Linking Ras to myosin function: RasGEF Q, a Dictyostelium exchange factor for RasB, affects myosin II functions

Subhanjan Mondal, Deenadayalan Bakthavatsalam, Paul Steimle, Berthold Gassen, Francisco Rivero, and Angelika A. Noegel

1Centre for Biochemistry, Institute of Biochemistry I, Medical Faculty and Centre for Molecular Medicine Cologne, University of Cologne, 50931 Cologne, Germany
2Department of Biology, University of North Carolina at Greensboro, Greensboro, NC 27402
3The Hull York Medical School and Department of Biological Sciences, University of Hull, HU6 7RX Hull, England, UK

As guanine nucleotide exchange factor (GEF) Q, a nucleotide exchange factor from Dictyostelium discoideum, is a 143-kD protein containing RasGEF domains and a DEP domain. We show that RasGEF Q can bind to F-actin, has the potential to form complexes with myosin heavy chain kinase (MHCK) A that contain active RasB, and is the predominant exchange factor for RasB. Overexpression of the RasGEF Q GEF domain activates RasB, causes enhanced recruitment of MHCK A to the cortex, and leads to cytokinesis defects in suspension, phenocopying cells expressing constitutively active RasB, and myosin-null mutants. RasGEF Q−/−mutants have defects in cell sorting and slug migration during later stages of development, in addition to cell polarity defects. Furthermore, RasGEF Q−/−mutants have increased levels of unphosphorylated myosin II, resulting in myosin II overassembly. Collectively, our results suggest that starvation signals through RasGEF Q to activate RasB, which then regulates processes requiring myosin II.

Introduction

The actin cytoskeleton is composed of actin, myosin, and several proteins that bind to them and play crucial roles in cell motility, cytokinesis, phagocytosis, and intracellular transport processes (Cooper, 1991; Matsumura, 2005). Coordinated cell movement requires preservative forces generated by polymerization of actin filaments at the leading edge and contractile forces via myosin motors at the rear of a cell. Myosin II, the conventional two-headed myosin, is also the primary motor protein required for cytokinesis in eukaryotes. Dictyostelium discoideum cells lacking MhcA show a plethora of defects, which include cytokinesis defect in suspension when grown on a solid support by a “traction-mediated” mechanism (De Lozanne and Spudich, 1987). These correspond to the localization of myosin at the contractile ring (cleavage furrow) during cytokinesis. MhcA−/− cells have a decreased chemotactic efficiency caused by reduction in cell polarity and an inability to suppress lateral pseudopods and retract the uropod (Wessels and Soll, 1990; Wessels et al., 1988). They also have a developmental defect, halting the developmental process shortly after cells have aggregated. The regulation of myosin II appears to differ between higher and lower eukaryotes.

In D. discoideum phosphorylation of myosin takes place at three threonine residues in the tail region by myosin II heavy chain kinases (MHCKs) (Luck-Vielmetter et al., 1990; Vaillancourt et al., 1988). Phosphorylated myosin is inactive and does not assemble into filaments, whereas unphosphorylated myosin II can spontaneously assemble into bipolar filaments. It is only these filaments that perform cellular myosin II functions (Egelhoff et al., 1993). Significant knowledge about the function of myosin II regulation has been derived from mutant myosin IIs: 3XALA myosin, where the three phosphorylatable threonines have been mutated to alanine, rendering it a poor substrate for MHCKs; and 3XASP myosin, where the three threonines were replaced by aspartate, mimicking the phosphorylated state. 3XALA myosin mutants show significant myosin overassembly in cytoskeletal fractions and form stable myosin II filaments, which accumulate...
in the rear cortex. Cells expressing 3XALA myosin are drastically impaired in cell migration and chemotaxis, making frequent turns and extending lateral pseudopods, which is caused by the inability to disassemble myosin filaments, and these cells have severely affected motility (Egelhoff et al., 1996; Stites et al., 1998; Heid et al., 2004). In contrast, 3XASP myosin does not assemble into bipolar filaments, is nonfunctional in vivo, and fails to complement cytokinesis and developmental defects of myosin II–null cells (Egelhoff et al., 1993).

Signaling pathways based on small GTPases of the Ras family regulate a myriad of cellular processes in eukaryotic cells. The D. discoideum genome encodes a large and varied family of Ras GTPases consisting of 15 Ras proteins. D. discoideum uses its Ras proteins to regulate several pathways controlling cell motility and polarity, cytokinesis, phagocytosis and pinocytosis, and multicellular development (Charest and Firtel, 2007).

D. discoideum expresses at least 25 Ras guanine nucleotide exchange factors (GEFs; Wilkins et al., 2005). However, it does not code for conventional receptor tyrosine kinases (RTKs), which are the major inputs for Ras signaling in higher eukaryotes (Eichinger et al., 2005). Functions of some of the RasGEFs are slowly being understood through mutant analysis. The gefA– (aimless) cells fail to aggregate upon starvation and are unable to synthesize and respond to cAMP (Insall et al., 1996; Kae et al., 2007), showing phenotypic similarities to rasC– cells, indicating that they may act to regulate activation of adenyl cyclase. The cyclic guanosine monophosphate binding proteins GbpC and D, which have RasGEF domains, show altered myosin II localization during chemotaxis (Bosgraaf et al., 2005). Cyclic guanosine monophosphate and GbpC induce myosin II filament formation, but its corresponding Ras GTPase has not been identified. GbpD is thought to activate Rap1 and regulate cell surface adhesion and motility (Kortholt et al., 2006). RasG, the most abundant Ras in vegetative cells and the closest relative to mammalian Ras, is thought to regulate several actin cytoskeleton–based processes like cell polarity and cytokinesis (Tuxworth et al., 1997). RasGEF Q appears to be required for maximal activation of RasG upon response to cAMP (Kae et al., 2007).

In this paper, we have focused on RasGEF Q. Our experiments identify RasB as a substrate for RasGEF Q. They further indicate that RasGEF Q acts upstream of RasB and regulates processes requiring myosin II, like cytokinesis, cell motility, and suppression of lateral pseudopods. Mutants lacking RasGEF Q show myosin overassembly caused by high levels of unphosphorylated myosin II and produce many random pseudopodia. Cells that overexpress the GEF domain of RasGEF Q have constitutively activated RasB, which is normally activated during aggregation upon a cAMP stimulus, and have defects in cytokinesis in suspension as do mhca– cells. Our results also imply an involvement of MHCK A as a downstream regulator of the signaling cascade. We observe that cells that overexpress the GEF domain have higher levels of MHCK A recruited to the cytoskeletal fractions, which occurs when MHCK A is activated in response to cAMP. Furthermore, RasGEF Q is involved in cell sorting and developmental patterning and slug motility.

### Results

#### Domain organization, expression pattern, and functional dissection of RasGEF Q

RasGEF Q, encoded by the gefQ gene, is a 1298-aa protein with a calculated molecular mass of 143,000. Apart from the RasGEF domains, it contains a DEP domain (a domain conserved among fly Dishevelled, worm Egl10, and mammalian Pleckstrin) separating the two RasGEF domains and a predicted coiled-coil region at the N terminus (Fig. 1A). RasGEF Q mRNA as examined by RT-PCR analysis of cDNA is present throughout development with elevated levels during aggregation and the loose mound stage (6–8 h of starvation; Wilkins et al., 2005). Monoclonal antibody K-70-187-1 generated against the DEP domain of RasGEF Q recognized a protein of the expected size, which was present in vegetative cells and in early development till the aggregation stage (6 h) but could not be detected later (Fig. 1B). Instead, a smaller and less intense band was seen at subsequent stages (Fig. 1B, asterisk). The smaller band could arise by translation from a downstream start (ATG) site at position 565. The sequence between both start sites is highly AT rich and could function as an alternative promoter.

To study the localization of RasGEF Q, we expressed RasGEF Q lacking the first 172 aa as a GFP fusion protein (GFP-RasGEF Q173). We observed that in fixed vegetative (Fig. 1C, bottom) and aggregation–competent cells (Fig. 1C, top), GFP-RasGEF Q173 was localized throughout the cytosol but was also enriched in the cortex, colocalizing with actin (Fig. 1C). When living cells expressing GFP-RasGEF Q173 were observed, cells appeared more flat and adhered to the surface, having long filopodia-like protrusions, and the protein was localized throughout the cytosol (Videos 1–4, available at http://www.jcb.org/cgi/content/full/jcb.200710111/DC1). To analyze the functions of different domains of RasGEF Q, we expressed the corresponding GFP fusion proteins in AX2. In fixed cells, the RasGEF domain (GFP-GEF) was present throughout the cytosol but was enriched at the cell cortex and was also present in the nucleus (Fig. 1D, D1, D1, arrowheads). Live cell analysis showed that the protein was present throughout the cells. It was also observed in the nucleus, and in moving cells it accumulated in extending pseudopods (Video 5). Cells expressing GFP-ΔGEF-GEFQ, which corresponds to the N-terminal domain (aa 173–654), distributed throughout the cytoplasm with enrichment in the cortex (Fig. 1D, second row). The DEP domain was present throughout the cytoplasm but did not show a particular enrichment either in fixed or in living cells (Fig. 1D, third row; and Video 6). The GFP fusion protein lacking the DEP domain (GFP-Δ-DEP-GEFQ) localized throughout the cytosol with slight enrichment in the cortical regions (Fig. 1D, fourth row).

#### RasGEF Q association with the actin cytoskeleton

Small GTPases of the Ras superfamily and their regulatory GEFs are known to be directly involved in the regulation of the cytoskeleton. To further investigate the colocalization of GFP-GEF with F-actin in the cortex, we used latrunculin A (LatA),
With the actin cytoskeleton we used 10 μM LatA, which forms 1:1 complexes with actin monomers and inhibits actin polymerization, and 20 μM cytochalasin D, a drug that binds to the growing or barbed end (+ end) of F-actin filaments and prevents addition of G-actin at these sites. Blebbistatin (used at 100 μM) is a drug that blocks the myosin heads and lowers the affinity of myosin for actin (Kovacs et al., 2004). We found that in control cells treated with DMSO (solvent for the drugs), GFP-RasGEF Q173 showed a cytosolic staining and was present in cortical regions of the cell colocalizing with actin. Upon treatment with LatA, the cells rounded up, the typical cortical actin staining was lost, and a patchy pattern appeared. GFP-RasGEF Q173 was present in the cytosol. On treatment with cytochalasin D, we observed the cells rounding up and actin staining in the cortex was fragmented. In this case, GFP-RasGEF Q173 was also seen in the periphery of the cell together with actin. Treatment with Blebbistatin did not alter the cell morphology or the actin staining and GFP-RasGEF Q173 was still enriched in the cell periphery (Fig. 2D). Thus, LatA that disrupts the cortical actin cytoskeleton also affects the localization of GFP-RasGEF Q172 at the cortex. Collectively, our results imply that RasGEF Q associates with F-actin in vitro and in vivo and that the C-terminal region containing the RasGEF domain may mediate this binding.
gefQ/H11002 cells initiate the developmental program, but in >50% of the mounds, multiple tips arise from a single mound by 13–14 h and, as a result, fruiting bodies are smaller than in AX2 (Fig. 3A, middle; and Video 8).

gefQ/H11002 cells formed slugs that were relatively smaller, their ability to move was greatly reduced, and they did not perform phototaxis toward a directed light source. In contrast, slugs from AX2 cells expressing GFP-GEF were able to move and perform phototaxis, but the migration was more disoriented compared with AX2. GFP-GEF slugs migrated at a mean angle of $\pm 80^\circ$, whereas AX2 slugs migrated at a mean angle of 25° toward the light. gefQ$^-$ cells expressing GFP-GEF or GFP-ΔGEF-QEQ showed slightly improved slug motility in phototaxis assays compared with gefQ$^-$ cells. A proportion of RasGEF Q-null cells have defects in developmental patterning and slug motility.

To study the functions of RasGEF Q in vivo we generated cells lacking RasGEF Q. gefQ$^-$ cells were generated by homologous recombination, screened by genomic PCR on genomic DNA, and confirmed by Southern and Western blotting and immunofluorescence analysis (Fig. S1, available at http://www.jcb.org/cgi/content/full/jcb.200710111/DC1). Multicellular morphogenesis can be described in its most basic form as a process where cells in a group undergo coordinated changes in cell shape and motility to form an organized structure to perform a particular function. The process of D. discoideum development is one such example of programmed multicellularization (Chisholm and Firtel, 2004). Involvement of the cytoskeleton in such processes that require continuous cellular changes is a prerequisite. When developed on nutrient-deficient agar plates, AX2 cells form aggregates by 8 h and tipped mounds by 13 h. The tip elongates to form a standing finger that falls down, becoming a migratory slug or pseudoplasmodium by 16 h. Development is completed by 20–24 h with the formation of fruiting bodies (Fig. 3A, top; and Video 7 available at http://www.jcb.org/cgi/content/full/jcb.200710111/DC1).

gefQ/H11002 cells were generated by homologous recombination, screened by genomic PCR on genomic DNA, and confirmed by genomic PCR on genomic DNA, and confirmed by Southern and Western blotting and immunofluorescence analysis (Fig. S1, available at http://www.jcb.org/cgi/content/full/jcb.200710111/DC1). Multicellular morphogenesis can be described in its most basic form as a process where cells in a group undergo coordinated changes in cell shape and motility to form an organized structure to perform a particular function. The process of D. discoideum development is one such example of programmed multicellularization (Chisholm and Firtel, 2004). Involvement of the cytoskeleton in such processes that require continuous cellular changes is a prerequisite. When developed on nutrient-deficient agar plates, AX2 cells form aggregates by 8 h and tipped mounds by 13 h. The tip elongates to form a standing finger that falls down, becoming a migratory slug or pseudoplasmodium by 16 h. Development is completed by 20–24 h with the formation of fruiting bodies (Fig. 3A, top; and Video 7 available at http://www.jcb.org/cgi/content/full/jcb.200710111/DC1). gefQ$^-$ cells initiate the developmental program, but in >50% of the mounds, multiple tips arise from a single mound by 13–14 h and, as a result, fruiting bodies are smaller than in AX2 (Fig. 3A, middle; and Video 8). gefQ$^-$ cells formed slugs that were relatively smaller, their ability to move was greatly reduced, and they did not perform phototaxis toward a directed light source. In contrast, slugs from AX2 cells expressing GFP-GEF were able to move and perform phototaxis, but the migration was more disoriented compared with AX2. GFP-GEF slugs migrated at a mean angle of $\pm 80^\circ$, whereas AX2 slugs migrated at a mean angle of 25° toward the light. gefQ$^-$ cells expressing GFP-GEF or GFP-ΔGEF-QEQ showed slightly improved slug motility in phototaxis assays compared with gefQ$^-$ cells. A proportion of

RasGEF Q-null cells have defects in developmental patterning and slug motility.

To study the functions of RasGEF Q in vivo we generated cells lacking RasGEF Q. gefQ$^-$ cells were generated by homologous recombination, screened by genomic PCR on genomic DNA, and confirmed by Southern and Western blotting and immunofluorescence analysis (Fig. S1, available at http://www.jcb.org/cgi/content/full/jcb.200710111/DC1). Multicellular morphogenesis can be described in its most basic form as a process where cells in a group undergo coordinated changes in cell shape and motility to form an organized structure to perform a particular function. The process of D. discoideum development is one such example of programmed multicellularization (Chisholm and Firtel, 2004). Involvement of the cytoskeleton in such processes that require continuous cellular changes is a prerequisite. When developed on nutrient-deficient agar plates, AX2 cells form aggregates by 8 h and tipped mounds by 13 h. The tip elongates to form a standing finger that falls down, becoming a migratory slug or pseudoplasmodium by 16 h. Development is completed by 20–24 h with the formation of fruiting bodies (Fig. 3A, top; and Video 7 available at http://www.jcb.org/cgi/content/full/jcb.200710111/DC1). gefQ$^-$ cells initiate the developmental program, but in >50% of the mounds, multiple tips arise from a single mound by 13–14 h and, as a result, fruiting bodies are smaller than in AX2 (Fig. 3A, middle; and Video 8). gefQ$^-$ cells formed slugs that were relatively smaller, their ability to move was greatly reduced, and they did not perform phototaxis toward a directed light source. In contrast, slugs from AX2 cells expressing GFP-GEF were able to move and perform phototaxis, but the migration was more disoriented compared with AX2. GFP-GEF slugs migrated at a mean angle of $\pm 80^\circ$, whereas AX2 slugs migrated at a mean angle of 25° toward the light. gefQ$^-$ cells expressing GFP-GEF or GFP-ΔGEF-QEQ showed slightly improved slug motility in phototaxis assays compared with gefQ$^-$ cells. A proportion of
the slugs formed could migrate toward the light source, although migration was greatly reduced, indicating that RasGEF Q is important for slug motility (Fig. 3 B).

*D. discoideum* serves as a model system to understand cell sorting. At the mound stage, an asymmetry is established and a fixed proportion of cell types is generated where the majority of the cells (nearly 80%) are destined to become spore cells and sort to the rear of a slug and 20% occupy the anterior tip, becoming the stalk cells that hold the spore mass in the fruiting body. Involvement of a particular protein in such cell-sorting mechanisms can be easily studied in *D. discoideum* by mixing strains together and allowing them to codevelop as a chimera. When 10% GFP-expressing AX2 cells was mixed with 90% unlabeled AX2 cells, GFP-labeled cells distributed evenly throughout the slug. However, when 10% GFP-labeled AX2 cells was mixed with 90% unlabeled AX2 cells, wild-type cells localized to the anterior prestalk region and mutants were present in the posterior prespore region of the slug. In a converse experiment where 10% GFP-labeled *gefQ* cells was mixed with 90% AX2 cells, mutant cells also sorted to the posterior (Fig. 3 C).

**Figure 3. Developmental defects in RasGEF Q-null cells (gefQ*).** (A) Development of *gefQ* cells plated on nonnutrient agar. The top shows wild-type tipped aggregate (13 h), migratory slug (16 h), and fruiting body (24 h). The middle shows that *gefQ* aggregates break up into smaller aggregates (13 h), multiple tipped structures (16 h), and fruiting bodies (24 h). The bottom shows development of cells overexpressing GFP-GEF. Bars, 200 μm. (B) Altered slug motility in phototaxis assays in *gefQ* and GFP-GEF-expressing cells. Wild-type AX2, GFP-GEF expressing AX2, and *gefQ* cells, as well as *gefQ* cells expressing GFP-GEF or GFP-ΔGEF-GEFQ, were allowed to develop on phosphate agar plates placed in a black opaque box for 36 h with a unidirectional light source from an open slit. Migratory pattern of slugs were determined by transferring slime trails and cellular materials onto nitrocellulose membrane. Membranes were stained with 0.1% amido black. (C) Altered cell-type spatial patterning in *gefQ* mutants. (a) 10% AX2 cells labeled with GFP was mixed with 90% unlabeled wild-type cells. (b) 10% labeled wild-type cells was mixed with 90% unlabeled *gefQ* cells. (c) 10% labeled *gefQ* cells was mixed with 90% AX2 cells and were codeveloped as a chimera. Images were taken at the slug stage using a fluorescent microscope (Leica DMR) at 5× magnification. Imaging medium was air at 22°C. Images were acquired with a camera (DC 350 FX; Leica). Bar, 200 nm.

Cytokinesis defect in suspension in cells overexpressing GFP-GEF and constitutively activated RasB

Further analysis revealed that the cells expressing GFP-GEF were defective in cytokinesis in suspension. When grown in suspension for 6 d, they attain a mean nuclei number of approximately six nuclei per cell, whereas wild-type AX2 and *gefQ/H11002* cells are mostly mono- or binucleated (Fig. 4, A and B). However, when grown on a plastic surface, GFP-GEF cells are predominantly mono- or binucleated, probably dividing by traction-mediated cytofission as occurs in *mhcA* cells (De Lozanne and Spudich, 1987; Neujahr et al., 1997).

Our results indicate that although karyokinesis is normal in GFP-GEF cells, the following cytokinesis is impaired. We also confirmed previous data on the localization and phenotype of cells expressing constitutively activated RasB (*RasB<sup>G12T</sup>, Sutherland et al., 2001). Overexpression of GFP-tagged *RasB<sup>G12T</sup>* caused cells to become multinucleated in suspension. The protein was slightly enriched in the nucleus (Fig. 4 C). Because overexpressors of the GEF domain and overexpressors of *RasB<sup>G12T</sup>* had phenotypic similarities, we hypothesized that RasGEF Q could be
Figure 4. Cells overexpressing GFP-GEF and constitutively activated RasB have a cytokinesis defect. (A) Cytokinesis is normal in wild-type AX2 and gefQ-/H11002 cells but is defective in GFP-GEF cells. Images were taken using a fluorescent microscope (DMR). Images were acquired with a camera (DC 350 FX). (B) The increase in the number of nuclei in GFP-GEF cells. GFP-GEF cells were grown in suspension, fixed at the indicated times, stained with DAPI, and the nuclei were counted. The data are the mean of three independent determinations ± SD. (C) Cytokinesis defect in cells overexpressing constitutively activated RasB(GFP-RasBCA; green). Cells were fixed with methanol and nuclei are visualized with DAPI (blue). Arrowheads indicate multinucleated cells. Images were taken using a fluorescent microscope (DMR). Images were acquired with a camera (DC 350 FX). Bars, 10 μm.

Figure 5. RasB activation by RasGEF Q and during development. (A) Physical association of GST-GEF and RasB. Glutathione Sepharose beads could precipitate RasB from AX2 cell lysates (Fig. 5 A). When cell lysates were pretreated with 100 μM GDP or 100 μM GTPγS, we found that GST-GEF bound preferentially to the GDP-bound form of RasB (Fig. 5 B), which is the preferred form for a RasGEF–Ras interaction. To determine if RasGEF Q actually activates RasB, we used GST-Byr2 Ras binding domain (RBD) to pull down GTP-bound active RasB from AX2, gefQ-/H11002, or GFP-GEF cells. Schizosaccharomyces pombe Byr2 is a Ras effector (MAPK/ERK kinase homologue) and binds to Ras in its activated (GTP-bound) form (Gronwald et al., 2001; Scheffzek et al., 2001). Cell lysates of AX2 and gefQ- at the growth (0 h) and aggregation (6 h) stage and GFP-GEF at 0 h were incubated with equal amounts of GST-Byr2(RBD) bound to glutathione Sepharose beads. We found that RasB is activated at 6 h in AX2 cells, whereas gefQ- cells are unable to activate RasB at either 0 or 6 h. GFP-GEF cells at 0 h have a high level of activated RasB, indicating that RasGEF Q acts as an exchange factor for RasB (Fig. 5 C). Expression of the GEF domain alone may act as a constitutively activated form of RasGEF Q. Our results also indicate that, although RasB is expressed throughout development (Daniel et al., 1993), it is activated upon starvation, thus implying a role for cAMP in its activation process. Because RasB is not activated in gefQ- cells, we can conclude that it is the only or the predominant exchange factor for RasB.

RasB is activated upon cAMP stimulation

To test whether RasB is activated upon response to cAMP, we used a GST-Byr2(RBD) to pull down activated Ras from cell lysates stimulated with cAMP. We observed an elevation in the levels of activated RasB within 10 s of stimulation with cAMP and decreasing by 60 s (Fig. 5 D, top). In a similar experiment using gefQ- cells expressing GFP-Δ-GEF-GEFQ, which also lacks the DEP domain, we saw no activation of RasB upon cAMP, further indicating that RasGEF Q is required for RasB activation (Fig. S2, available at http://www.jcb.org/cgi/content/full/jcb.200710111/DC1). We also observed that in cells...
overexpressing the DEP domain, the RasB activation was greatly reduced and delayed (Fig. 5 D, bottom). As overexpression of the GEF domain acts as a constitutively activated form of RasGEF Q, the DEP domain that resides between the RasGEF domains might serve as a possible autoregulatory domain in the activation process of RasGEF Q. Further on, in a GST pull-down experiment, GST-DEP could pull down GFP-GEF from cell lysates of cells overexpressing GFP-GEF, indicating that the two domains can physically interact (Fig. 5 E). To further test whether the DEP domain acts as an autoregulatory domain, we used AX2 cells expressing GFP-Δ-DEP-GEFQ, which is specifically lacking the DEP domain, and determined the amount of activated RasB in growing cells using GST-Byr2–coated beads. Cells overexpressing GFP-Δ-DEP-GEFQ have activated RasB even at the vegetative state, which is similar to cells expressing the GEF domain alone, further supporting that the DEP domain has autoregulatory functions in the protein (Fig. 5 F).

Role of RasGEF Q in regulating myosin II function

Defects in Ras pathways result in chemotaxis defects (Sasaki and Firtel, 2005, 2006; Charest and Firtel, 2006). To examine whether RasGEF Q had any effect on chemotactic-induced cell migration, we compared the migration of aggregation-competent gefQ− and parental AX2 cells. During migration toward an exogenous CAMP source, wild-type cells are well polarized and produce pseudopodia exclusively at the leading edge and very few lateral pseudopods. In contrast, gefQ− cells produce more random pseudopodia (4.6 per cell per 10 min) than wild-type cells (1.7 per cell per 10 min; Table I) and have an increased frequency of turning (Fig. 6, A and B; and Videos 9 and 10, available at http://www.jcb.org/cgi/content/full/jcb.200710111/DC1), showing similarities to 3XALA myosin mutants. Surprisingly, the cell motility parameters (speed, persistence, and direction change) were not significantly altered (Table II).

In chemotaxing cells, myosin II typically localizes to the posterior cortical regions of polarized cells, where it is required for retraction of the cell body and suppression of lateral pseudopods. When we stained gefQ− cells for myosin, we observed an increased myosin staining in the cortex that was not restricted to the rear and also an elevated myosin level throughout the cytoplasm (Fig. 7 A). To test this further, we measured the amounts of myosin II present in preparations of cytoskeletal ghosts of gefQ− and AX2 cells both from growing and aggregation-competent stages. In this assay, the amount of myosin II recovered reflects the amount of filamentous myosin associated with the actin cytoskeleton in the living cell. Myosin II filament assembly and disassembly is an extremely dynamic process and, in D. discoideum, it depends largely on the levels of myosin heavy chain phosphorylation. Also, the level of myosin II in the cytoskeletal fractions in AX2 cells is significantly higher in aggregation-competent cells than in growing cells. In contrast, gefQ− cells had a high level of myosin II in the cytoskeletal fractions obtained from growing cells, which was comparable to that in aggregating AX2 cells, and there was no significant rise upon reaching aggregation competence (Fig. 7 B, top). Total myosin II levels in both AX2 and gefQ− cells were comparable in vegetative and aggregation-competent cells (Fig. 7 B, bottom).

The cause for higher levels of filamentous myosin II in gefQ− cells could be because of higher levels of unphosphorylated myosin II that can spontaneously form filaments. To test this hypothesis, we determined the phosphorylation status of myosin II in vegetative AX2 and gefQ− cells. We used 2D gel electrophoresis to examine the changes in the isoelectric point (pI) of phosphorylated versus unphosphorylated myosin II. We observed myosin II as a distinct spot in a Western blot using myosin II antibodies. We found that in gefQ− cells, myosin II had a higher pI than myosin II in AX2 cells, implying that in gefQ− cells, myosin was predominantly in the unphosphorylated state (Fig. 7 C). From these results, we conclude that the higher levels of unphosphorylated myosin II in gefQ− cells lead to higher levels of filamentous myosin II and involve MHCKs in the process.

RasGEF Q regulates Myosin II through MHCK A

The presence of higher amounts of unphosphorylated myosin II in gefQ− cells indicated that probably myosin phosphorylation is affected. MHCK A is a major kinase regulating myosin II phosphorylation. In GST pulldown experiments, we found that GST-GEF could coprecipitate myosin II and MHCK A from cell lysates under conditions that dissociate actin–myosin complexes by the addition of 5 mM ATP. Actin was absent from the precipitate. When cell lysates were preincubated with LatA to

Table I. Lateral pseudopod formation by cells crawling in buffer and in a spatial cAMP gradient

<table>
<thead>
<tr>
<th>Cell strain</th>
<th>Number of cells</th>
<th>0–2 lateral pseudopods per 10 min</th>
<th>3–5 lateral pseudopods per 10 min</th>
<th>&gt;5 lateral pseudopods per 10 min</th>
<th>Mean frequency of lateral pseudopods per cell per 10 min</th>
</tr>
</thead>
<tbody>
<tr>
<td>Buffer</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AX2</td>
<td>31</td>
<td>9.6</td>
<td>45.16</td>
<td>45.16</td>
<td>5.19</td>
</tr>
<tr>
<td>gefQ−</td>
<td>33</td>
<td>0</td>
<td>21.21</td>
<td>78.78</td>
<td>7.03</td>
</tr>
<tr>
<td>cAMP gradient</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AX2</td>
<td>35</td>
<td>82.85</td>
<td>17.14</td>
<td>0</td>
<td>1.71</td>
</tr>
<tr>
<td>gefQ−</td>
<td>29</td>
<td>6.9</td>
<td>65.5</td>
<td>27.50</td>
<td>4.65</td>
</tr>
</tbody>
</table>

Images were taken at a magnification of 40× every 6 s. In all cases, cells were analyzed for 10 min. χ² test, performed between AX2 and gefQ− cells on data of the three categories of lateral pseudopods formed, showed highly significant (P > 0.001) difference between AX2 and gefQ− cells in both buffer and a cAMP gradient.
analyzed the amounts of MHCK A associated with cytoskeletal fractions, as the cytoskeleton-associated protein represents the active autophosphorylated form of MHCK A. We found that gefQ/H11002 cells and AX2 cells have similar amounts of MHCK A associated with the cytoskeletal fractions. In contrast, cells overexpressing the GEF domain had at least twofold higher levels of MHCK A associated with the cytoskeletal fractions (Fig. 8 B).

To investigate if activated Ras could transduce signals for regulation of myosin II, we used the GST-Byr2(RBD) to pull down active Ras from GFP-GEF cells at 6 h and found MHCK A in pulldown eluates with active RasB (Fig. 8 C). Pulldown eluates did not contain myosin II. Thus, MHCK A, which directly regulates myosin II phosphorylation, may either bind directly to active Ras or associate with complexes containing active Ras, suggesting that it might be regulated by Ras upon activation.

disrupt the cytoskeleton, the association with myosin II and MHCK A was totally abolished (Fig. 8 A). These results indicate that an intact cytoskeleton is required for bringing a signaling complex together, where RasGEF Q can bind to MHCK A and myosin II in an F-actin-dependent manner.

We then examined MHCK A in gefQ− cells and in cells overexpressing GFP-GEF. Under normal conditions, MHCK A is localized throughout the cytosol. Upon chemoattractant stimulation, MHCK A associates with the cytoskeleton and localizes to the cell cortex (Steimle et al., 2001). Association with the actin cytoskeleton causes a drastic increase in the autophosphorylation activity of MHCK A, which is then activated (Egelhoff et al., 2005). Using a monoclonal antibody that detects both the phosphorylated (~145 kD) and unphosphorylated (130 kD) forms of MHCK A (Steimle et al., 2001), we found that gefQ− cells and cells overexpressing GFP-GEF have both unphosphorylated and autophosphorylated MHCK A. We then analyzed the amounts of MHCK A associated with cytoskeletal fractions, as the cytoskeleton-associated protein represents the active autophosphorylated form of MHCK A. We found that gefQ− cells and AX2 cells have similar amounts of MHCK A associated with the cytoskeletal fractions. In contrast, cells overexpressing the GEF domain had at least twofold higher levels of MHCK A associated with the cytoskeletal fractions (Fig. 8 B).

Figure 6. Chemotactic behavior of gefQ− cells. (A) Computer-generated cell tracks of gefQ− and AX2 cells during chemotactic migration in a spatial cAMP gradient using DIAS. Arrowheads indicate turns initiated by formation of lateral pseudopods in gefQ− cells. (B) Shape changes of aggregation-competent gefQ− and AX2 cells during chemotactic migration were analyzed by DIAS. Images were taken every 6 s but only every third frame is shown. The green areas indicate new membrane protrusions, the red areas indicate retractions, and the arrows indicate the direction of migration.

Published June 2, 2008
In the next section, we explore the role of RasGEF Q in regulating myosin II functions. Our studies on RasGEF Q reveal that it is required for regulation of myosin II–based cellular functions, like cytokinesis and cell shape during chemotaxis, and also affects late developmental decisions. We provide evidence for RasB being a substrate for RasGEF Q and propose that regulation of myosin II functions by RasGEF Q occurs predominantly through RasB. Cells lacking RasGEF Q show myosin II overassembly associated with the inability to suppress lateral pseudopods, which is similar to that observed in 3XALA myosin II mutants. We show that the myosin overassembly is caused by higher levels of unphosphorylated myosin II in these cells, so the defect in myosin phosphorylation might arise from an inability to activate MHCKs. Cells that overexpress the GEF domain of RasGEF Q have a cytokinesis defect in suspension, and these cells also have high levels of constitutively activated RasB. We identified RasB as the substrate for RasGEF Q through in vivo and in vitro binding assays and found that RasB is activated upon cAMP, which indicates an involvement of cAMP and cAMP receptors (seven transmembrane G protein–coupled receptors [GPCRs]) in the process of activation.

We note that RasGEF Q associates with F-actin. The C-terminal region containing the catalytic GEF domain is a possible region involved in F-actin association. The cortical localization of both GFP-RasGEF Q173 and GFP-GEF are sensitive to Latrunculin A, indicating that an intact cytoskeleton is required for localization of RasGEF Q to the cortex. We also note that RasGEF Q can associate with myosin II and MHCK A, which is also sensitive to Latrunculin A. These results indicate that the F-actin cytoskeleton acts as a scaffold to recruit the signaling complex and that when the F-actin network is disassembled the signaling components do not meet. Myosin II is an F-actin cross-linking protein and, upon a cAMP stimulus, MHCK A localizes to the cell cortex with the help of F-actin. At this point when all the signaling components are assembled, it is critical for RasGEF Q to be in its active state to elicit downstream effects. Signaling components like RasGEFs are active only temporarily, the activation has to be appropriately controlled, and the downstream signals are amplified by orders of magnitude. It is likely that RasGEF Q is active for a very short time after a cAMP stimulus only.

We ruled out the possibility that RasGEF Q might activate RasG, another Ras isoform. Cells lacking RasG show a cytokinesis defect (Tuxworth et al., 1997), whereas in cells in which overexpress the GEF domain of RasGEF Q resulting in constitutively high levels of active Ras, we see a cytokinesis defect and, thus, activation of RasG might be independent of RasGEF Q. We also provide a function for the less well understood function of the DEP domain in RasGEF Q, as our results point to the DEP domain
MhckA mediate regulators of myosin II are MHCKs. GST-GEF can associate through MHCK A. GST-GEF can associate with myosin II and MHCK A in a manner that is sensitive to Lat A treatment. (B) Cytoskeletal fractions from wild-type AX2, AX2 cells overexpressing GFP-GEF, and gefQ cells were prepared as described in Materials and methods. Supernatant and pellet fractions were resolved by SDS-PAGE and immunoblotted using MHCK A–specific monoclonal antibody. The graph below represents the mean of two independent experiments and shows the amount of MHCK A present in the pellet fractions as the percentage of the total MHCK A content. (C) Presence of MHCK A in fractions containing active RasB. Active RasB was pulled down from GFP-GEF (6 h) cells using GST-Byr2[RBD]. The precipitates were tested for the presence of MHCK A and myosin II heavy chain.

Figure 8. RasGEF Q regulates myosin II through MHCK A. (A) GST-GEF can associate with myosin II and MHCK A in a manner that is sensitive to Lat A treatment. (B) Cytoskeletal fractions from wild-type AX2, AX2 cells overexpressing GFP-GEF, and gefQ cells were prepared as described in Materials and methods. Supernatant and pellet fractions were resolved by SDS-PAGE and immunoblotted using MHCK A–specific monoclonal antibody. The graph below represents the mean of two independent experiments and shows the amount of MHCK A present in the pellet fractions as the percentage of the total MHCK A content. (C) Presence of MHCK A in fractions containing active RasB. Active RasB was pulled down from GFP-GEF (6 h) cells using GST-Byr2[RBD]. The precipitates were tested for the presence of MHCK A and myosin II heavy chain.

The GEF domain of RasGEF Q has the ability to coprecipitate MHCK A and myosin II in an F-actin–dependent manner. In accordance with the fact that RasGEF Q regulates myosin II functions by regulating MHCK A, we observed that cells overexpressing the GEF domain have a twofold higher level of MHCK A associated with cytoskeletal fractions. This is the result of MHCK A activation by autophosphorylation, whereupon it associates with the actin cytoskeleton in aggregation-competent cells that are stimulated with cAMP (Steimle et al., 2001). Thus, overexpression of the GEF domain causes larger amounts of MHCK A to be activated. In contrast, MHCK A distribution in cytoskeletal fractions is normal in gefQ cells, indicating that RasGEF Q plays a role in facilitating MHCK A recruitment to the cytoskeleton and that other (probably passive) processes are important for returning the kinase to the cytosol. Furthermore, the C terminus of RasGEF Q, which harbours the GEF domain, has the potential to bind to F-actin directly in F-actin cosedimentation assays. These results also suggest that acting as an autoregulatory domain of RasGEF Q. Under vegetative conditions when RasB is not activated, the DEP domain can bind to the GEF domain and RasGEF Q is in an inactive conformation. Upon starvation, GPCRs can induce a conformational change upon cAMP binding whereby the DEP domain inhibition is released and, thus, GPCRs activate RasGEF Q, which activates RasB.

We observed that myosin in gefQ cells has a higher pI, possibly because of higher levels of unphosphorylated myosin II. A higher level of unphosphorylated myosin II is the cause of myosin overassembly in the cortex in gefQ cells. This also implies a role of MHCK A in the process. In D. discoideum, the most immediate regulators of myosin II are MHCKs. D. discoideum has four MHCKs (A–D), among which MHCK A has been most extensively studied. MhckA cells exhibit a partial, but significant, level of myosin II overassembly because of higher levels of unphosphorylated myosin II. Overexpression of MHCK A elicits defects comparable to those observed in myosin II–null cells, namely a blocked cytokinesis in suspension and arrested development in the mound stage (Kolman et al., 1996). In chemotaxing cells, MHCK A relocates to the actin rich cortex in the anterior of the cell, where it presumably functions to phosphorylate and disassemble myosin II at the leading edge (Steimle et al., 2001).

The process of D. discoideum development is an example of programmed multicellularization (Chisholm and Firtel, 2004), where cells that form and organize the multicellular organism undergo continuous coordinated changes in shape and motility that require the cytoskeleton. D. discoideum tip formation is an event that can serve as a model to understand similar developmental processes in other organisms. Normally, only one tip arises from a mound and this apical tip serves as an organizer to control morphogenesis of the organism by acting as a cAMP oscillator from which waves are initiated and propagated posteriorly (Siegert and Weijer, 1992; Siegert and Weijer, 1995). Mounds from gefQ cells give rise to supernumerary tips and, as a result, smaller fruiting bodies are formed. Besides gefQ cells, mutations in other components of signal transduction cascades lead to similar defects. A defect in Scar, a WASP-related protein identified in a mutant screen which suppresses phenotypes of cAR2 cells, also leads to a multiple-tipped phenotype (Bear et al., 1998) as well as overexpression of an activated RasB(G12T) (Reymond et al., 1986). Similarly, a double knockout
of two isoforms of phosphatidylinositol-3-kinase (PI3K1/2) and overexpression of the phosphotyrosine phosphatase PTP1 also resulted in the multiple-tip phenotype (Howard et al., 1992; Zhou et al., 1995).

Multiple tips arising from gefQ mounds may result from the formation of more than one oscillator (or embryonic organizer). It is also possible that a single embryogenic organizer subdivides to form multiple organizers, causing the multiple-tip phenotype. The tip of the slug is also critical in sensing light and cells were allowed to develop to the migratory slug stage. Slime trails and cellular material were transferred onto a nitrocellulose membrane. Membranes were stained with staining solution (0.1% amido black in 20% isopropanol and 10% acetic acid) for 15 min, destaining solution (20% isopropanol and 10% acetic acid) for 15 min, washed with water, and air dried.

For development in chimeras, gefQ cells and wild-type cells were transfected with pBsr-GFP for expression of GFP to mark the different cell types. 90% wild-type cells was mixed with 10% gefQ cells expressing GFP or 90% gefE cells was mixed with 10% GFP-expressing wild-type cells and allowed to codevelop. For control 10% GFP-expressing wild-type cells was mixed with 90% wild-type cells. Images were taken at the slug stage using a fluorescent microscope (DMR; Leica).

Generation of gefQ cells and cells expressing RasGEF Q domains

For generation of the knockout vector, cDNA clone SLH890 (procured from the D. discoideum cDNA project, Tsukuba, Japan) encompassing nt 1798–3987 of gefQ cloned in pSPORT (Invitrogen) was used. The plasmid was digested with BsaB1 to release a 55-kb fragment and the neomycin resistance cassette (Witke et al., 1987) was inserted by blunt end ligation. The resulting replacement vector was linearized by digesting with Sall and transformed into AX2 by electroporation. Transformants were selected in nutrient medium containing 7 μg/ml G418. Independent clones were screened for the disruption of the gefQ gene by PCR using genomic DNA, Southern blotting, immunofluorescence, and Western blot analysis. For Southern blot analysis, a probe encompassing nt 690–990 of the cDNA was used.

For expression of RasGEFQ<sup>173</sup>, a fragment encoding the protein from aa 173–1298 was cloned into pDex79 and expressed as a GFP fusion protein in AX2 cells. For expression of the N-terminal fragment ΔGEFQ fused to GFP at its N terminus, a 1.4-kb fragment encoding aa residues 172–654 was cloned into pBsr (Mohrs et al., 2000). For expression of the DEP domain as a GFP-tagged protein fused at the N terminus, a 450-bp fragment encoding residues 683–833 was cloned into pBsr. For expression of RasGEFQ<sup>173</sup> and RasGEFQ<sup>173</sup> cells and cells expressing RasGEF Q domains

For generation of the knockout vector, cDNA clone SLH890 (procured from the D. discoideum cDNA project, Tsukuba, Japan) encompassing nt 1798–3987 of gefQ cloned in pSPORT (Invitrogen) was used. The plasmid was digested with BsaB1 to release a 55-kb fragment and the neomycin resistance cassette (Witke et al., 1987) was inserted by blunt end ligation. The resulting replacement vector was linearized by digesting with Sall and transformed into AX2 by electroporation. Transformants were selected in nutrient medium containing 7 μg/ml G418. Independent clones were screened for the disruption of the gefQ gene by PCR using genomic DNA, Southern blotting, immunofluorescence, and Western blot analysis. For Southern blot analysis, a probe encompassing nt 690–990 of the cDNA was used.

For expression of RasGEFQ<sup>173</sup>, a fragment encoding the protein from aa 173–1298 was cloned into pDex79 and expressed as a GFP fusion protein in AX2 cells. For expression of the N-terminal fragment ΔGEFQ fused to GFP at its N terminus, a 1.4-kb fragment encoding aa residues 172–654 was cloned into pBsr (Mohrs et al., 2000). For expression of the DEP domain as a GFP-tagged protein fused at the N terminus, a 450-bp fragment encoding residues 683–833 was cloned into pMCS (Weber et al., 1999). The same fragment was recloned into pGEX-4T1 (GE Healthcare) for expression of GST-DEP in bacteria. For expression of the C-terminal domain containing the catalytic GEF domain as a GFP fusion fused at the N terminus, a 1.2-kb fragment encoding residues 910–1298 was cloned into pMCS. The same fragment was recloned into pGEX-4T1 for expression of GSTGEF in bacteria. A construct lacking the DEP domain [GFP-ΔDEP-GEFQ] was generated by digesting pDex79/GFPΔrasGEFQ<sup>173</sup> with NaeI and Sall and ligating it with a PCR-amplified fragment encoding aa 818–1298 preserving the NaeI site. The resulting plasmid, which lacks the DEP domain, was introduced into AX2 cells. Cells lacking myosin heavy chain can aggregate but fail to proceed beyond the mound stage of development. The regulatory light chain of myosin has also been thought to be required for directional sorting of prestalk EcmAO cells at the tip of a developing mound (Clow et al., 2000). Although RasGEF Q transcripts are present throughout development, a protein of higher molecular mass is present in the first 6 h of development and a smaller isoform generated by an alternative promoter is present in low amounts during later stages of development. This smaller form of the protein might have functions in regulating processes in late development.
Generation of RasGEF Q monoclonal antibodies

The procedure used to generate RasGEF Q monoclonal antibodies was as described previously (Schleicher et al., 1984). The DEP domain of RasGEF Q (residues 683–833) was used for immunization of four female BALB/c mice (Lingnau et al., 1996). mAbs K-70-187-1 and K-70-102-1 were used in this study. They recognize a protein of 143 kD in whole cell homogenates of wild-type Ax2 cells, which is absent in gefQ cells.

Actin binding assay

All purified proteins used in the study were clarified by centrifugation at 120,000 g for 60 min at 4°C. D. discoideum actin was isolated as described previously (Haugwitz et al., 1991). Actin sedimentation assays were performed as described previously (Jung et al., 1996). In brief, 5 μM G-actin was polymerized in the presence or absence of 60 μg/μl 1 μM GST-GEF or 20 μg/μl 1 μM GST by addition of 0.1 vol of 10x polymerization buffer (100 mM imidazol, pH 7.6, 20 mM MgCl₂, 10 mM EGTA, 1 M KCl, and 5 mM ATP) for 30 min at room temperature. The final reaction volume was 70 μl. Binding to F-actin was determined by high-speed centrifugation at 120,000 g for 1 h at 4°C. Cross-linking of filaments was analyzed by low-speed centrifugation at 12,000 g for 1 h at 4°C. Equal amounts of pellet and supernatant were resolved by SDS-PAGE (10% acrylamide) and proteins were visualized by Coomassie brilliant blue staining.

In vitro binding assays with GST fusion protein and analysis of cAMP-induced activation of RasB

For interaction with cytoskeletal proteins, 5 × 10⁷ AX2 cells were lysed in lysis buffer (LB, 25 mM Tris/HCl, pH 7.5, 150 mM NaCl, 5 mM EDTA, 0.5% Triton X-100, and 1 mM DTT, supplemented with protease inhibitors (Sigma-Aldrich) with 5 mM ATP added) with or without a preincubation with 10 μM Lat A (Sigma-Alrichr) and incubated with equal amounts of GSTGEF-bound beads for 3 h at 4°C. Beads were washed with wash buffer (25 mM Tris/HCl, pH 7.5, 150 mM NaCl, and 5 mM EDTA) and the pulldown eluates were analyzed in Western blots. Monoclonal antibodies recognizing actin (Simpson et al., 1984) or myosin II (Pagh and Gerisch, 1986) and a polyclonal antibody against MHCK A (provided by T. Engelhoff, Case Western Reserve University, Cleveland, OH; Kolman et al., 1996) were used.

For interaction of GST-GEF with RasB, 5 × 10⁷ AX2 cells were lysed by sonication in LB without Triton X-100 and membrane and nuclear-enriched pellet fraction separated by centrifugation at 100,000 g for 30 min at 4°C. The pellet fraction was resuspended in LB containing 1% Triton X-100. The pellet down-formation was described as the interaction of GST-GEF with cytoskeletal proteins. For analysis of binding preference of GST-GEF for GTP- or GDP-bound RasB, cell lysates from 5 × 10⁷ AX2 cells were lysed in 1 ml LB. One 1-ml aliquot was pretreated with 100 μM GDP and 5 mM MgCl₂, and another one with 100 μM GTP-7S and 5 mM MgCl₂ for 1 h, and the pulldown reaction was done as described for the interaction of GST-GEF with cytoskeletal proteins. Eluates were probed with RasB-specific polyclonal antibodies (provided by G. Weeks, University of British Columbia, Vancouver, Canada; Sutherland et al., 2001).

Activation of RasB was assayed by performing pulldown with beads coated with the GST-fused Ras binding domain of S. pombe Byr2 (supplied by G. Praefcke, University of Cologne, Cologne, Germany; Granwald et al., 2001; Scheffzek et al., 2001). 5 × 10⁷ AX2 and gefQ cells were harvested at the vegetative stage and aggregation-competent (6 h) stages and GFP-GEF-expressing cells were harvested at the vegetative stage. Cells were lysed in LB and incubated with equal amounts of GST-Byr2-bound beads. Pulldown eluates were immunoblotted and probed with RasB antibody.

CAMP-induced activation of RasB in aggregation-competent AX2 cells was done according to Kae et al. (2004). Cells were stimulated with 500 nM cAMP for 10 min. The samples were spun at 100,000 g for 4 min. Supernatants were discarded and pellet fractions washed once with NP-40 buffer. The pellet fractions were dissolved in 2× SDS-PAGE sample buffer (Laemml, 1970) and proteins resolved by SDS-PAGE (% acrylamide) and visualized by Coomassie brilliant blue staining. Protein bands were scanned and changes in myosin II content in the cytoskeleton quantified using Image J software (National Institutes of Health). For isolation of cytoskeletal fractions for analyzing MHCK A, 1.5 × 10⁷ cells were lysed in containing 0.1 M MES pH 6.8, 2.5 mM EGTA, 5 mM MgCl₂, 0.5 mM ATP, and 0.5% Triton X-100, supplemented with protease inhibitors, briefly vortexed, and then spun at 100,000 g for 1 min. Supernatant fractions were precipitated with acetone. Pellet and supernatant fractions were resolved by SDS-PAGE and immunoblotted using MHCK A-specific monoclonal antibody (Steine et al., 2001). The level of MHCK A in both the pellet and supernatant fractions was quantified by densitometric analysis of the scanned blot using Image J. The percentage of MHCK A in the pellet fraction was determined by dividing the value obtained for the band in the pellet by the total from the bands in the pellet and supernatant. Preparation of cytoskeletal fractions using saponin was done using a buffer containing 50 mM Tris/HCl, pH 7.6, 100 mM NaCl, 10 mM NaF, 1 mM EDTA, 1 mM EGTA, 2% Saponin, 10% glycerol, and 1 mM DTT, supplemented with protease inhibitors (de Curtis and Malachnich, 1997).

Analysis of cell shape and migration

Aggregation-competent AX2 and RasGEF Q- cells were plated onto glass coverslips and allowed to settle for 15 min in Soerensen phosphate buffer and melaninex experiments were performed with microinjected cells filled with 10⁻⁴ M CAMP attached to a micromanipulator system at 22°C. The micropipette tip was carefully moved to touch the surface of the glass coverslip. Images were recorded at intervals of 6 s using an inverse microscope (40x objective; DML; Leica) and a conventional charge-coupled device video camera using OPTIMAS 6.0 software (Optimas Corporation) and analyzed using Dynamic Image Analysis software (DIAAS, Solar Technologies; Wessels et al., 1998).

2D SDS-PAGE

2D gel electrophoresis was performed using an adaptation of previously described protocols (Clemen et al., 2005). D. discoideum cells were lysed in lysis buffer (7 M urea, 2 M thiourea, 4% CHAPS, 40 mM Tris, 2% IGF buffer, 2% DTT, 1 mM PMSF, and protease inhibitors (Roche) containing bromophenol blue at room temperature and centrifuged at 16,000 g for 5 min. Samples of supernatants (250 μl) were diluted with rehydration buffer to a volume of 350 μl and applied to the IEF strips (18 cm; pH 3–10; non-linear) via rehydration technique for 12 h at 50 V. The strips were then focused on the IEFphor system (GE Healthcare) with a current limit of 50 μA per strip at 20°C with the following program: 1 h at 200 V, 1 h at 500 V, 1 h at 1000 V; gradient to 8000 V in 1 h, and a final focusing step at 8000 V for 28 kVh. After IEF, the strips were briefly rinsed with water and prepared for the second dimension by a two-step equilibration and cysine alkylation process. The strips were incubated twice in equilibration buffer (50 mM Tris/HCl, pH 8.8, 6 M urea, 30% vol/vol glycerol, and bromophenol blue) for 12 min, in which 1% [wt/vol] DTT (step one) or 4% [wt/vol] iodoacetamide were added, respectively. Subsequently, the strips were loaded on SDS gels (8% acrylamide) and resolved in the second dimension. Gels were subjected to immunoblotting using myosin II-specific monoclonal antibody mAb 56–396-2 (Pagh and Gerisch, 1986).

Miscellaneous methods

For treatment with drugs, cells were treated with 10 μM Lat A, 20 μM cytochalasin D, or 100 μM blebbistatin in nutrient medium with shaking for 40 min. Cells were fixed with 3% paraformaldehyde and stained for F-actin using TRITC-labeled phallolidin (Sigma-Aldrich) or cold methanol, and actin was detected with mAb act1–7. For staining myosin II, aggregation-competent cells were allowed to settle on coverslips and were fixed using methanol (–20°C) and stained for myosin II using mAb 56–396-2 (Pagh and Gerisch, 1986) and images were captured using a laser scanning confocal microscope (TCS-SP; Leica). For quantitative analysis, initial scans using AX2 cells were used to optimize the scanning parameters and, subsequently, gefQ cells were scanned. Images were acquired using the accompanying Leica software. This software was also used to generate pseudo-3D projections from 2D images, in which the z axis represents intensity distribution over the scanned area. In all cases, temperature was maintained at 22°C and cells were mounted on coverslips using gelvatol. Monoclonal antibodies recognizing csA (Berthold et al., 1985), actin (Simpson et al., 1984), and GFP (Niozegel et al., 2004) were used for Western blotting.
Online supplemental material

Fig. S1 shows the scheme for generation of gfpQ cells and verification of mutants by genomic PCR, Southern blotting, Western blotting, and immunofluorescence studies. Fig. S2 shows that gfpQ cells overexpressing GFP-3G-GEF-QEF do not show RasB activation. Videos 1 and 3 show localization of GFP-RasGEF-Q173 in AX2 cells and 2 and 4 show the corresponding phase-contrast images, respectively. Video 5 shows localization of GFP-GEF and 6 shows the localization of GFP-DEP in AX2 cells. Video 7 shows development of wild-type AX2 strain and 8 shows development of gfpQ cells. Video 9 shows migration of AX2 cells toward a cAMP source and 10 shows migration of gfpQ cells toward a cAMP source. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.200710111/DC1.

We thank R. Müller for experimental help, Dr. M. Schiefele for discussion, Dr. T. Egelhoff for polyclonal antibodies against MyHC A2, Dr. G. Weeks for RasB antibody and RasBp121-pVE II construct, and Dr. G. Praefcke for the GST-By2(1RD) expression vector.

This work was supported by the Deutsche Forschungsgemeinschaft (NO 113/17-1 to A.A. Noegel and RI 1034/4 to F. Rivero), the Fonds der Chemischen Industrie, the Prostate Project of the Medical Faculty, University of Cologne, and National Institutes of Health (grant 2R15GM065789-02 to P. Steimle).

Submitted: 17 October 2007  
Accepted: 1 May 2008

References


re-arrangement of the actin system and formation of the cleavage furrow. J. Cell Sci. 110:123–137.


