Tracking individual secretory vesicles during exocytosis reveals an ordered and regulated process

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Post-Golgi secretory vesicle trafficking is a coordinated process, with transport and regulatory mechanisms to ensure appropriate exocytosis. While the contributions of many individual regulatory proteins to this process are well studied, the timing and dependencies of events have not been defined. Here we track individual secretory vesicles and associated proteins in vivo during tethering and fusion in budding yeast. Secretory vesicles tether to the plasma membrane very reproducibly for \(\sim 18\) s, which is extended in cells defective for membrane fusion and significantly lengthened and more variable when GTP hydrolysis of the exocytic Rab is delayed. Further, the myosin-V Myo2p regulates the tethering time in a mechanism unrelated to its interaction with exocyst component Sec15p. Two-color imaging of tethered vesicles with Myo2p, the GEF Sec2p, and several exocyst components allowed us to document a timeline for yeast exocytosis in which Myo2p leaves 4 s before fusion, whereas Sec2p and all the components of the exocyst disperse coincident with fusion.

Introduction

The functional organization of eukaryotic cells is dependent on the faithful packaging of cargos into membrane-bound vesicles and their transport to and fusion with the appropriate membrane. Exocytosis is an essential process and allows a cell to secrete molecules and peptides, regulate the composition of its plasma membrane, and enable growth (Brennwald and Rossi, 2007); defects in specific steps can lead to severe human diseases and conditions including Charcot-Marie-Tooth syndrome and X-linked mental retardation (D’Adamo et al., 1998; Zhao et al., 2001). Budding yeast is an attractive model in which to study exocytosis due to the large collection of characterized mutants and well-established conservation of function in mammalian cells (Novick et al., 1980; Salminen and Novick, 1987; Liu and Bretscher, 1989; Johnston et al., 1991).

Post-Golgi secretory trafficking in yeast begins as secretory vesicles mature from the trans-Golgi network via Rab cascades and an unknown scission event (Ortiz et al., 2002). After the transition from Rab11 homologue Ypt31/32p to Rab8 homologue Sec4p, the exocyst tethering complex, through Sec15p, binds active Sec4-GTP (Guo et al., 1999). Transport-competent secretory vesicles then bind to and activate the myosin-V motor Myo2p, through direct binding to both Sec4-GTP and Sec15p (Jin et al., 2011; Santiago-Tirado et al., 2011; Donovan and Bretscher, 2012). Rapid polarized transport along formin-nucleated actin cables delivers secretory vesicles to sites of growth in the bud where the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, and Exo84p) then engages to physically tether the vesicle to the plasma membrane (TerBush and Novick, 1995; Evangelista et al., 2002; Schott et al., 2002; Luo et al., 2014). Finally, regulatory interactions between exocyst components (Sivaram et al., 2005; Morgera et al., 2012), SNARE proteins (Lehman et al., 1999), GTPase activating proteins (GAPs; Gao et al., 2003), and SM proteins (Carr et al., 1999; Scott et al., 2004; Togneri et al., 2006) contribute to the final stage of exocytosis, vesicle fusion, though the timing and order of events is still undefined.

Here we present the first timeline of events for yeast exocytosis of individual secretory vesicles. We show that vesicles physically tether to the plasma membrane for a short period of time (\(\sim 18\) s). Two-color imaging shows that the myosin-V motor Myo2p leaves the vesicle before fusion, but other components associated with vesicles, including the GEF Sec2p and the exocyst complex, leave the vesicle at the moment of fusion. Further, we reveal dependencies in this timeline by exploring how defects in Sec4-GTP hydrolysis, Myo2p motors, an SM protein, and exocyst components affect tethering and fusion. Given the conservation of this pathway in mammalian cells, these results are likely widely applicable.

Results and discussion

Individual secretory vesicle tethering and fusion events can be followed in vivo

Yeast cells contain \(~ 7,000\) molecules of Sec4p, of which \(~ 4,000\) molecules are present in a growing bud (Donovan and
Vesicle tethering time is uniform and lengthened by delaying Rab GTP hydrolysis or inhibiting membrane fusion

We first sought to determine the length of time that vesicles are tethered to the cortex in wild-type cells. Their location after tethering was tracked in three dimensions, though for presentation purposes here we show maximum projection still frames or kymographs (Fig. 1, A and B). The tethering time at the cortex was remarkably consistent, with an average of 18.1 ± 4.2 s ($n = 22$; Fig. 1 C and Video 1), which suggests that a timed order of events regulates the tethering and fusion processes. This length of time also fits well with observed Myo2p motor recycling, as motors associated with secretory vesicles only reside in the bud for ~30 s (which includes transit and recycling times; Donovan and Bretscher, 2012). Some vesicles used in this analysis were tracked near the distal end of the bud while others were tracked at the sides. As the bud is growing isotropically at this cell stage, it is not surprising that we did not detect a difference in tethering and fusion dynamics between these two populations (Fig. 1 C).

Having revealed the consistency in tethering time before fusion, we examined the consequence of delaying the critical Sec4-GTP hydrolysis event. The constitutively active Sec4-Q79L mutant shows a 30% reduced hydrolysis rate in vitro, likely due to the mutation affecting the phosphoryl-binding site in the Rab protein (Walworth et al., 1992). We did not detect any change in expression compared with the wild-type protein (Fig. S2 A). In cells where chromosomal Sec4-Q79L was GFP-tagged, the tethering time of vesicles entering the bud increased 2.5-fold and was far more variable at 45.6 ± 11.7 s ($n = 15$; Fig. 1, D and E; and Video 2). This implies that the timing of Sec4-GTP hydrolysis occurs before fusion and regulates post-tethering activities of the vesicle. Further analysis of the vesicle-position data showed that the vesicles did not “wander” on the plasma membrane any faster than in wild-type cells, with each moving no more than ~125 nm/s when tethered to the cortex (Fig. 1 F). There was, however, an eightfold increase in the number of vesicle untethering events in GFP-Sec4-Q79L cells. In these events, the vesicles are tethered to the cortex for several seconds but then are observed untethering in an aborted fusion event (Fig. 1 G and Fig. S2 B). This suggests that a window of opportunity exists for the fusion event to occur, and, if missed, a regulatory mechanism untethers the vesicle for another attempt at an alternate site. The nature of this correction mechanism is unknown. These data, in sum, show that the Sec4-GTP hydrolysis event regulates the tethering time, and if delayed results in an increase of aborted vesicle fusion events.

We next sought to determine how inhibiting certain key steps in exocytosis affects vesicle tethering and fusion at the single-vesicle level. Sec6p is a core member of the exocyst complex involved in both tethering and signaling at fusion sites (TerBush and Novick, 1995; Sivaram et al., 2005; Morgan et al., 2012). Importantly, the exocyst complex becomes disassembled and its function disrupted in the sec6-4 temperature-sensitive mutant (TerBush and Novick, 1995; Lamping et al., 2005). At the permissive temperature, vesicle tethering times increased to 23.1 ± 5.6 s ($n = 16$; Fig. 2, A and C). However, these cells showed no difference in vesicle wandering velocity or in aborted tethering events compared with wild type (Fig. 1, F and G), so this minor, but significant, delay likely reflects a defect in a previously unappreciated role in regulating downstream fusion events. Importantly, by examining kymographs of the entire bud cortex, we were unable to detect any
Timing of secretory vesicle tethering and fusion

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lasting vesicle tethering events at the restrictive temperature after a 5-min shift (Fig. 2, D and E). This supports the longstanding hypothesis that the exocyst functions as a physical tether at sites of exocytosis (TerBush and Novick, 1995; Luo et al., 2014), and validates that the tethering we have documented in wild-type cells is mediated by the exocyst.

We next visualized tethering and fusion in a mutant of the SM protein Sec1p, which has been proposed to stimulate assembled SNARE complexes to complete fusion (Scott et al., 2004). The time from tethering to fusion at the permissive temperature was 19.8 ± 5.5 s (n = 15; Fig. 2, B and C), which is not significantly different from wild type. Short 5-min shifts to the restrictive temperature showed that vesicles remained tethered to the cortex, with no clear fusion events being detected (Fig. 2 f). We also did not detect any increase in aborted tethering events at the permissive temperature, but there was a slight decrease in the mobility of the vesicle on the cortex (Fig. 1, f and g). Therefore, when the SM protein is rendered nonfunctional, tethering continues, indicating that the dissociation of the tethering complex requires the function of the SM protein.

The myosin-V Myo2p regulates the time of secretory vesicle tethering

We have described conditional mutations in the cargo-binding domain of the essential myosin-V, Myo2p, that fail to transport
secretory vesicles at the restrictive temperature (Schott et al., 1999). One of these alleles, myo2-13, is misregulated at both the permissive and restrictive temperatures, and is therefore hyperpolarized in the bud, as it has a reduced ability to deactivate (Donovan and Bretscher, 2012). The time of tethering before fusion in the myo2-13 mutant at the permissive temperature is extended to 27.9 ± 7.5 s (n = 15; Fig. 3, A and D), revealing that a mutant motor protein can influence the vesicle tethering time. This delay may indicate that fusion requires timely release of the motor, or because Myo2p itself participates in a dependent event and the myo2-13 allele is defective in this function.

To distinguish between these possibilities, we examined tethering in two additional active mutants. We recently showed that Myo2p undergoes a head-to-tail regulatory interaction in vivo through acidic residues in the head and basic residues in the tail; disruption of this interaction renders the motor hyperactive and therefore hyperpolarized in the bud (Donovan and Bretscher, 2015). Analysis of secretory vesicle tethering in two active mutants (myo2-3DR and myo2-RAKA) shows that they do not enhance the tethering time, indicating that some function other than unregulated motor activity is defective in the myo2-13 allele (Fig. 3, B–D). One avenue by which the motor might control tethering is through its interaction with exocyst component Sec15p, which was shown to interact with the tail of Myo2p (Jin et al., 2011). However, this interaction is disrupted by the myo2-RAKA allele, which indicates that the interaction of Myo2p with Sec15p does not contribute to the extension of the tethering time seen in the myo2-13 allele. Thus, our data imply that Myo2p contributes to the timing of events during exocytosis, but that the mechanism is unrelated to its state of activation. To this point, our results show that it is possible to follow exocytosis of individual secretory vesicles, and that the time of tethering by the exocyst is influenced by the activity state of Sec4p, an SM protein, and the motor Myo2p that delivered the vesicle.

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Myo2 leaves the tethered secretory vesicle 4 s before fusion

Our earlier studies revealed that Myo2p remains associated with secretory vesicles at sites of exocytosis, and that its release requires exocyst complex tethering and Sec4-GTP hydrolysis (Donovan and Bretscher, 2012). To explore the fate of Myo2p present on secretory vesicles during the tethering and fusion steps of exocytosis, we colocalized the vesicle/fusion marker GFP-Sec4 with Myo2p on the bud cortex over time (Fig. 4, A and E). Most events showed a gradual tapering of Myo2p intensity on the secretory vesicle before complete disappearance (Fig. 4, B). Because Myo2p’s association with vesicles is dependent on Sec4-GTP binding (Santiago-Tirado et al., 2011; Donovan and Bretscher, 2012),
one explanation for this result is that we are capturing “rolling” Sec4-GTP hydrolysis events of the ∼50 Sec4p molecules on the vesicle from ∼10–4 s before fusion. While we were unable to directly measure Sec4-GTP levels at the fusion site (such as through construction of a probe), it may be that the Sec4-GTP associated with the exocyst or SNARE apparatus is protected from the activity of the Sec4p GAPs Msb3p and Msb4p until a signal triggers fusion.

The GEF Sec2p and the exocyst remain associated with secretory vesicles up to the time of fusion

The GEF Sec2p is associated with secretory vesicles and is critical for the activation of Sec4p necessary for both secretory vesicle transport and binding to the exocyst (Walch-Solimena et al., 1997; Guo et al., 1999). It is not known if Sec2p remains with secretory vesicles during tethering, as it might dissociate to allow inactivation of Sec4-GTP by GAPs Msb3p/4p (Gao et al., 2003). It was therefore of considerable interest to see at which point Sec2p leaves secretory vesicles. In a strain with chromosomally tagged GFP-Sec4 and Sec2-3×mCherry, Sec2p was found to remain associated with secretory vesicles up to the point of fusion (Fig. 4, C and E). This may indicate that the GEF is required for some portion of the fusion event, such as keeping some of the pool of vesicle-localized Sec4p in a GTP-bound state or regulating the exocyst complex through its interaction with Sec15p (Mizuno-Yamasaki et al., 2010; Stalder et al., 2013).

Sec4-GTP hydrolysis has been postulated to regulate several events at the bud cortex, including its association with Myo2p and the exocyst, as well as regulating proper SNARE assembly (Guo et al., 1999; Grosshans et al., 2006; Santiago-Tirado et al., 2011; Donovan and Bretscher, 2012). Exocyst component Sec15p directly binds to Sec4p in a GTP-dependent manner and has been proposed to link the rest of the exocyst complex to the vesicle (Guo et al., 1999). We were able to detect some Sec4p/Sec15p colocalization on vesicles in the mother cell, but did not detect significant Sec4p or exocyst component overlap with the trans-Golgi marker Sec7p; this is consistent with the model that at least some components of the exocyst complex load onto vesicles before transport (Boyd et al., 2004; Fig. S3).

In contrast to Myo2p, Sec15-3×mCherry appeared to leave at the moment GFP-Sec4 disappears, which implies it is leaving at the fusion event (Fig. 4, D and E). This was intriguing because the Rab’s interactions with both Myo2p and Sec15p are regulated by GTP hydrolysis; however, as the exocyst is essential for exocytosis, it is conceivable that Sec15p must be present at sites of fusion until the end of the event. Further, the exocyst is well integrated to plasma membrane–localized Rho proteins Rho1p, Rho3p, and Cdc42p (Robinson et al., 1999; Guo et al., 2001; Zhang et al., 2001) and Sec2p via a phosphoryl regulation (Stalder et al., 2013), both of which may keep it from freely diffusing away. Our data showing that Sec15p remains with the vesicle until fusion are also similar to a recent observation in a mammalian vesicle fusion study, which found that the exocyst component Sec8 is present on vesicles at fusion sites but then leaves ∼2 s after vesicle fusion (Rivera-Molina and Toomre, 2013).

The exocyst is a nearly megadalton complex, with dimensions of 13 × 30 nm in a closed form (Hsu et al., 1998). As Sec15p is found on vesicles right up to the moment of fusion, this suggests that the complex must either disassemble or rearrange to accommodate the fusion of the 80-nm secretory vesicle. To better understand this result, we explored the behavior of additional exocyst complex components. We chose to tag Sec3p because it physically contacts the cortex through Rho proteins, and Sec5p because it is present on secretory vesicles but does not contact Sec15p (Guo et al., 1999, 2001; Zhang et al., 2001). In both cases, exocyst components left secretory vesicles at the same time as Sec15p, suggesting that the exocyst does not disassemble before fusion and may instead rearrange to accommodate vesicle fusion (Fig. 4, F–H). Additional evidence that the exocyst does not disassemble before fusion comes from fluorescence loss in photobleaching (FLIP) experiments, in which the mother cell is continuously bleached and the fluorescence intensity of protein in the bud is monitored over time; thus, the relative rates of recycling from the bud can be compared for different proteins. All exocyst proteins were observed to recycle from the bud at similar rates (Fig. 4 I), with ∼70% of the population for all components being in the mobile fraction. This suggests that the exocyst complex recycles from the bud as a single unit and therefore must later break up into “v-exocyst” and “t-exocyst” components for another round of tethering.

Despite thirty years of work dissecting post-Golgi secretion in budding yeast, the precise temporal localizations of dif-
different components at the cell cortex during exocytosis has not been achieved until now. A timeline of events summarizing our results is presented in Fig. 5. Several interesting questions are raised by this analysis. It is tempting to speculate that the Rab hydrolysis event is the master timing control for vesicle fusion given the delay between wild-type and hydrolysis-impaired mutants, though this could be due to other factors such as the mutant impairing SNARE assembly. Further, it is striking to see just how immobile tethered vesicles are on the plasma membrane, and we cannot offer an explanation for this phenomenon. As the proteins tracked in this study are highly conserved through evolution, these results are likely widely applicable. This study sets the stage, using additional mutants and altering the levels of key components, to fully dissect these events and establish how vesicle tethering, motor release, GTP hydrolysis, and membrane fusion events are coordinated, corrected, and timed.

Materials and methods

Yeast strains and constructs

Cells were grown and selected for using standard molecular biology techniques (Sherman, 2002). Yeast transformations were performed using lithium acetate–based methods (Gietz et al., 1995). In brief, log phase cultures were transformed for 45 min at 42°C with the vector/PCR product in a mixture of ~40% wt/vol PEG-3350 (Sigma-Aldrich), 0.1 M lithium acetate (Sigma-Aldrich), and 0.28 mg/ml SS carrier DNA (Sigma-Aldrich). Transformants were always
selected for on appropriate synthetic media. Table S1 shows the strains used in this study.

**DNA constructs**

GFP-Sec4 was chromosomally integrated into strains using the endogenous promoter and locus (Donovan and Bretscher, 2012). In brief, this vector contains 400 nt of the SEC4 promoter, followed by GFP, SEC4, and the SEC4 terminator. Colocalization experiments were performed with either 3xGFP or 3xmCherry fused to the C terminus of the protein of interest. All PCR-amplified fragments were sequenced after ligation to ensure fidelity. Myo2-3xmCherry was created by removing a 3xGFP module from pRS306-ctaa3-3xGFP and ligating a 3xmCherry module between the BamHI and NotI restriction sites. The vector was then cut with a unique HindIII site for integration at the 3′ end of the endogenous MYO2 gene. Strains containing Sec15-3xmCherry were created by ligating a PCR-amplified fragment of the 3′ end of SEC15 (1,008 nt) between restriction sites HindIII and BamHI in the pRS306 vector. A 681-nt fragment of the SEC15 3′ untranslated region was ligated upstream, between XhoI and HindIII, while the 200 nt fragment of the SEC15 terminator was amplified and ligated between the SacI and NotI sites. After ligation of the 3xmCherry module between BamHI and NotI, the construct was linearized with the unique HindIII site to integrate 3xmCherry immediately 3′ of the SEC15 gene. A similar strategy was done for Sec2-3xmCherry, using a unique SpeI cut site to linearize and integrate. Sec3p and Sec5p were tagged with 3xGFP by amplifying the 3′ 1,000 nt of each gene sequence and ligating into a pRS303-3xGFP-ADH1 construct between the BamHI and Sall restriction sites. Each gene fragment has a unique ClaI restriction site; when linearized, 3xGFP integrated at the 3′ end of the gene in question. The plasmid pSSEC7-DsRed.M1 × 6, which contains SEC7 driven from the TP1 promoter followed by six tandem dsRed genes, was a gift from the B. Glick laboratory (University of Chicago, Chicago, IL). The CEN plasmid used in GFP-Ypt31 studies was a gift from the R. Collins laboratory (Cornell University, Ithaca, NY) and contains the endogenous promoter. The plasma membrane marker used in our control experiments was the CEN plasmid pRS415-pTOM3-mCherry (2X Ist2928–948), which lasts for 18 s in wild-type cells. Myo2p motors are released gradually, with all dissociated ~4 s before fusion. This may indicate that Sec4-GTP is also hydrolyzed on a continuum. Finally, the GEF Sec2p and the exocyst complex are released at the moment of vesicle fusion, which then likely breaks into vesicle-associated and plasma membrane–associated components for another round of tethering. Not shown is the recycling event of the SNARE proteins, Sec4p by GDI, or the recycling of the unknown component of the receptor complex.

**Vesicle tethering assay**

“Vesicles” in this assay are defined as GFP-Sec4–positive puncta. All assays were done in strains grown to mid-log phase in appropriate synthetic media containing dextrose. Live cell imaging of log-phase cells was performed at 21°C or after a 5-min shift to 35°C where appropriate. Cells were imaged on a 35-mm MatTek dish (Ashland) pretreated with 0.05 mg/ml Concanavalin A (EY Laboratories, Inc.).

Micrographs were taken on a spinning disc confocal microscope system (CSU-X; Intelligent Imaging Innovations) using an inverted microscope (DMi600B; Leica) and a camera (CoolSnap HQ2; Photometrics). Micrographs were captured using the 100×/1.46 NA objective lens with 2x binning, for an effective pixel resolution of ~14 μm². Movies were taken in a z stack of 5 planes (covering 2.5 μm), each with 150-ms exposure times from a 488-nm laser, for a time resolution of ~1.32 s per frame. This allows for the capture of about half of the bud in late G2 phase. Photobleaching of the entire bud was performed using a Vector photomanipulation system (Intelligent Imaging Innovations) with a 1-ms dwell time and a raster block size of 10.

GFP-Sec4–positive vesicles entering the bud after FRAP were tracked in three dimensions in Slidebook 5.0 using the “Mean Adjusted Center of Intensity” manual particle tracking tool. This finds the coordinates of the center of the object (weighted by intensity values that are above the mean intensity). Vesicles were tracked by eye until one was observed tethering to the membrane. The manual particle tracker tool was then used to measure the particle’s location in 3D space of the multiplaned image until it disappeared. Only those vesicles that contacted the membrane from the cytoplasm, were unambiguous throughout their time there (that is, no other vesicle appeared next to it or overlapped with it), and quickly vanished in the middle three planes of the five plane image were used. This last criterion was included to prevent sampling vesicles that might drift out of the field of view in the z direction. Statistics related to the path of the vesicle were then obtained from Slidebook 5.0 and exported for work in Microsoft Excel and GraphPad Prism. Aborted tethering events for different strains were scored as the...
vesicles that dissociated from the cortex after being tethered for at least four consecutive frames (~5 s) of 20 separate movies. Imaging projections were also created in Slidebook 5.0.

Colocalization experiments
Colocalization microscopy of tethered Sec4p, Myo2p, Sec15p, Sec3p, and Sec5p was performed by imaging a single bottom plane of the cell. This was done to increase time resolution to <1 s, and because it was found that tethered vesicles in wild-type cells are relatively immobile on the plasma membrane (Fig. 1 G). GFP-Sec4 channel was captured for 120 ms per frame while the 3xmCherry-tagged protein was captured for 750 ms per frame. For exocyst component colocalization, Sec15-3xmCherry was captured for 500 ms while either Sec3-3xGFP or Sec5-3xGFP were captured for 400 ms. The times of disappearance for proteins analyzed were calculated by observing movie frames and comparing time stamps. Colocalization of GFP-Ypt31 and Sec7-6xdsRed in the mother cell was performed for the indicated strains at different exposure times as needed. FLIP photobleaching experiments were performed by imaging the cell every 2 s while photobleaching the mother cell every 6 s using the Vector control system (Intelligent Imaging Innovations) with 1 ms dwell time and a raster block size of 20.

Western blotting
Log phase cell cultures were washed once in ice-cold water, spun down, and resuspended in 1× Laemmli sample buffer. 4 × 1 min bead disruption was then done to break open the cells, with 1 min on ice in between runs. Samples were then boiled for 30 s at 95°C and resolved on a 12% SDS-PAGE gel. After transfer and blocking, membranes were probed with anti-Sec4p (generated in rabbit against full-length Sec4p missing its CAX box motif) and loading control anti-Zw11p (also known as the G6PDH enzyme; generated in rabbit against the full-length protein).

Statistics
Student’s t test and one-way analysis of variance (ANOVA) were used to determine statistical significance between datasets. A 95% confidence interval (P < 0.05) was considered significant.

Online supplemental material
Fig. S1 shows control bleach experiments and colocalization between GFP-Sec4–marked vesicles and a plasma membrane marker. Fig. S2 provides protein expression control blots and an example of an aborted transformation of intact yeast cells by the LiAc/SS-DNA/PEG procedure. Fig. S3 shows colocalization data for Rab proteins, the trans-Golgi network protein Sec7p, and exocyst components. Videos 1 and 2 show examples of bleached cells used in vesicle tracking studies for wild-type GFP-Sec4 and GFP-Sec4-Q79L strains, respectively. Table S1 shows the strains used in this study. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.201501118/DC1.

Acknowledgements
We would like to thank members of the Bretscher laboratory for helpful discussions and for reading this manuscript. We also thank C. Boone, E. Bi, P. Novick, R. Collins, B. Glick, and S. Emr for strains and constructs used in this study.

This work was supported by the National Institutes of Health (grant GM39066).

The authors declare no competing financial interests.

Author contributions: K.W. Donovan designed and performed experiments and contributed to the manuscript. A. Bretscher designed experiments and contributed to the manuscript.

Submitted: 29 January 2015
Accepted: 15 June 2015

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Timing of secretory vesicle tethering and fusion


Figure S1. Bleaching the bud does not interrupt or inhibit exocytosis, and secretory vesicles marked by GFP-Sec4 tether to the plasma membrane before fusion. (A) Small-budded cells were bleached with the same settings used in vesicle tracking assays. There was no difference in the growth of the bud of bleached or unbleached samples, indicating that the bleach event does not cause defects in exocytosis. Differential interference contrast images were adjusted for presentation. The red circle indicates the bleach area. Bar, 2 µm. (B) Still frame of medium budded cell showing vesicle marker GFP-Sec4 and plasma membrane marker pRS415-pTOM3-mCherry-(2X Ist2928-946) after the bleach event. Vesicles marked by GFP-Sec4 clearly contact the plasma membrane (arrowheads), as indicated by the normalized line scan graph. The image and line scan are representative of n = 25 cells analyzed. Bars, 2 µm. (C) The GAP-null msb3Δ msb4Δ strain contains cortex-localized GFP-Sec4 throughout the mother cell, likely due to reduced rates of GTP hydrolysis. Free GFP-Sec4 diffuses quickly throughout the plasma membrane as determined by a FRAP experiment bleaching a small area on the mother cell. Arrowheads point to cortex-localized GFP-Sec4 pool in this mutant. Bars, 2 µm. Error bars indicate standard deviation.
Figure S2. **Constitutively active Sec4-Q79Lp expresses similarly to wild type, and an example of an aborted tethering event in a GFP-Sec4-Q79L cell.** (A) Expression of Sec4p and Sec4-Q79Lp, as probed with an Sec4p antibody generated in a rabbit. The glucose-6-hydrogenase enzyme Zwf1p was used as a loading control. (B) Still frame micrographs of an abortive tethering event in the GFP-Sec4-Q79L strain. Arrowheads point to a vesicle that docked for ~5 s before untethering and reentering the bud cytoplasm. Bar, 2 µm.
Figure S3. **Colocalization of exocyst complex subunits, Rabs, and trans-Golgi network markers.** (A) Still frame micrographs showing colocalization of the Rab GFP-Ypt31 and the trans-Golgi marker Sec7-6xdsRed. Arrowheads show examples of overlap. Bar, 5 µm. (B) Still frame micrographs of the Rab GFP-Sec4 and the trans-Golgi marker Sec7-6xdsRed. There was no significant overlap. Bar, 5 µm. (C) Still frame micrographs of the exocyst component Sec15-3xGFP and the trans-Golgi marker Sec7-6xdsRed. There was no significant overlap. Bar, 5 µm. (D) Still frame micrographs of the exocyst component Sec5-3xGFP and the trans-Golgi marker Sec7-6xdsRed. There was no significant overlap. Bar, 5 µm. (E) Still frame micrographs of the Rab GFP-Sec4 and the exocyst component Sec15-3xmCherry. Some GFP-Sec4 puncta in the mother cell were positive for Sec15-3xmCherry. Bar, 2 µm.
Video 1. **Wild-type GFP-Sec4 vesicle tracking example from Fig. 1 (a and b).** Bleach event of the entire bud occurs at 5.1 s. Newly formed vesicles can then be observed entering the bud, docking with the plasma membrane, and disappearing in a frame-to-frame event. Images were analyzed by time-lapse spinning disk confocal microscopy (DMI600B, Leica; CSU-X, Yokogawa Electric Corporation) using Slidebook 5.0 software (Intelligent Imaging Innovations). Each frame is ~1.28 s.

Video 2. **GFP-Sec4-Q79L vesicle tracking example from Fig. 1 d.** Wild-type cells expressing chromosomally integrated GFP-Q79L-Sec4 during a bleach event. A bleach event of the entire bud occurs at 5.1 s. Newly formed vesicles can then be observed entering the bud, docking with the plasma membrane, and disappearing in a frame-to-frame event. Images were analyzed by time-lapse spinning disk confocal microscopy (DMI600B, Leica; CSU-X, Yokogawa Electric Corporation) using Slidebook 5.0 software (Intelligent Imaging Innovations). Each frame is ~1.28 s.
Table S1. Summary of yeast strains

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NA, not applicable.