A fluorescent resonant energy transfer–based biosensor reveals transient and regional myosin light chain kinase activation in lamella and cleavage furrows

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Approaches with high spatial and temporal resolution are required to understand the regulation of nonmuscle myosin II in vivo. Using fluorescence resonance energy transfer we have produced a novel biosensor allowing simultaneous determination of myosin light chain kinase (MLCK) localization and its \([Ca^{2+}]_i/calmodulin\)-binding state in living cells. We observe transient recruitment of diffuse MLCK to stress fibers and its in situ activation before contraction. MLCK is highly active in the lamella of migrating cells, but not at the retracting tail. This unexpected result highlights a potential role for MLCK-mediated myosin contractility in the lamella as a driving force for migration. During cytokinesis, MLCK was enriched at the spindle equator during late metaphase, and was maximally activated just before cleavage furrow constriction. As furrow constriction was completed, active MLCK was redistributed to the poles of the daughter cells. These results show MLCK is a myosin regulator in the lamella and contractile ring, and pinpoints sites where myosin function may be mediated by other kinases.

Introduction

Phosphorylation of the 20-kD regulatory light chain (RLC)* regulates nonmuscle myosin II activity. RLC phosphorylation sites can be categorized into inhibitory and activating based on their effects on myosin function. Phosphorylation of Ser-19 and Thr-18 stimulates myosin activity, whereas Ser-1, Ser-2, and Thr-9 phosphorylation is inhibitory. Ser-19 can be phosphorylated by several kinases, including myosin light chain kinase (MLCK) (Sellers et al., 1981; Ikebe et al., 1986), Rho kinase (Amano et al., 1996), and p21-activated kinase (PAK) (Chew et al., 1998; Zeng et al., 2000). MLCK also phosphorylates RLC at Thr-18 (Ikebe et al., 1986). Thr18-ser19 diphosphorylation maximally activates myosin ATPase in vitro (Sellers et al., 1981), and produces maximal isometric tension development in thrombin-stimulated endothelial cells (Goeckeler and Wyszolmerski, 1995). Phosphorylation of RLC at Ser-1, Ser-2, or Thr-9 by protein kinase C (Ikebe et al., 1987) or Cdc2 kinase (Satterwhite et al., 1992; Mishima and Mabuchi, 1996) inhibits myosin activity and decreases the Km of MLCK for RLC (Turbedsky et al., 1997).

The kinases that phosphorylate the RLC are regulated by distinct upstream signals, such as \([Ca^{2+}]_i/calmodulin\) and Rho family GTPases. In addition, many of these pathways interact. For example, cdc42-activated PAK phosphorylates RLC at Ser-19 (Chew et al., 1998; Zeng et al., 2000) and inhibits MLCK, preventing Thr-18 phosphorylation (Sanders et al., 1999; Goeckeler et al., 2000). This complexity suggests that cells spatially and temporally compartmentalize their signals. How these different kinases are targeted to their sites of action remains unre-
solved, in part due to our inability to follow these molecular events dynamically.

MLCK is a $[Ca^{2+}]/calmodulin$-dependent kinase implicated in nonmuscle contraction (Goecckler and Wysolmerski, 1995), cytokinesis (Poperechnaya et al., 2000), stress fiber formation (Chrzansowska-Wodnicka and Burridge, 1996), and motility (Kishi et al., 2000). The MLCK gene encodes two different kinases, a 210-kD MLCK (MLCK$_{210}$) expressed primarily in nonmuscle cells, and a differentially spliced isoform of 108–125 kD, MLCK$_{125}$ (Poperechnaya et al., 2000). Although previous immunolocalization studies have localized MLCK to stress fibers as well as the cleavage furrow of dividing cells (de Lanerolle et al., 1981; Guerriero et al., 1981), the dynamics of MLCK activation in these regions is unknown. The formation and maintenance of stress fibers are believed to require RLC phosphorylation (Chrzanowska-Wodnicka and Burridge, 1996), consistent with the stress fiber association of MLCK. However, despite localization of MLCK to stress fibers, myosin is not fully activated as further contraction can be induced. This suggests myosin can be further potentiated to produce maximal contraction.

In addition, we do not know if MLCK activation precedes or follows stress fiber localization. The convergence of multiple signals on myosin highlights the possibility of regionalized myosin regulation by distinct pathways. These unresolved issues underscore the need to dissect these pathways spatially and temporally. As the best characterized RLC kinase, MLCK is an ideal target for dynamic localization of activation state.

Using fluorescence resonant energy transfer (FRET) between blue (BFP) and green (GFP) fluorescent proteins, Rosomer et al. (1997) developed a fluorescent indicator protein (FIP) that detected $[Ca^{2+}]/calmodulin$ changes in live cells. Here we report the engineering of a novel biosensor, created by fusing the FIP to the MLCK COOH terminus, that detects the calmodulin binding state of MLCK. Since $[Ca^{2+}]/calmodulin$-binding activates MLCK, this sensor provides a representation of the activation state of MLCK. Using this approach, we observed that localized MLCK activation along stress fibers precedes cell contraction, demonstrating that MLCK activity can be modulated in situ on stress fibers to mediate the extent of myosin contractility. Activated

![Figure 1](image-url). **MLCK-FIP is a FRET-based $[Ca^{2+}]/calmodulin$ sensor with activity and regulation similar to wild-type MLCK.** (A) Schematic diagram of MLCK-FIP. The fluorescent indicator protein (FIP) consists of BFP linked to GFP via the $[Ca^{2+}]/calmodulin$-binding domain derived from MLCK. In the absence of $[Ca^{2+}]/calmodulin$, the coiled $[Ca^{2+}]/calmodulin$ binding domain allows FRET between the fluorophores. When $[Ca^{2+}]/calmodulin$ (yellow cylinder) is present, it binds and activates MLCK and binds between the fluorophores disrupting FRET. (B) MLCK-FIP shows $[Ca^{2+}]/calmodulin$ dependent kinase activity. Lysates from mock-transfected COS-7 cells or cells transiently expressing MLCK-FIP, wild-type MLCK were tested for their ability to phosphorylate RLC in a $[Ca^{2+}]/calmodulin$-dependent fashion. Endogenous kinase activity was evident only after prolonged exposure of the autoradiograph. (C) MLCK-FIP phosphorylates RLC at rates similar to wild-type MLCK. The activity of immunoprecipitated MLCK-FIP and wild-type MLCK was tested using three RLC concentrations. Amounts of immunoprecipitated kinase were determined using a standard curve of known MLCK concentrations detected by anti-MLCK pAb (bottom).
MLCK was also observed within the protruding lamella, localizing activated MLCK to where significant myosin reorganization occurs. During cell division, MLCK was enriched at the spindle equator during metaphase and at the poles of the daughter cells as cleavage furrow contraction was completed. In addition, observation of areas where MLCK is under represented identifies sites where myosin activity may be regulated by other pathways.

Results
Construction of a sensor to detect MLCK localization and calmodulin binding state
MLCK is activated by calmodulin binding. To detect calmodulin binding to MLCK, the FIP was linked to the MLCK COOH terminus. In the absence of bound calmodulin, the coiled conformation of the calmodulin binding domain (CBD) linking the BFP and GFP facilitates FRET upon BFP excitation (Fig. 1 A). When MLCK-FIP encounters increased concentrations of \([\text{Ca}^{2+}]_{i}/\text{calmodulin}\), the CBD in both MLCK and the FIP bind calmodulin, changing its conformation, activating MLCK, and disrupting FRET. By exciting BFP and monitoring the emission from GFP, the subcellular localization and the calmodulin-binding state of MLCK can be simultaneously monitored in living cells, allowing us to infer MLCK activation state.

MLCK-FIP has wild-type calmodulin-dependent RLC kinase activity
To test the regulation of MLCK-FIP, we assessed its ability to phosphorylate RLC. Lysates from COS-7 cells overexpressing either wild-type MLCK or MLCK-FIP were incubated with RLC. In the presence of \([\text{Ca}^{2+}]_{i}/\text{calmodulin}\), lysates from wild-type MLCK and MLCK-FIP showed significantly higher activities than mock-transfected cell lysates or when \(\text{Ca}^{2+}\) was omitted (Fig. 1 B). This result demonstrated the \([\text{Ca}^{2+}]_{i}/\text{calmodulin}\) dependence of the MLCK-FIP, showing that the FIP did not interfere with normal MLCK regulation.

To assess the enzymatic properties of MLCK-FIP, we compared the rates of RLC phosphorylation mediated by MLCK-FIP or wild-type MLCK at three different subsaturating RLC concentrations. This approach was necessary because the bacterially expressed RLC precipitated at high concentration, limiting our ability to determine MLCK kinetics at high RLC concentrations. MLCK-FIP and wild-type MLCK were expressed in COS-7 cells and immunoprecipitated using an MLCK-specific antibody. The amount of recombinant MLCK-FIP and wild-type MLCK was determined by comparing their intensity on an immunoblot to that of a standard curve (Fig. 1 C, bottom). Since endogenous kinase activity was not detected, the activity in the immunoprecipitates represented the expressed kinase activity (a faint endogenous band of MLCK\(_{125}\) was evident only after prolonged exposure, unpublished data). Immunoprecipitates containing equal amounts of wild-type MLCK and MLCK-FIP were used in the in vitro kinase assay. Fig. 1 C shows that both wild-type MLCK and MLCK-FIP phosphorylate RLC at indistinguishable rates at all three substrate concentrations tested. Since the recombinant RLC was buffered in high salt to prevent precipitation, both wild-type MLCK and MLCK-FIP–phosphorylated RLC to a maximum of 1 mol phosphate incorporated per mole RLC, consistent with previous findings that the MLCK-mediated diphosphorylation of RLC is sensitive to high ionic strength (Ikebe and Hartshorne, 1985). These results demonstrate

Figure 2. MLCK-FIP detects \([\text{Ca}^{2+}]_{i}/\text{calmodulin}\) changes in vitro and in vivo. (A) Partially purified MLCK-FIP in buffer containing 1 \(\mu\text{M}\) calmodulin was exposed to increasing free \(\text{Ca}^{2+}\). Emission scans (using 380 nm excitation) were obtained at increasing \(\text{CaCl}_2\) concentrations. (B) COS-7 cells overexpressing MLCK-FIP were treated with 1 \(\mu\text{M}\) ionomycin, and ratio imaging used to monitor the \([\text{Ca}^{2+}]_{i}/\text{calmodulin}\) binding to MLCK-FIP. Relative \([\text{Ca}^{2+}]_{i}/\text{calmodulin}\) binding (representing MLCK activity) is displayed using intensity-modulated display with blue indicating bound calmodulin (active MLCK) and red showing little bound calmodulin (inactive MLCK) as shown in the ratio bar.
that MLCK-FIP has the same \([\text{Ca}^{2+}]_4/\text{calmodulin-dependent kinase activity as wild-type MLCK.}\)

**MLCK-FIP detects changes in \([\text{Ca}^{2+}]_4/\text{calmodulin concentrations in vitro**

Next, we ascertained the ability of MLCK-FIP to detect \([\text{Ca}^{2+}]_4/\text{calmodulin changes in vitro. MLCK-FIP was purified, and the emission spectrum was determined following excitation at 380 nm in the presence of increasing amounts of CaCl\(_2\). Fig. 2 A shows that MLCK-FIP displays decreased FRET, detected by decreased 509 nm emission, in response to increased \([\text{Ca}^{2+}]_4\) concentration. Decreased GFP emission was accompanied by a corresponding increase in BFP emission (448 nm), consistent with loss of FRET. This result, consistent with the behavior of FIP (Romoser et al., 1997), shows that MLCK-FIP effectively detects changes in \([\text{Ca}^{2+}]_4/\text{calmodulin concentration.}\)

**MLCK-FIP detects \([\text{Ca}^{2+}]_4/\text{calmodulin changes in vivo**

The simultaneous monitoring of MLCK localization and \([\text{Ca}^{2+}]_4/\text{calmodulin binding requires two measurements, one to determine the amount of FRET (corresponding to activity state) and a second to determine MLCK-FIP intensity (corresponding to distribution). Relative MLCK activity (\([\text{Ca}^{2+}]_4/\text{calmodulin binding state) is represented by a ratio of intensity from the FRET acceptor (GFP emission at 510 nm caused by stimulation of the donor at 380 nm), F\(_{\text{FRET}}\) divided by the intensity of the acceptor (at 510 nm) produced by direct stimulation of the acceptor (at 460 nm), F\(_{\text{GFP}}\). Since F\(_{\text{GFP}}\) is obtained by direct excitation of the GFP, the intensity is not affected by FRET, thus providing an independent measurement of MLCK concentration. However, it is important to note that F\(_{\text{GFP}}\) cannot distinguish between changes in path length and MLCK concentration. Regions with significant difference in thickness will have difference in F\(_{\text{GFP}}\) intensities. Caution needs to be applied when comparing MLCK concentration in cellular regions with significant difference in thickness.

To test MLCK-FIP detection of \([\text{Ca}^{2+}]_4/\text{calmodulin changes in live cells, MLCK-FIP spectra were monitored following \text{Ca}^{2+} ionophore, ionomycin, treatment of MLCK-FIP transfected COS-7 cells. COS-7 cells were chosen because they significantly overexpress recombinant proteins and have high transfection efficiency. As shown in Fig. 2 B, the high protein expression level resulted in a generally diffuse localization of MLCK-FIP. Prior to the ionomycin treatment, ratio images indicate that MLCK-FIP was not in the calmodulin-bound state (red, MLCK inactive). A dramatic loss of FRET was seen immediately after ionomycin treatment (Fig. 2 B), indicated by a shift from red to green or blue, showing that MLCK-FIP bound calmodulin and was therefore activated. This result shows that MLCK-FIP detects \([\text{Ca}^{2+}]_4/\text{calmodulin changes in live cells. It also shows that there was sufficient calmodulin to allow MLCK-FIP to detect increased \([\text{Ca}^{2+}]_4/\text{calmodulin binding even when MLCK-FIP was overexpressed.}\)

The data in Fig. 2 B is displayed using Intensity-Modulated Display (IMD) (Tsien and Harootunian, 1990), in which the FRET/GFP ratio determines color, and the intensity of the F\(_{\text{GFP}}\) determines the color intensity. In this method, the pixel values 0–255 are divided into 16 bins (0–15, 16–31, etc.) to represent FRET levels. Within each bin, the lowest number represents the lowest F\(_{\text{GFP}}\) intensity while the highest number represents the highest intensity. For example, in the 0–15 bin representing the smallest FRET ratio, a pixel value of 0 would represent a small amount of calmodulin-bound MLCK (activated), while 15 would represent a large amount of calmodulin-bound MLCK. Similarly, in the 240–255 bin (representing the highest FRET and therefore the lowest amount of bound calmodulin or relatively inactive kinase) a value of 240 represents little inactive kinase while 255 represents a large amount of inactive kinase. This mathematical manipulation provides a dynamic two-dimensional display of MLCK regulation.

**Regions with MLCK-FIP activation exhibit highly phosphorylated RLC**

If MLCK-FIP accurately reflects the activation state of MLCK, cellular regions with \([\text{Ca}^{2+}]_4/\text{calmodulin-bound
MLCK should correspond with regions of increased RLC phosphorylation. To test this, we compared the MLCK-FIP ratio image with the distribution of phosphorylated RLC using a polyclonal antibody specific for RLC phospho-Ser-19 (Matsumura et al., 1998). PTK-2 cells expressing MLCK-FIP were imaged to obtain a $F_{\text{FRET}}/F_{\text{GFP}}$ ratio (Fig. 3 A, left), then immediately fixed and double-stained for myosin heavy chain and phosphorylated RLC. The level of RLC phosphorylation is displayed as a ratio of phosphorylated RLC to total myosin (Fig. 3 A, right). Myosin associated with stress fibers throughout lamella had highly phosphorylated RLC. The $F_{\text{FRET}}/F_{\text{GFP}}$ ratio image shows a strong correlation between MLCK$_{125}$ activation and RLC phosphorylation. In addition, the MLCK-FIP suggests that MLCK is highly active within the lamella where very little myosin was observed. In this region, myosin is organized into clusters of bipolar filaments that appear as spots undergoing retrograde movement (Verkhovsky and Borisy, 1993; Verkhovsky et al., 1995). This pattern of myosin organization within lamella suggests that there is a pool of diffuse myosin that becomes more highly organized. The fact that MLCK-FIP is highly activated in this region suggests that active MLCK$_{125}$ may mediate this myosin reorganization.

Our results suggested that MLCK$_{125}$ localized to stress fibers. To confirm this, we assessed colocalization of MLCK-FIP and F-actin by comparing the MLCK-FIP image with rhodamine-phalloidin staining of fixed cells. Fig. 3 B clearly shows the colocalization of MLCK-FIP with phalloidin stained stress fibers.

**Localized MLCK activation precedes regional cellular contraction**

MLCK activation has been implicated in nonmuscle cell contraction (Goeckeler and Wysolmerski, 1995) and correlates with isometric tension development in permeabilized endothelial cells (Wysolmerski and Lagunoff, 1991). We examined how MLCK–calmodulin interaction correlated with cell contraction in transiently transfected PTK-2 cells. PTK-2 cells were used because of their high transfection efficiency, prominent stress fiber network, and the fact that they express MLCK-FIP at significantly lower levels than COS-7 cells, whose ultra-high expression level would have interfered with the imaging of cytoskeletal structures. Fig. 4 shows two different examples of contracting PTK2 cells. Cell contraction was characterized by stress fibers shortening and decreased cell margins. The $F_{\text{FRET}}/F_{\text{GFP}}$ ratios are displayed in a three-dimensional plot with color indicating MLCK activity state as shown in the ratio bar (bottom), and height indicating fluorescence intensity of directly stimulated GFP. Regions with abundant MLCK-FIP are represented by peaks of

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**Figure 4.** Transient recruitment and activation of MLCK$_{125}$ along contracting stress fibers. Ratio images of two contracting cells (out of four observed). The intensity of MLCK-FIP is represented by the peak height (high peaks indicate enrichment of MLCK) while the MLCK-FIP $[\text{Ca}^{2+}]_c$/calmodulin-binding state is displayed by the color. Red (high ratio) represents inactive kinase, while blue indicates $[\text{Ca}^{2+}]_c$/calmodulin-bound kinase. Arrows indicate regions where diffuse MLCK is recruited to stress fibers, and arrow heads show sites of in situ activation of MLCK-FIP. Please refer to Videos 1 and 2 (available at http://www.jcb.org/cgi/content/full/jcb.200110161/DC1) for the dynamic MLCK profile.
increased height. Fig. 4, A–D, (and Video 1) shows that transient and highly localized MLCK<sub>125</sub> enrichment and apparent activation along stress fibers precedes cellular contraction. Diffuse MLCK–FIP (Fig. 4 A) became increasingly associated with stress fibers before contraction (Fig. 4, B and C, arrows). MLCK–FIP also showed regulated activity in situ along stress fibers (Fig. 4, B–D, arrowheads), where the activity first increased at the start of contraction, then decreased as contraction ends. Fig. 4, E–H (Video 2), show another example. These results demonstrate that MLCK<sub>125</sub> can associate with stress fibers, although based on previous results (Poperechnaya et al., 2000) its association with the cytoskeleton may be more transient than that of MLCK<sub>210</sub>. Videos are available at http://www.jcb.org/cgi/content/full/jcb.200110161/DC1.

**MLCK<sub>125</sub> is activated in the lamella of migrating cells**

Since MLCK<sub>125</sub> bound calmodulin in the lamella of stationary cells, we investigated its behavior in the extending lamella of PTK2 cells stimulated to migrate by hepatocyte growth factor/scatter factor. Fig. 5 suggests MLCK activation in the lamella of motile PTK-2 cells based on increased calmodulin binding. Since the F<sub>FRET</sub> image and the F<sub>GFP</sub> image are taken sequentially, we worried that movement might create a motion artifact that could be misinterpreted as a loss of FRET (MLCK activation). Two lines of evidence argue against this. First, extending lamellas continue to show active MLCK-FIP (Fig. 3) after fixation. Second, alternating the order of collection of the FRET and GFP images did not alter the MLCK-FIP activation profile (unpublished data).

MLCK-FIP in the lamella associated with a meshwork resembling actin, consistent with MLCK<sub>125</sub> binding to F-actin. The level of MLCK activation was consistently higher in the leading lamella than the retracting tail (eight out of nine cells observed), where myosin contractility has been postulated to dislodge focal adhesions during cell movement. Previous studies (Matsumura et al., 1998) showed elevated RLC phosphorylation in the tail, raising the possibility that MLCK may not be responsible for phosphorylating RLC in the tail. Perhaps one of the other RLC-targeting kinases regulates myosin at the retracting tail.

**During cytokinesis MLCK<sub>125</sub> is activated at both the cleavage furrow and the poles**

Myosin is dramatically reorganized during cytokinesis, with phosphorylated RLC enriched in the midzone of mitotic spindle during late anaphase, before the constriction of cleavage furrow (Matsumura et al., 1998). MLCK<sub>210</sub> has been localized to the cleavage furrow and the cortical regions of dividing cells, whereas MLCK<sub>125</sub> remained diffuse (Poperechnaya et al., 2000). Fig. 6 A shows MLCK-FIP during cytokinesis in transiently transfected NRK cells. MLCK intensity and FRET profile were measured along a dividing cell during cytokinesis (dotted red line) and is shown in Fig. 6 B. Significant MLCK enrichment occurred at late metaphase (indicated by equatorial alignment of chromosomes, phase image not shown) at the equator of the spindle, and showed moderate levels of calmodulin binding. Immediately before constriction of the cleavage furrow at late anaphase (red arrowhead, time: 7:30), MLCK<sub>125</sub> appeared maximally activated. The surge of activity at the cleavage furrow was immediately followed by recruitment of active MLCK<sub>125</sub> to the polar regions of the daughter cells. MLCK<sub>125</sub> intensity at the spindle midzone dropped following the onset of cleavage furrow contraction (Fig. 6 B, left), but was maximally activated until cleavage was complete (Fig. 6 B, right). MLCK at the poles showed high level of calmodulin binding especially within the lamella and ruffles.

## Discussion

To extend our understanding of myosin regulation during cell motility, we produced a biosensor able to both localize MLCK and provide information regarding its activation state in living cells. Since MLCK is regulated by [Ca<sup>2+</sup>]<sub>/calmodulin binding, we adopted a strategy to detect colocaliza-
tion of MLCK125 and its activator, [Ca\(^{2+}\)]/calmodulin, by fusing the FIP to the COOH terminus of MLCK125. Binding of [Ca\(^{2+}\)]/calmodulin to the regulatory site in MLCK-FIP activates the kinase (Fig. 1 B) while binding to the FIP domain disrupts FRET between the GFP-based donor and acceptor (Fig. 2). We showed that the biosensor retained the regulation and enzymatic properties of that of wild-type MLCK, and detected [Ca\(^{2+}\)]/calmodulin changes in vivo. These results suggest that MLCK-FIP provides an indication of MLCK activation state in living cells.

Several factors affect the accuracy with which MLCK-FIP reports MLCK activation state. The first is the requirement for the two [Ca\(^{2+}\)]/calmodulin binding domains in MLCK-FIP to have similar calmodulin binding properties. Romoser et al. (1997) have shown [Ca\(^{2+}\)]/calmodulin binding to MLCK and FIP to be comparable. A second factor is that MLCK-FIP must accurately reflect the MLCK localization. The most distinctive pattern of MLCK localization is its association with stress fibers (de Lanerolle et al., 1981; Guerrero et al., 1981; Matsumura et al., 1998; Lin et al., 1999; Poperechnaya et al., 2000). As shown in Fig. 3 B, MLCK-FIP shows stress fiber localization. Thus, at least for the most identifiable sites, MLCK-FIP displays the same localization as wild-type MLCK. Third, to accurately reflect activity, MLCK-FIP must also localize to cellular regions with high levels of RLC phosphorylation. Fig. 3 A shows that regions where myosin RLC is most heavily phosphorylated also exhibit high levels of MLCK-FIP activation. There are also regions, particularly the leading edge, where MLCK activity is high but where there is relatively little myosin. The possible reasons for this are discussed below, but there is generally good agreement between higher levels of RLC phosphorylation and MLCK-FIP activation.

Since activation state is inferred from calmodulin binding, could there be situations where calmodulin binding might not accurately reflect MLCK activation? MLCK is phosphorylated by several kinases, including PAK, CaM kinase II, and PKA. CaM kinase II or PKA phosphorylation of Ser-992, which is located in the [Ca\(^{2+}\)]/calmodulin binding domain, decreases MLCK125-calmodulin binding efficiency (Payne et al., 1986; Ikebe and Reardon, 1990; Tansey et al., 1992). In addition, bound calmodulin blocks phosphorylation of this site. MLCK is also phosphorylated by PAK at residues Ser-439 and Ser-991 (Goecckeler et al., 2000). Ser-439 phosphorylation has been postulated to affect protein–protein interactions, but there is no direct experimental test.
of this idea. Like Ser-992, calmodulin binding blocks PAK-mediated phosphorylation of Ser-991 (Goeckeler et al., 2000). Although it is debatable if PAK phosphorylation reduces calmodulin binding (Sanders et al., 1999), it is easy to imagine that phosphorylation of these sites blocks calmodulin binding and prevents MLCK activation. Ser-991 and Ser-992 are present in both the calmodulin-binding domains of MLCK-FIP. Thus, if PAK, PKA, or CaM kinase II were to phosphorylate these sites in both calmodulin-binding domains, affecting calmodulin binding, the MLCK-FIP would accurately reflect the activation state of MLCK. On the other hand, if phosphorylation were to regulate MLCK independently of calmodulin binding, which has not been demonstrated, MLCK-FIP might not accurately display the MLCK activity. Another case where MLCK-FIP might not accurately reflect MLCK activity is regulation through the nucleotide-binding domain of the MLCK catalytic core, a drug target for inhibitors such as KT-5926. Despite these caveats, our results suggest MLCK-FIP reflects MLCK activity and provides the best tool available to study the dynamic regulation of MLCK in vivo.

### Transient enrichment of calmodulin-bound MLCK<sub>125</sub> induces contraction

Although MLCK has been directly implicated in mediating cellular contraction in permeabilized endothelial cells (Wyssolmerski and Lagunoff, 1991) and isolated stress fibers (Katoh et al., 2001), the dynamic aspects of how MLCK regulates myosin function are poorly understood. This is complicated by the existence of two isoforms of MLCK. The vertebrate MLCK gene produces two kinases (Birukov et al., 1998): (a) a 108–125-kD MLCK (MLCK<sub>125</sub>) found in both smooth muscle and nonmuscle cells; and (b) a 210-kD MLCK (MLCK<sub>210</sub>) expressed in nonmuscle cells, consisting of MLCK<sub>210</sub> with a 900–amino acid NH<sub>2</sub>-terminal extension (Poperenchnaya et al., 2000). The MLCK-FIP described in this report is based on MLCK<sub>25</sub>, although MLCK<sub>210</sub>-FIP is in development. Since antibodies against MLCK<sub>125</sub> also recognize MLCK<sub>210</sub>, immunolocalization cannot distinguish between these isoforms. GFP-MLCK<sub>210</sub> associates with stress fibers with high affinity (Poperenchnaya et al., 2000), suggesting it can be activated in situ. GFP-tagged MLCK<sub>125</sub> localizes differently in different cell types. Poperenchnaya et al. (2000) showed MLCK<sub>125</sub> to be largely diffuse in the cytoplasm, while Lin et al. (1997, 1999) observed filament-bound MLCK<sub>125</sub>. The short MLCK isoform also contains a high affinity actin-binding motif (Smith et al., 1999). Consistent with Lin et al. (1997, 1999), we observed MLCK-FIP in association with stress fibers. We also observed recruitment of additional MLCK-FIP to stress fibers as they contract (Fig. 4). This suggests that stress fiber association of MLCK<sub>125</sub> may be regulated and transient, providing a basis to reconcile the previous contradictory observations.

Rho kinase has been proposed to induce a slow and sustained contractility to maintain tension along stress fibers, whereas MLCK mediates a rapid but transient contraction (Katoh et al., 2001). The rapid enrichment of MLCK<sub>125</sub> activity on stress fibers is consistent with in vitro kinetic studies. The $K_m$ of MLCK for RLC is higher than Rho kinase, suggesting that it may work optimally at high local RLC concentration. The high $V_{max}$ of MLCK is ideal to mediate rapid myosin activation. Our studies with MLCK-FIP suggest that localized contraction is mediated by a combination of transient association of MLCK with stress fibers and localized MLCK activation.

### MLCK and directed cell movement

Previous in vitro biochemical studies show that RLC phosphorylation mediates myosin assembly into bipolar filaments (Ikebe et al., 1988; Trybus and Lowey, 1988; Katoh and Morita, 1996). In the leading lamella, apparently diffuse myosin becomes organized into clusters of bipolar filaments (DeBiasio et al., 1988; Verkhovsky and Borisy, 1993; Verkhovsky et al., 1995). Localization of highly activated MLCK-FIP in this region suggests that MLCK<sub>125</sub> could regulate myosin organization. Consistent with this, reducing MLCK expression limits lamellipodial extension in smooth muscle cells after platelet-derived growth factor treatment (Kishi et al., 2000). Since the protrusion of lamellipodia is driven mainly by actin polymerization (reviewed in Higgs and Pollard, 2001), the mechanism by which myosin contributes to motility in the lamella of a migrating cells is unclear. Fig. 7 presents a model suggested by the observation of activated MLCK in the lamella. Myosin II filaments aggregate in the lamella to form ribbon-like structures that may exert tension required to bundle loosely aligned actin filaments (Verkhovsky et al., 1995). We suggest that MLCK-mediated myosin activation may lead to contraction in the region where myosin spots coalesce to form a meshwork of stress fibers (Fig. 7). Myosin-mediated contraction of the cytoskeleton in this region would exert force between the lamella and cell center as proposed previously (Lauffen-
MLCK is activated in cleavage furrow and cortex during cytokinesis
MLCK-FIP has also provided insight into the regulation of cytokinesis. MLCK-FIP was localized to the spindle midzone during late metaphase before its activation. Calcium and calmodulin dynamics complement the MLCK dynamics we observe during cytokinesis. Elevation of free Ca\(^{2+}\) begins in anaphase, and persists through daughter cell separation (Tombs and Borisy, 1989). During mitosis, calmodulin is concentrated at the spindle poles and in the cortex (Li et al., 1999). Cortical calmodulin is redistributed to the equator before cleavage furrow formation. Using a sensor (Torok and Trentham, 1994) that detects calmodulin binding to Ca\(^{2+}\) and its target, only equatorial calmodulin interacts with downstream effector(s) (Li et al., 1999). Enrichment of MLCK\(_{125}\) at the equator before its activation suggests that MLCK localization is not dependent on [Ca\(^{2+}\)]/calmodulin. Interaction between MLCK and [Ca\(^{2+}\)]/calmodulin, indicated by loss of FRET, does not correlate with MLCK-FIP intensity during cytokinesis. These data argue against the possibility that MLCK-FIP is mislocalized to regions of high [Ca\(^{2+}\)]/calmodulin. The differential distribution of Ca\(^{2+}\) and calmodulin in cultured mammalian cells led to the suggestion that calmodulin might be involved in positioning of the cleavage furrow (Li et al., 1999). However, the dynamics of MLCK-FIP suggests that the contractile machinery may already be in place, and calmodulin activates contraction locally.

MLCK-FIP accumulated at the midzone until contraction was initiated. During this time, the MLCK became increasingly associated with calmodulin and thus activated (Fig. 6 A, red arrowhead). Once contraction began, the amount of MLCK-FIP in the cleavage furrow began to decrease, although what remained was highly activated (Fig. 6 B). As contraction proceeded, MLCK both accumulated and was activated at the poles. In contrast, [Ca\(^{2+}\)]/calmodulin from the cortical pool is redistributed to the equator (Li et al., 1999). The lack of [Ca\(^{2+}\)]/calmodulin at the poles of the daughter cells suggests that MLCK\(_{125}\) may remain active as the kinase translocates from the equator to the poles. Following cleavage furrow contraction, myosin, monitored by GFP-RLC, follows a similar translocation from the furrow to the poles (unpublished data). It is first concentrated at the equator during late metaphase, and then accumulates at the poles after constriction of cleavage furrow has occurred. It is unclear what molecular mechanism is responsible for this redistribution. Perhaps MLCK is transported by the same mechanism as myosin, or even by association with the redistributing myosin.

The localization of active MLCK to the new leading edges of the daughter cells after cytokinesis is consistent with our model that myosin is required for the pulling force between the nucleus and lamellipodia. MLCK recruitment to the poles where extensive cell spreading occurs may activate myosin to facilitate the separation of the two daughter cells in the same way we suggest myosin contractility might pull the nucleus forward during migration.

Conclusion
Our data have documented the recruitment of MLCK to various cytoskeletal structures during contraction, motility, and cytokinesis. The ability to simultaneously infer MLCK activity from calmodulin binding and monitor its localization highlights the lack of a direct correlation between localization and enzymatic activity, providing an important reminder that the localization of a protein cannot be automatically translated into its activity. The biosensor can easily be adapted to study other [Ca\(^{2+}\)]/calmodulin-dependent proteins in vivo, such as calmodulin-dependent protein kinase II. Understanding the spatio-temporal dynamics of other kinases could advance our understanding of the signal transduction pathways important for directed cell migration.

Materials and methods
Generating the MLCK-FIP and wild-type MLCK constructs
Both the BFP and GFP cDNAs were PCR-amplified from the appropriate vectors of the “Living Colors” GFP vector series purchased from CLONTECH Laboratories, Inc. Overlapping primers were designed to join the two fluorophores via a linker GT55RRNNKTNKHRAVRGI55TGA. Bold letters denote the [Ca\(^{2+}\)]/calmodulin binding domain derived from MLCK, whereas the rest of the amino acids are linker sequence. Underlined letters represent MLCK\(_{125}\) Ser-991 and Ser-992 equivalents. The FIP cDNA was first subcloned into pcDNA3 vector, to generate the pcDNA3/FIP construct. To fuse the MLCK\(_{125}\) cDNA in frame into pcDNA3/FIP, murine MLCK\(_{125}\) cDNA (EMBL/GenBank/DDBJ accession no. P29294) was PCR amplified with the downstream primer designed to mutate the stop codon to code for alanine. The MLCK\(_{125}\) cDNA was then subcloned into BamHI sites of pcDNA3/FIP, and was sequenced in its entirety to rule out any PCR-related mutation. The final pcDNA3/MLCK\(_{125}\)-FIP construct contains the murine MLCK\(_{125}\) linked to the FIP via a short linker containing the arbitrary amino acid sequence encoded by vector sequence. This construct encodes the 185-kD MLCK-FIP recombinant protein.

To generate the pcDNA3 vector expressing the wild-type MLCK\(_{125}\), the murine MLCK\(_{125}\) was PCR-amplified to engineer the KpnI and BamHI sites for subcloning into pcDNA3 vector. The positive clones were sequenced to ensure the absence of PCR-related mutation. The construct expresses the 125-kD wild-type MLCK\(_{125}\).

Cell culture and transfection
PTK2 kangaroo rat epithelial cells (a gift from Dr. Robert Goldman, Northwestern University, Evanston, IL) were cultured in MEM (GIBCO-BRL) supplemented with 10% FCS, and 0.1 mM nonessential amino acids. The nor-
nal rat kidney (NRK) epithelial cell line was a gift from Dr. Yu-Li Wang (University of Massachusetts Medical School, Worcester, MA). NRK cells were cultured in F12 Kaighn’s modified medium (Sigma-Aldrich), supplemented with 10% FCS. COS-7 cells were kindly provided by Dr. Kathleen Green (Northwestern University, Evanston, IL) and were maintained in DMEM supplemented with 10% FCS. All cell lines were maintained in an atmosphere of 5% CO2 at 37°C. 

Transfection was performed by electroporation. Cells were trypsinized and pelleted by centrifugation. The cell pellets were resuspended in 1 ml appropriate medium. 200 μl of the resuspended cells were mixed with 7–10 μg DNA containing 13 μg sheared salmon sperm DNA and electroporated in 4-mm cuvettes using Bio-Rad Laboratories Gene Pulser set at 200 ohms, 900 V, and 250 μF. Following this transfection efficiency (70–90%) for most cell types at a wide range of cell density except NRK cells, in which ~10–15% could be transfected. Peak protein expression levels observed 18–48 h posttransfection for all cell lines.

Reagents, proteins, and antibodies

Polyclonal rabbit anti-MLCK antibody and purified MLCK-FIP was provided by Dr. Robert Wyssolmerski (St. Louis University, St. Louis, MO). Ionomycin and calmodulin were purchased from Calbiochem. Protein-A sepharose was purchased from Amersham Pharmacia Biotech, pp2b rabbit polyclonal antibody specific for Ser-19–phosphorylated RLC was obtained from Dr. Fumio Matsumura. Monoclonal antisynemin heavy chain antibody was purchased from Covance. Texas red–conjugated goat anti–mouse IgM and Cy5-conjugated donkey anti-rabbit IgG were purchased from Jackson ImmunoResearch Laboratories.

Protein expression and purification

Myosin II RLC cDNA was cloned into pETi-1b vector (Novagen) for the expression of His-tagged RLC, and protein expression was induced in BL21 by 0.4 mM IPTG for 3 h. Bacterial pellet was lysed in lysis buffer A (5 mM imidazole, 0.5 mM NaCl, 20 mM Tris-HCl, pH 7.9) containing 6 M urea and protease inhibitors. Following sonication, cell lysate was precleared by 0.4 mM IPTG for 3 h. Bacterial pellet was lysed in lysis buffer A (500 mM imidazole, 250 mM NaCl, 10 mM Tris-HCl, pH 7.9). The eluted protein was dialyzed against diethyl sulfoxide buffer A (20 mM MOPS, pH 7.2, 250 mM NaCl, 1 mM MgCl2, 1 mM MgCl2) with stepwise decrease of imidazole concentration from 500 to 250 mM. Lower imidazole concentration resulted in massive protein precipitation. Cleaving the His tag did not eradicate the precipitation problem.

MLCK-FIP and wild-type MLCK were overexpressed in COS-7 cells for purification. Cell lysates were collected from 16 confluent 10-cm cell cultures. Cells were lysed in 35 ml of lysis buffer B (10 mM MOPS, pH 6.8, 5 mM MgCl2, 1.25 mM EGTA, 1 mM EDTA, 10% glycerol, 1% NP-40) containing protease inhibitors. Lysates were sonicated briefly in sonicator buffer and pre cleared with 50,000 g centrifugation, and loaded onto His-Bind column (Novagen) pre equilibrated with the same buffer. After washing the column with washing buffer B (60 mM imidazole, 0.5 mM NaCl, 20 mM Tris-HCl, pH 7.9), the eluted protein was dialyzed against diethyl sulfoxide buffer A (500 mM imidazole, 250 mM NaCl, 10 mM Tris-HCl, pH 7.9). The eluted protein was dialyzed against diethyl sulfoxide buffer A (20 mM MOPS, pH 7.2, 250 mM NaCl, 1 mM CaCl2, 1 mM MgCl2) with stepwise decrease of imidazole concentration from 500 to 250 mM. Lower imidazole concentration resulted in massive protein precipitation. Cleaving the His tag did not eradicate the precipitation problem.

MLCK-FIP and wild-type MLCK were overexpressed in COS-7 cells for purification. Cell lysates were collected from 16 confluent 10-cm cell cultures. Cells were lysed in 35 ml of lysis buffer B (10 mM MOPS, pH 6.8, 5 mM MgCl2, 1.25 mM EGTA, 1 mM EDTA) and the FRET ratio depicted by the line color. We have avoided cells with saturated pixels to minimize error on ratio calculation.

To correlate the relative activity of MLCK-FIP with the extent of RLC phosphorylation in vivo, PTK-2 cells transiently expressing MLCK-FIP were plated on gridded coverslips. The ratio images of MLCK-FIP were obtained as described, and the cells were immediately fixed. The coverslips were blocked with PBS containing 0.1% BSA and 1:20 dilution of normal goat serum. Double immunofluorescence was performed with antomyosin mAb and pp2b polyclonal antiphosphorylated RLC antibody. Primary antibody incubation performed at 37°C for 1 h. After washing in PBS, the secondary antibody was performed at 37°C for 30 min with Texas red–conjugated goat anti–mouse IgM, and Cy5-conjugated donkey anti–rabbit IgG. Immunofluorescence images were taken with ZEISS LSM 510 confocal microscope and ratio of the images performed on MetaMorph 4.5. software.

Online supplemental materials

There are videos relating to Figs. 4–6 available online. Video 1 corresponds to Fig. 4, A–D; Video 2 corresponds to Fig. 4, E–H; Video 3 corresponds to Fig. 5, A–D; Video 4 corresponds to Fig. 5, E–H; and Video 5 corresponds to Fig. 6.

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