Mutations in the relay loop region result in dominant-negative inhibition of myosin II function in Dictyostelium

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Received July 8, 2002; revised August 29, 2002; accepted September 4, 2002

INTRODUCTION

The N-terminal, globular domain of myosin interacts with actin filaments, producing force and movement in an ATP-dependent fashion. High-resolution structural data of this domain show the myosin motor to be composed of a central core, which contains the nucleotide-binding site and is structurally related to G-proteins (Vale, 1996). Extensions to this central core form the actin-binding site and the relay, converter and lever arm regions. A major function of these three regions is the amplification of the small conformational changes occurring at the active site to the large changes required for the movement of actin filaments (Geeves and Holmes, 1999).

The central core structure consists of seven β-strands and six α-helices and contains a group of conserved sequence motifs, termed switch-1 and switch-2, that contact the nucleotide at the rear of the nucleotide-binding pocket and act as γ-phosphate sensors. Switch-1 and switch-2 move towards each other when ATP is bound and move away from each other when ADP occupies the binding pocket, with switch-2 undergoing a large conformational change, whereas switch-1 contributes only minor conformational changes. The resulting conformational states are referred to as closed (ATP bound) and open (ADP or no nucleotide bound). Outside the nucleotide-binding pocket, conformational changes during the transition from open to closed are limited to a subset of regions and nearly all of them take place by rigid-body rotations of secondary and tertiary structure elements (Rayment et al., 1993; Dominguez et al., 1998; Kollmar et al., 2002). Therefore, the core and its extensions can be regarded as communicating functional units with substantial movement occurring in only a few residues. Some of the largest rotations in the angles of Φ and Ψ bonds are observed in the relay region, which serves as a central communication hub (Geeves and Holmes, 1999). Closure of the γ-phosphate-binding site results in the formation of a sharp kink in the switch-2 helix and a 60° twisting near its end, which is part of the relay region (Figure 1). This motion affects the angular position of the

Dominant-negative inhibition is a powerful genetic tool for the characterization of gene function in vivo, based on the specific impairment of a gene product by the coexpression of a mutant version of the same gene product. We describe the detailed characterization of two myosin constructs containing either point mutations F487A or F506G in the relay region. Dictyostelium cells transformed with F487A or F506G myosin are unable to undergo processes that require myosin II function, including fruiting-body formation, normal cytokinesis and growth in suspension. Our results show that the dominant-negative inhibition of myosin function is caused by disruption of the communication between active site and lever arm, which blocks motor activity completely, and perturbation of the communication between active site and actin-binding site, leading to an ~100-fold increase in the mutants’ affinity for actin in the presence of ATP.
leverage arm and the actin-binding site. Communication to the actin-binding site follows the path of the polypeptide chain, whereas a cluster of highly conserved hydrophobic residues mediates the coordinated movement of the relay region and converter region in response to conformational changes in the nucleotide-binding site. Hydrophobic interactions mediated by these residues are critical for at least two functions: residues Y494, I499, W501, F692 and F745 link the end of the relay helix to the converter domain, with the effect that both move as a rigid unit; residues N483, F487, F506, L508 and I687 appear to be important for stabilizing the bent form of the relay helix, which is present in the hydrolytically competent closed state of myosin (Kollmar et al., 2002). Here, we examine myosin motor domain and full-length constructs containing point mutations leading to the substitution of either residue F487 or F506. Constructs with point mutations F487A, F506A and F506G were generated. However, as all three constructs showed similar or identical properties, we only report results obtained with F506G and selected results obtained with F487A.

RESULTS AND DISCUSSION

In the *Dictyostelium* system, the functionality of a mutant myosin can be easily assessed *in vivo*. Normal cytokinesis, growth in suspension culture, capping of cell surface receptors and sporogenesis are processes that require a functional myosin II in *Dictyostelium* (De Lozanne and Spudich, 1987). Complementation of myosin null cells (Manstein et al., 1989) with F487A- and F506G-myosin did not restore the functional defects, indicating that the point mutations disrupt the motor function. Additionally, we found that expression of the mutant myosins interferes with normal myosin II function in a dominant-negative way. Wild-type cells transformed with F487A- or F506G-myosin were unable to undergo fruiting-body formation and cytokinesis and failed to grow in suspension (Figure 2). Partial impairment of myosin II function in *Dictyostelium* has been reported previously for the coexpression of the tail portion of myosin II, which leads to the formation of single-headed myosin II and interferes with cytokinesis but not sporogenesis (Burns et al., 1995). Dominant mutations have been described for the *Caenorhabditis elegans* body wall myosin UNC-54 (Bejsovec and Anderson, 1990) however, mutations of the equivalent residues in the ATP and actin-binding sites of *Dictyostelium* myosin II have no dominant-negative effect.

To determine the cause of the dominant-negative effect of the F487A or F506G full-length constructs, we produced the point mutations separately in the myosin motor domain construct M761-2R (Anson et al., 1996). M761-2R consists of the first 761 amino acids of the motor domain of *Dictyostelium discoideum* myosin II fused to two α-actinin repeats in place of the native light chain binding domain. M761-2R displays S1-like kinetic and motile properties (Kurzawa et al., 1997; Kliche et al., 2001). The mutant constructs will be referred to as F487A-2R and F506G-2R.

Differential scanning calorimetry (DSC) was used to examine whether the elimination of a singe phenylalanine residue from the cluster of highly conserved hydrophobic residues is sufficient to disrupt the coordinated movement of the relay and converter regions. DSC is sensitive to conformational changes that occur in the globular motor portion of myosin following strong binding to F-actin or the formation of stable ternary complexes with ADP and P$_i$ analogues (Levitsky et al., 1998; Ponomarev et al., 2000). In the case of wild-type myosin, discrete increases in the thermal stability of the protein are observed, which reflect the transitions between open in the absence of nucleotide, open in the presence of ADP, closed in the presence of ATP and ADP-P$_i$, analogues and open in the presence of ADP and F-actin (Figure 3). The difference between the maximum of the thermal transitions for actin-free and actin-bounded F506G-2R ($\Delta T_m = 4.7^\circ C$) is 20% smaller than that observed with a wild-type construct ($\Delta T_m = 6.0^\circ C$) (Ponomarev et al., 2000), indicating differences in the coupling between nucleotide- and actin-binding sites. Furthermore, the calorimetric traces for the thermally induced unfolding of F506G-2R complexed with ADP, ADP-V$_p$, ADP-BeF$_3$ or ADP-AlF$_4$ show similar shifts of the maximum of the thermal transition ($T_m$) relative to the $T_m$ value observed for nucleotide-free F506G-2R (Figure 3). These results are in good agreement with a model where nucleotide binding leads to an $\sim$4°C stabilization of the motor domain. However, additional increases in $T_m$ as observed for the wild-type protein upon formation of stable ternary complexes with ADP and P$_i$ analogues, require closure of the P$_i$ binding pocket and the concerted movement of relay region and converter.

Additional support for the disruption of the coordinated movement of relay region and converter by the point mutations comes from the loss of the characteristic enhancement in tryptophan
fluorescence, which has been widely exploited for the kinetic characterization of myosins. Crystal structures show Trp501 or the equivalent residue in vertebrate smooth muscle myosin to change from a more exposed environment in open to a less exposed, hydrophobic environment in closed structures. In agreement with these changes in microenvironment, ATP binding to Dictyostelium myosin II, which favours the closed state, leads to a 25% increase in the intrinsic fluorescence of Trp501 (Batra and Manstein, 1999). In contrast, addition of excess ATP to F506G-2R and F487A-2R results in a 4–6% decrease in intrinsic fluorescence (data not shown).

Disruption of the coordinated movement of the relay and converter regions is predicted to greatly reduce or abolish motor activity. F506G-2R and F487A-2R did not move actin filaments in vitro motility assays (Kron and Spudich, 1986). Mixing assays, allowing an estimate of the duration for which the mutant construct is attached to actin during a catalytic turnover (Giese and Spudich, 1997), were used to measure the inhibition of rabbit HMM motility by F506G-2R. At a one-to-one ratio of rabbit HMM to F506G-2R, we observed a >3-fold reduction in velocity, whereas a one-to-one mixture of rabbit HMM with the corresponding wild-type construct reduced the velocity of rabbit HMM by only 35%. Higher ratios of F506G completely inhibited velocity (data not shown). These results suggest that the mutant constructs do not only disrupt the communication between the nucleotide-binding site and the lever arm but that the mutations affect a kinetic step resulting in prolonged actin attachment.

Stopped-flow analysis of F487A-2R and F506G-2R showed that the second-order rate constants for ATP binding ($k_{1}$/$k_{-1}$) and ADP binding ($k_{6}/k_{7}$), rigor binding to actin ($k_{a, b, k_{A}}$), and coupling between actin binding and ADP affinity ($K_{AD}/K_{D}$) are not affected by the mutations (Tables I and II). In contrast, steady-state measurements revealed large differences in the interaction with actin and ATP between the mutant and wild-type constructs. F487A-2R and F506G-2R exhibit 2- to 5-fold elevated basal ATPase activity (0.12 and 0.3 s$^{-1}$), reduced $k_{cat}$ values of ∼0.4 s$^{-1}$, and a 50- (F506G) to 270-fold (F487A) increased actin affinity in the presence of ATP ($K_{app}$). A value for the $K_{app}$ of 135 µM was determined for M761-2R. As the small differences between $k_{basal}$ and $k_{cat}$ make a more exact determination of $K_{app}$ difficult, we used single turnover kinetics with mantATP as substrate to confirm the increased actin affinity of the mutant constructs in the presence of nucleotide (Figure 4). Three phases could be distinguished following mixing of mantATP and F487A-2R: (1) an initial fast rise of the fluorescence signal, (2) a plateau phase and (3) a slow decrease of the fluorescence signal, where phases 1 and 3 reflect the binding of mantATP and dissociation of mantADP, and phase 2 monitors the duration of the hydrolysis reaction. Addition of increasing amounts of F-actin led to a linear acceleration of the
rate of mantADP dissociation. When the same experiment was
repeated with F506G-2R, only two phases could be distin-
guished in the absence of actin; a fast rise in fluorescence,
followed by a plateau with no signal decrease occurring during
the next 1000 s. Quenched-flow experiments revealed that the
nucleotide was hydrolysed with a rate of 0.06 s⁻¹ (data not
shown), indicating that the plateau was caused by slow dissocia-
tion of the hydrolysis products and not by a limiting hydrolysis
rate. Addition of actin led to the reappearance of phase 3, indi-
cating acceleration of the rate of mantADP dissociation. The
increase in the \( k_{\text{obs}} \) of phase 3 with increasing actin concentra-
tion is a measure of the efficiency with which actin binds to the
M·mantATP or M·mantADP-Pᵢ complex. For F506G-2R, the
increase in \( k_{\text{obs}} \) with increasing actin concentration could be
fitted to a hyperbola with \( K_{0.5} = 1 \) µM (Figure 4B). This value is
similar to that determined for the \( K_{\text{app}} \) of F506G-2R.

Our results confirm the importance of the relay loop region as
a communication zone, mediating conformational information
between the converter domain, the nucleotide-binding site and
the actin-binding site. They demonstrate the importance of a
conserved hydrophobic cluster for the efficient conformational
coupling between the active site and the lever arm and show
that changes in the relay loop perturb communication between
the active site and the actin-binding site. The high degree of
conservation in this region suggests that the generation of
myosin constructs containing mutations equivalent to F506G,
F506A and F487A will provide a powerful tool to dissect the
functional properties of myosins from all classes in vivo and in
more complex systems than Dictostelium.

**METHODS**

**Plasmid construction.** Enzymes were obtained from MBI-
Fermentas (St Leon-Roth, Germany) and New England Biolabs
(Frankfurt, Germany). *Escherichia coli* strain XL1Blue (Strata-
gene, Heidelberg, Germany) was used for amplification of plas-
mids. The expression vectors used for the production of mutant
myosin constructs were based on the extrachromosomal vector
pDXA-3H (Manstein *et al.*, 1995). M761-2R and full-length
myosin constructs were generated using plasmids pDH12
(Kurzawa *et al.*, 1997) and pDH (Furch *et al.*, 1999), respec-
tively. All DNA constructs were confirmed by sequencing.

**Protein production and purification.** Plasmids were transformed
into Orf and mhcA- cells by electroporation. Transformants were
grown at 21 °C in HL-5C medium and selected in the presence of
10 µg/ml G418 and 100 U/ml penicillin-streptomycin. Screening for the production of the recombinant myosins and
protein purification was performed as described previously
(Manstein and Hunt, 1995). M761-2R and full-length
myosin constructs were generated using plasmids pDH12
(Kurzawa *et al.*, 1997) and pDH (Furch *et al.*, 1999), respect-
ively. All DNA constructs were confirmed by sequencing.

**Dictostelium manipulation.** Synchronous morphological
differentiation was induced by starvation on MMC agar (20 mM
MES, 2 mM MgCl₂, 0.2 mM CaCl₂, and 2% w/v Bacto agar)
adjusted to pH 6.8. Structures from various stages of develop-
ment were visualized using an Olympus B061 microscope and a
Sony SSC-M370CE video camera. A Hamamatsu Argus-20 was
used for contrast enhancement and transfer of images to a
Table I. Transient kinetic analysis of mutants and wild-type myosin

<table>
<thead>
<tr>
<th>Nucleotide</th>
<th>Rate constant</th>
<th>M761–2R</th>
<th>F506G-2R</th>
<th>F487A-2R</th>
</tr>
</thead>
<tbody>
<tr>
<td>ATP</td>
<td>$K_1 k_{12}$ (M$^{-1}$s$^{-1}$)</td>
<td>$7.0 \pm (0.4) \times 10^5$</td>
<td>$6.7 \pm (0.2) \times 10^5$</td>
<td>$6.2 \pm (0.1) \times 10^5$</td>
</tr>
<tr>
<td></td>
<td>$k_{21} + k_{31}$ (s$^{-1}$)</td>
<td>$28 \pm (4)$</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td>$k_{22}$ (s$^{-1}$)</td>
<td>–</td>
<td>$&gt;500$</td>
<td>$&gt;250$</td>
</tr>
<tr>
<td>mantATP</td>
<td>$K_1 k_{12}$ (M$^{-1}$s$^{-1}$)</td>
<td>$8.1 \pm (0.2) \times 10^5$</td>
<td>$5.3 \pm (0.1) \times 10^5$</td>
<td>$9.1 \pm (0.4) \times 10^5$</td>
</tr>
<tr>
<td>ADP</td>
<td>$k_6/K_7$ (M$^{-1}$s$^{-1}$)</td>
<td>no signal</td>
<td>$9 \pm (0.1) \times 10^5$</td>
<td>$22 \pm (0.7) \times 10^5$</td>
</tr>
<tr>
<td></td>
<td>$K_D$ (µM)</td>
<td>$7.1 \pm (0.5)$</td>
<td>$1.6 \pm (0.2)$</td>
<td>$3.1 \pm (0.4)$</td>
</tr>
<tr>
<td>mantADP</td>
<td>$k_{10}$ (M$^{-1}$s$^{-1}$)</td>
<td>$4.8 \pm (0.1) \times 10^5$</td>
<td>$5.0 \pm (0.3) \times 10^5$</td>
<td>$13.2 \pm (1.1) \times 10^5$</td>
</tr>
<tr>
<td></td>
<td>$k_{d1}$ (s$^{-1}$)</td>
<td>$1.34 \pm (0.1)$</td>
<td>$0.34 \pm (0.04)$</td>
<td>$0.8 \pm (0.1)$</td>
</tr>
<tr>
<td></td>
<td>$K_D$ (µM)</td>
<td>$2.8 \pm (0.2)$</td>
<td>$0.68 \pm (0.1)$</td>
<td>$0.61 \pm (0.1)$</td>
</tr>
</tbody>
</table>

Binding and hydrolysis of ATP by myosin was analysed in terms of the seven-step model shown above (Bagshaw et al., 1974).

Table II. Transient kinetic analysis of actin with mutants and wild-type myosin

<table>
<thead>
<tr>
<th>Nucleotide</th>
<th>Rate constant</th>
<th>M761–2R</th>
<th>F506G-2R</th>
<th>F487A-2R</th>
</tr>
</thead>
<tbody>
<tr>
<td>ATP</td>
<td>$K_1 k_{12}$ (M$^{-1}$s$^{-1}$)</td>
<td>$5.7 \pm (0.4) \times 10^5$</td>
<td>$4.8 \pm (0.2) \times 10^5$</td>
<td>$3.7 \pm (0.2) \times 10^5$</td>
</tr>
<tr>
<td></td>
<td>$k_1$ (s$^{-1}$)</td>
<td>$1000$</td>
<td>$500$</td>
<td>$400$</td>
</tr>
<tr>
<td></td>
<td>$k_{22}$ (s$^{-1}$)</td>
<td>$-500$</td>
<td>$&gt;1000$</td>
<td>$&gt;1000$</td>
</tr>
<tr>
<td>ADP</td>
<td>$K_{AD}$ (µM)</td>
<td>$182 \pm (28)$</td>
<td>$44 \pm (6)$</td>
<td>$84 \pm (9)$</td>
</tr>
<tr>
<td></td>
<td>$k_{AD}$ (M$^{-1}$s$^{-1}$)</td>
<td>$&gt;0.5 \times 10^6$</td>
<td>$&gt;0.5 \times 10^6$</td>
<td>$&gt;0.2 \times 10^6$</td>
</tr>
<tr>
<td></td>
<td>$k_{AD}$ (s$^{-1}$)</td>
<td>$&gt;100$</td>
<td>$&gt;20$</td>
<td>$&gt;20$</td>
</tr>
<tr>
<td></td>
<td>$K_{AD}/K_D$</td>
<td>$24 \pm (3)$</td>
<td>$28 \pm (4)$</td>
<td>$27 \pm (3)$</td>
</tr>
<tr>
<td>Actin binding to myosin</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ATP</td>
<td>$k_{1a}$ (M$^{-1}$s$^{-1}$)</td>
<td>$8.0 \pm (0.1) \times 10^3$</td>
<td>$2.7 \pm (0.3) \times 10^5$</td>
<td>$8.0 \pm (0.1) \times 10^5$</td>
</tr>
<tr>
<td></td>
<td>$k_{1A}$ (ms$^{-1}$)</td>
<td>$2.5 \pm (0.4)$</td>
<td>$1.6 \pm (0.3)$</td>
<td>$5.0 \pm (1)$</td>
</tr>
<tr>
<td></td>
<td>$K_A$ (nM)</td>
<td>$3.1 \pm (0.5)$</td>
<td>$5.9 \pm (0.7)$</td>
<td>$6.2 \pm (0.8)$</td>
</tr>
<tr>
<td></td>
<td>$K_{DA}$ (nM)</td>
<td>$79.5 \pm (14)$</td>
<td>$162 \pm (23)$</td>
<td>$168 \pm (29)$</td>
</tr>
<tr>
<td></td>
<td>$k_{DA}$ (µM$^{-1}$s$^{-1}$)</td>
<td>$0.14 \pm (0.01)$</td>
<td>$0.11 \pm (0.01)$</td>
<td>$0.28 \pm (0.02)$</td>
</tr>
<tr>
<td></td>
<td>$k_{DA}$ (s$^{-1}$)</td>
<td>$11.1 \times 10^{-3}$</td>
<td>$17.8 \times 10^{-3}$</td>
<td>$47.0 \times 10^{-3}$</td>
</tr>
<tr>
<td></td>
<td>$k_{DA}/k_A$</td>
<td>$4.4 \pm 0.6$</td>
<td>$11.1 \pm 1.3$</td>
<td>$9.4 \pm 0.8$</td>
</tr>
</tbody>
</table>

Actomyosin interactions were analysed in terms of the schemes shown above (Millar and Geeves, 1983; Siemankowski and White, 1984).
DSC experiments were performed on a DASM-4M differential scanning microcalorimeter (Institute for Biological Instrumentation, Puschchino, Russia) as described previously (Ponomarev et al., 2000). Transition temperatures (T_m) were determined from the maximum of the temperature dependence of the molar heat capacity. Calorimetric enthalpies (ΔH_m) were calculated from the area under the excess heat capacity curves.

In vitro motility was measured using standard sliding-filament assay methods at 30°C (Kron and Spudich, 1986; Anson et al., 1996).

ACKNOWLEDGEMENTS

We thank S. Zimmermann for excellent technical assistance in the generation of expression vectors, M.L.W. Knetsch for help and stimulating discussions and M. Kollmar for contributing Figure 1, and K. C. Holmes for encouragement and continuous support. The work presented was supported by the Max-Planck-Society, Deutsche Forschungsgemeinschaft grants MA 1081/5-2 (to D.J.M.), Ku-1288/2-2 (to F.J.K.), GK388 (to G.T.), Wellcome Trust grant 055841 (to M.A.G.), and INTAS-RFBR Grant IR-97-577 (to D.I.L., D.J.M. and M.A.G.).

REFERENCES


Macintosh 9500. DAPI staining was performed as described previously (De Lozanne and Spudich, 1987).

**Protein characterization.** Fluorescence emission spectra were recorded at 20°C in a SLM 8000 fluorescence spectrophotometer. Transient kinetic and single turnover measurements were performed using a Hi-tech Scientific SF-61DX2 stopped-flow spectrophotometer as described previously (Furch et al., 1999). All concentrations refer to the concentration of the reactants after mixing in the stopped-flow observation cell. Steady-state ATPase activities were determined at 25°C using a linked enzyme assay and analysed as described previously (Furch et al., 1998). A notation is used that distinguishes between rate and equilibrium constants in the presence and absence of actin by using bold (k_\text{cat}, K_1) versus italic type (k_\text{cat}, K_1); subscript A and D refer to actin (K_A) and ADP (K_D), respectively.
Dominant-negative myosin mutations


DOI: 10.1093/embo-reports/kvf214


