could also influence these behaviors.

For CTx, it is known that loss of even a single GM1 binding site results in significant loss of toxicity (11,22). This loss of toxicity has been hypothesized to reflect a requirement for multivalent binding to scaffold GM1 into nanodomains to support subsequent membrane trafficking steps (11). Our results demonstrating a role of multivalent binding in CTxB's raft partitioning and domain stabilization strongly support this hypothesis. Finally, we note that many toxins and viruses utilize a multivalent glycolipid

binding strategy to gain access to host cells (23,24). Further, clustering of glycolipids has been hypothesized to play a role in many cellular functions (25–28). Our results validate the underlying assumption in these biological scenarios that clustering of glycolipids enables raft partitioning and stabilization.

SUPPORTING MATERIAL

Supporting Materials and Methods, seven figures, and one table are available at [http://www.biophysj.org/biophysj/supplemental/S0006-3495\(16\)31035-9](http://www.biophysj.org/biophysj/supplemental/S0006-3495(16)31035-9).

AUTHOR CONTRIBUTIONS

A.K.K., K.R., W.I.L., and M.G.J. designed research; K.R., T.H.W., D.J.C., and M.G.J. performed research; K.R. contributed analytic tools; K.R., T.H.W., and M.G.J. analyzed data; K.R., A.K.K., M.G.J., W.I.L., and D.J.C. wrote the article; and all authors reviewed the final manuscript.

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SUPPORTING CITATIONS

References (29–47) appear in the Supporting Material.

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