Actin Depolymerizing Factor Stabilizes an Existing State of F-Actin and Can Change the Tilt of F-Actin Subunits

Vitold E. Galkin,* Albina Orlova,* Natalya Lukoyanova,* Willy Wriggers,† and Edward H. Egelman*

*Department of Biochemistry and Molecular Genetics, University of Virginia Health Sciences Center, Charlottesville, Virginia 22908; †Department of Cell Cultures, Institute of Cytology RAS, St. Petersburg, Russia; ‡Institute of Theoretical and Experimental Biophysics RAS, Puschino, Russia; †Department of Molecular Biology, The Scripps Research Institute, La Jolla, California 92037

Abstract. Proteins in the actin depolymerizing factor (ADF)/cofilin family are essential for rapid F-actin turnover, and most depolymerize actin in a pH-dependent manner. Complexes of human and plant ADF with F-actin at different pH were examined using electron microscopy and a novel method of image analysis for helical filaments. Although ADF changes the mean twist of filament, we show that it does this by stabilizing a preexisting F-actin angular conformation. In addition, ADF induces a large (~12°) tilt of actin subunits at high pH where filaments are readily disrupted. A second ADF molecule binds to a site on the opposite side of F-actin from that of the previously described ADF binding site, and this second site is only largely occupied at high pH. All of these states display a high degree of cooperativity that appears to be an integral part of F-actin.

Key words: actin • ADF • cooperativity • electron microscopy • image processing

Introduction

Actin dynamics play a major role in cell motility, cytokinesis, and endocytosis. The rapid polymerization/depolymerization of actin filaments in the cell, especially under the leading membrane edge, requires an efficient protein machinery that can provide a fast response to extracellular stimuli (Chen et al., 2000; Pollard et al., 2000). A large number of actin binding proteins have been shown to participate in the assembly, disassembly, and rearrangement of the cytoskeleton. Proteins in the actin depolymerizing factor (ADF)/cofilin family are essential, conserved, and widespread actin depolymerizing factors that interact with F-actin in a strong cooperative manner (Hawkins et al., 1993; Hayden et al., 1993; Blanchin and Pollard, 1999). All members of the ADF/cofilin family are small proteins that contain between 118 and 168 amino acids (13–19 kD), and most depolymerize actin more rapidly at higher pH (Yonezawa et al., 1985; Bernstein et al., 2000). The exceptions to this pH dependence are Acanthamoeba thaliana ADF1 (p-ADF) and human ADF (h-ADF), molecules that share only 31% identity.

Two possible mechanisms of actin depolymerization were proposed for ADF/cofilin proteins. It was suggested that ADF depolymerizes actin due to a severing activity (Cooper et al., 1986; Maciver et al., 1991). Carlier (1998) proposed that the acceleration of treadmilling via the enhancement of the off-rate at the barbed end of the filament by ADF/cofilin proteins is responsible for actin filament destabilization (Carlier and Pantaloni, 1997). A combination of both mechanisms has also been suggested (Theriot, 1997), and the main question involves the relative contribution of each of these mechanisms to actin filament shortening (Du and Frieden, 1998; Moriymama and Yahara, 1999).

A growing body of evidence suggests that the geometry and internal dynamics of actin filaments might be functionally important in the interaction between F-actin and many actin-binding proteins. For example, in muscle, it has been shown using mutations (Drummond et al., 1990), cross-linking (Prochniewicz and Yanagida, 1990; Kim et al., 1998), and proteolysis (Schwyter et al., 1990) that modifications can be made to F-actin that do not prevent the binding of myosin and do not inhibit the activation of myosin's ATPase activity but do prevent the generation of force. The variability in the structure of F-actin may be important in this context. In an ideal actin filament, actin subunits are related to each other by an axial rise of 27 Å
and a rotation of \( \sim 167^\circ \). This symmetry operation can generate every subunit in a filament, given a single subunit. Because subunit \( n \) will be rotated \( \sim 26^\circ \) from both subunits \( n - 2 \) and \( n + 2 \), the resulting filament can also be described by a helix containing two \( \sim 700\)-Å-pitch axially staggered strands that crossover in projection at average intervals of \( \sim 350 \) Å. However, early electron microscopic observations showed that the actual crossover points of negatively stained actin filaments were far from uniform in their length (Hanson, 1967). A subsequent model suggested that this arises from an unusual property of F-actin where subunits have the ability to rotate within the filaments, although the axial rise per subunit is quite fixed (Egelman et al., 1982). It was proposed that this rotational symmetry of F-actin might help the cell to use a single highly conserved protein in several different structures. Human cofilin was observed to change the twist of actin by \( \sim 5^\circ \) per subunit when it was bound stoichiometrically to F-actin (McGough et al., 1997), and it was proposed that this change in actin symmetry was responsible for the destabilization of the actin filament. Later, using a mutant cofilin that bound to actin but did not destabilize the filament, it was suggested that the change in twist induced by cofilin could be uncoupled from subunit dissociation (Pope et al., 2000). Thus, there is no clear picture for the role of the change in actin’s twist in the mechanism of ADF/cofilin-induced actin depolymerization.

We have used a new approach for image analysis of helical filaments (Egelman, 2000) to examine both pure actin filaments and complexes of F-actin with p- and h-ADF. This new approach allows us to analyze tens of thousands of short segments within filaments, without the need to assume a fixed helical symmetry for a long filament. This approach is therefore sensitive to variations in helical symmetry between different segments, as well as to differences in the occupancy of the ADF molecules bound to F-actin. Using this method, we show that segments of pure actin can be found in an ADF/cofilin-like state of twist in the absence of other proteins. Furthermore, the ADF–actin complex can exist with a twist close to that of the normal actin state. We find that under conditions where actin filaments are readily depolymerized, two molecules of ADF bind per actin subunit, and not one as has been believed previously. We also find that under these conditions of filament destabilization some actin subunits undergo a large tilt from their positions in normal F-actin that causes the breakage of the longitudinal contacts within the actin filament. These results provide new insight into the internal dynamics of F-actin, suggesting that they may be even larger in magnitude than previously imagined, and suggest that certain actin-binding proteins in the cell may have evolved to regulate these internal dynamics as part of cellular control of the cytoskeleton.

Materials and Methods

Protein Preparation and EM

Actin was prepared from rabbit skeletal muscle (Strzelecka-Golaszewski et al., 1980) and isolated as Ca\(^{2+}\)–G-actin by chromatography over a Superdex-200 column using the AKTA Explorer HPLC system (Amersham Pharmacia Biotech). G–Ca\(^{2+}\)–actin was diluted to a final concentration of 0.5 mg/ml by 5 mM Pipes buffer, pH 6.5, or 5 mM Tris buffer, pH 7.7. Ca\(^{2+}\) was replaced with Mg\(^{2+}\) by incubating G-actin with 0.2 mM EGTA and 0.2 mM MgCl\(_2\) for 10 min at room temperature. G-actins were polymerized by 0.1 M KCl and 2 mM MgCl\(_2\) by incubating 2 h at room temperature and then overnight at 4°C. F-actins were spun down in a TLX-120 tabletop ultracentrifuge (Beckman Coulter), and pellets were homogenized in fresh F buffers (0.1 mM KCl, 1 mM MgCl\(_2\), 15 mM Tris buffer, pH 7.7, or Pipes buffer, pH 6.5) and diluted to final concentrations of 2–4 \(\mu\)M p-ADF (Carlier et al., 1997) and h-ADF were a gift from Dr. M.-F. Carlier (Laboratory of Enzymology and Structural Biochemistry, Gif-Sur-Yvette, France). ADFs were diluted by F buffers to final concentrations of 3–6 \(\mu\)M.

Negatively stained samples were prepared by incubation for 10 min in tubes of 2 \(\mu\)M actin with 6 \(\mu\)M ADF or by decoration on the grid, where one drop (6 \(\mu\)l) of 2 \(\mu\)M actin was applied to 300-mesh copper grids coated with carbon for 1 min, and then two separate drops (6 \(\mu\)l each) of 4 \(\mu\)M ADF were added for 30 s–2 min. The grids were rinsed with two drops of 1% uranyl acetate.

Specimens were examined in a JEOL 1200 EX11 electron microscope at an accelerating voltage of 80 kV and a nominal magnification of 30,000×. Negatives were densitometered with a Leaf 45 scanner, using a raster of 4 Å/pixel.

Image Analysis

The references for initial multireference cross-correlation analysis were generated using layer lines extracted from an atomic model of the F-actin filament (Holmes et al., 1990). The symmetry of this model was changed by complexing the layer lines (from a 13/6 helix) as follows: \( l_1 = 1; n = 1; l_2 = 1; n = 2; l_3 = 1; n = 3; l_4 = 1; n = 4; l_5 = 5; n = 1; l_6 = 6; n = 4; l_7 = 7; n = 1; l_8 = 8; n = 3; l_9 = 12; n = 2; l_{10} = 13, n = 0; l_{11} = 14, n = 2. \) The subsequent procedure for iterative helical real space reconstruction was described (Egelman, 2000). Segments of pure F-actin and F-ADF–actin complexes were placed in 100 × 100 pixel boxes (\( \sim 400 \times 400 \) Å), and these were cross-correlated against reference projections using a real space radius of 42 pixels in the search. Thus, the cross-correlation search involved \( \sim 12 \) subunits. The search for helical symmetry within the asymmetric volume generated by back-projection involved nine subunits, eliminating possible end effects that are present due to the geometry of the reconstruction (Egelman, 2000). Typically, \( \sim 10\% \) of filament segments were excluded during the iterations, based on poor cross-correlations against the reference volumes. The resolution of the reconstructions was determined by generating two independent reconstructions from each data set after randomly dividing the images into two equal subsets. The correlation coefficients from each of these pairs of reconstructions was \( > 0.5 \) with a resolution of \( \sim 25 \) Å for the ADF-actin complexes and \( \approx 30 \) Å for both the pure and naked actin. Using the 3e criterion (Saxton and Baumeister, 1982) rather than the correlation coefficient, the estimate for resolution is \( \sim 20 \) Å for the ADF–actin complexes and \( \sim 25 \) Å for both the pure and naked actin.

The cross-correlation procedure was used to discriminate ADF-bound and naked actin segments in a similar manner to that described for sorting by symmetry. We term actin “naked” when patches of undecorated actin are found within ADF-decorated actin filaments, in contrast to “pure” F-actin, which refers to actin filaments in the absence of any additional proteins. References were created by imposing a symmetry of 162.0° on the pure F-actin reconstruction as well as on the fully ADF-decorated actin filaments to distinguish segments by the presence or absence of the ADF, rather than by symmetry. The reconstruction algorithm was then iterated many times in each cycle, eliminating those segments that had a poor cross-correlation coefficient against the continuously updated naked actin reconstruction. This was continued (for 60–250 cycles) until a stable solution was found with respect to both symmetry and the number of segments identified as naked actin. The validation of this sorting procedure was that reconstructions of segments from ADF-decorated filaments that were selected by higher cross-correlation against the pure F-actin reference than against the ADF–actin reference looked like undecorated actin.

Surface thresholds were determined by using 125% of the expected molecular volume of pure actin, and 100% of the expected molecular volume for both the 1:1 or 2:1 ADF–actin complexes, assuming a partial specific volume of protein of 0.75 cm\(^3\)/g.

Fitting of Actin and ADF Monomer Structures

The missing DNase-1 binding loop was added to the actin structure (Protein Data Bank entry 1EOY) as described (Wriggers and Schulten, 1999). h-ADF coordinates were obtained from PDB entry 1AK6 (Hatamaka et al., 1996). The fitting of atomic models into EM reconstructions was carried out by the Image Processing Group.
ried out with the Situs package v1.4 (Wriggers et al., 1999). The fitting method takes advantage of topology-representing neural networks that represent the shape features and three-dimensional density distribution of both atomic and low-resolution data by a discrete number of vectors (Wriggers et al., 1998). It was shown that this docking approach reconstructs atomic models of undecorated actin filament structures with a precision of one order of magnitude above the nominal resolution of the underlying low-resolution map (Wriggers et al., 1999). The main innovation implemented in Situs v1.4 is the addition of distance constraints between adjacent vectors. The resulting distance-constrained vectors freeze the degrees of freedom that are inessential for the docking and thereby provide robustness against the effects of noise and experimental uncertainty (Wriggers and Birmanns, 2001). Five vectors were used per actin subunit, and two vectors per ADF molecule. Helical boundary conditions were applied since rigid body docking was performed, intramolecular distances (derived from the atomic structures) were constrained, using the SHAKE algorithm (van Gunsteren and Berendsen, 1977), whereas intermolecular distances remained free. The resulting vectors provided anchor points for a least squares fitting of individual molecules (Wriggers et al., 1998).

To test the fitting algorithm for the ADF-decorated volume, we compared the model resulting from a fit of G-actin to the ADF-decorated volume with the Holmes model. The root mean square deviation of the resulting model from the symmetry corrected Holmes model was only 1.76 A, demonstrating the reliability of the skeleton-based docking approach. After the docking of actin, the resolution of the resulting F-actin model was lowered to 20 A using the Situs pdbblur utility (Wriggers and Birmanns, 2001). The amplitude of the simulated actin map was varied systematically to match the actin surface in the experimental map at like threshold levels. Subsequently, the simulated actin map was subtracted from the experimental data set. Single molecule densities of the primary and secondary ADF molecules were isolated with Situs as described (Wriggers et al., 1999). Finally, the ADF structure was docked to the single molecule densities. There was a sixfold degeneracy in the vector rms deviation score for the primary ADF, but only one of the possible solutions was consistent with the biochemical information on the consensus binding interface with actin (Yonezawa et al., 1991; Lappalainen et al., 1997; Van Troys et al., 1997; Ono et al., 1999). The shape-based docking was unambiguous in the case of the second ADF, and no biochemical data was used in this case to help orient the molecule.

Results

Rotational Variability of Pure F-Actin Allows It to Exist in the ADF/Coﬁlin-like Twist State

The unusual twist previously reported for coﬁlin-decorated actin ﬁlaments (changing F-actin from ~167°–162° of rotation per subunit) was observed at pH 6.6 where stable filaments of actin–coﬁlin complex can be observed (McGough et al., 1997). At higher pH, coﬁlin will depolymerize actin ﬁlaments more efﬁciently. To determine the distribution of twist angle for pure F-actin at pH 6.5, we examined 10,800 segments of Mg2+-actin polymerized at pH 6.5. The frequency distribution of the images according to their twist (Fig. 1 a) is based on finding which of 27 reference ﬁlaments with angular rotations per subunit of 152°–179° generates the highest cross-correlation when projections of the images are compared with the raw images. This distribution is extremely broad, and the dispersion has two components: the intrinsic variability of the twist of pure F-actin (Egelman et al., 1982), and the poor signal-to-noise ratio present in segments of F-actin that contain only ~12 subunits. Model calculations show, as expected, that the dispersion in cross-correlation against references with different symmetries will increase as the signal-to-noise ratio is decreased. The iterative helical real space reconstruction (IHRSR) method (Egelman, 2000), however, allows us to take subsets sorted as shown in Fig. 1 a and find if they yield a stable solution. The sub-

sets from the far left (<156°) and the far right (>170°) of the distribution gave symmetries, after multiple iterations, that were either close to the central part of the distribution or had no stable solution. Thus, we can dismiss those outlying symmetries as being due to errors in the initial sorting by twist because of noise or heterogeneity.

The frequency distribution of stable solutions (Fig. 1 b) must be an underestimate of the dispersion of average twist of filament segments containing ~12 subunits. The reason that this is an underestimate is due to the way that these solutions have been obtained. We consider a solution stable if we can show that it converges to a particular
helical symmetry independent of the starting point for the iterative procedure. Fig. 1 c illustrates this for two different subsets, 158° and 166°. It can be seen, for example, that the 158° solution is reached whether the iterations are started from a model having 151.5°, 162°, or 166° rotation per subunit. Similarly, the 166° solution is found whether the iterations start from 162° or 170°. Thus, we have high confidence that each stable solution corresponds to a real state for the average twist of 12 F-actin subunits, but we cannot exclude the possibility that other average states, further from the mean, actually exist. When the entire data set was combined, an overall symmetry of 166.1° was found. Keeping in mind that cofilin changes the mean twist of actin filaments to ~162° (McGough et al., 1997), it can be seen (Fig. 1 b) that ~5–10% of segments of pure F-actin can be found with a mean twist of 162°, or even 158°, without ADF/cofilin bound. Since the 158° state is so far from anything that has been described previously, we were interested to see if this was associated with filament ends, because the untwisting of actin was proposed as a mechanism of actin depolymerization (McGough et al., 1997). By selecting segments that were only close to filament ends, we did not see any significant increase in the frequency of this state. Our results suggest that these segments are randomly distributed within actin filaments.

The three-dimensional reconstructions of pure actin from the 158° subset (Fig. 2 a) and from the 166° subset (Fig. 2 c) obtained by the IHRSR method have an obviously different twist. To exclude the possibility that this difference in twist is an artifact of the three-dimensional reconstruction
method, actin images from each of the two sets were averaged together. The resulting two-dimensional averages (Fig. 2, b and d) have approximately the same difference in crossover lengths, as can be seen in the three-dimensional reconstructions (Fig. 2, a and c). We have also used cryo-EM on unstained frozen-hydrated actin filaments and find a similar distribution of twist (data not shown), excluding the possibility that the variation in twist is due to specimen preparation. Thus, cofilin/ADF do not induce a new state of twist in F-actin, but either stabilize a particular state of twist in which pure actin can be found or shift the overall distribution of twist by \( \sim 5^\circ \). The results below suggest that the former possibility is more likely.

**Symmetry of ADF–Actin Complexes**

h-ADF is more efficient at disrupting rabbit muscle actin filaments than is p-ADF, and this difference is more obvious at high pH (Ressad et al., 1998). We have therefore used incubations of p- and h-ADF with F-actin at both pH 6.5 and 7.7 (Fig. 3). We observed that h-ADF bound to F-actin at pH 6.5 more slowly than p-ADF (Fig. 3, com-
pare a with b). After 2 min of incubation on the grid, fila-
ments were fully decorated with p-ADF, but only partial
decoration was noticed for h-ADF. Full occupancy was
reached for h-ADF only after 10 min of incubation (Fig. 3
d). There were no differences in EM pictures between
p-ADF–decorated actin after 2 min incubation on the grid or
10 min incubation in tubes, except filaments were shorter
after the longer incubation (Fig. 3, a and c). But h-ADF–
decorated F-actin appeared quite different from p-ADF
after 2 min incubation on the grid, as well as after 10 min
incubation in tubes (Fig. 3, compare a, c, and d). Approxi-
mately 30% of filaments decorated with h-ADF appeared
more massive and were stained more darkly (Fig. 3 d,
black arrow), and no such filaments were found in p-ADF
samples. For h-ADF–actin filaments at pH 7.7, ~70%
were darkly stained (Fig. 3 f, black arrow), as opposed to
~30% found at pH 6.5 (Fig. 3 d, black arrow). No filaments
containing regions of both dark and light staining were
found. The pH 7.7 h-ADF–actin filaments were sorted
into two subsets, based upon this staining, before subse-
quent image analysis.

Stable solutions were sought for p-ADF and h-ADF
complexes with F-actin at both pH 6.5 and 7.7, after the
procedure described for pure F-actin, and these are shown
in Fig. 4 a. Several contrasts exist with the distribution for
pure F-actin (Fig. 1 b). The means of the twist distribution
for all ADF–actin complexes were ~162°, but segments of
actin filaments decorated with ADF could also be found in
states with an average twist of 164°–165°, close to the nor-
mal F-actin twist. The dispersion in the twist distributions
is greatly reduced compared with pure F-actin, consistent
with the notion that ADF may be preferentially stabilizing
an existing state or states of F-actin out of several possible
states. By combining all images from each group, rather
than searching for subsets that yielded stable solutions, the
overall symmetries all converged to ~162°, except for the
p-ADF complex, pH 7.7, where the average symmetry was
~163°.

Reconstruction of the ADF–F-Actin Complexes by the
Single Particle Approach

Three-dimensional reconstructions were generated for dif-
ferent subsets of the ADF–actin complexes using the
IHRSR method (Fig. 5). To assist in interpreting the mass
due to ADF, we have superimposed an ADF–actin, pH 6.5,
reconstruction (Fig. 5 a), on a pure F-actin reconstruc-
tion (Fig. 5 a), and the difference density in Fig. 5 b is very
similar to what has previously been described for cofilin
(McGough et al., 1997). The most striking difference with
previous work, however, is the visualization of a second
ADF molecule bound to a site on the opposite side of the
actin subunit from the primary ADF. This second h-ADF
can be seen partially in Fig. 5 d (pH 6.5) and more fully in
Fig. 5 f (pH 7.7). The second ADF was completely absent
in the case of the lightly stained h-ADF, pH 7.7, set (Fig. 5
f). The difference in appearance of the second ADF be-
tween Fig. 5, d and f, could be due to the difference in
binding modes of ADF at different pH. The dark and light
staining of the h-ADF–actin filaments in the EM images
(Fig. 3, d and f) is due, therefore, to the presence or ab-
sence, respectively, of a second ADF molecule bound to
many actin subunits.

A second ADF molecule is not apparent in the whole
set reconstructions of p-ADF–actin complexes at either
pH 6.5 or 7.7 (Fig. 5, c and e). We were able, however, to
find traces of the second ADF molecule for the p-ADF
complex at pH 7.7. When a subset containing ~15% of
these images, isolated using cross-correlation procedures,
was reconstructed, a weak density due to the second ADF
was observed (data not shown). This suggests that the sec-
ond site is available for the p-ADF as well, but its occu-
pancy is significantly lower than that of h-ADF.

Binding of ADF Induces a Change in the Tilt of the
Actin Subunit

It has been shown that the binding of ADF (Hayden et al.,
1993; Hawkins et al., 1993; Ressad et al., 1998) and cofilin
(McGough et al., 1997) to F-actin is a cooperative process.
actin subunits at pH 7.7 causes an apparent breakage of the contact between subdomain 4 of one protomer and subdomain 3 of the protomer above it on the same long-pitch strand (Fig. 6 d, red arrow). It also shifts the contact between subdomain 2 of one protomer from subdomain 1 of the subunit above it to subdomain 3 of the subunit above. Overall, the disruption of the longitudinal contacts within the actin filaments may be the most important factor in destabilization of the filament as a result of this tilt of the actin subunit.

Constructing an Atomic Model of F-Actin with Two ADFs Bound per Subunit

We have shown that heterogeneity can exist within the ADF–actin filaments due to variations in twist, the presence of undecorated actin segments, as well as the presence of one or two ADF molecules per actin subunit. We have attempted to eliminate much of this heterogeneity within the set of h-ADF–actin complexes, at pH 7.7 and have generated a reconstruction from 2,116 segments found in the center of the twist distribution (162°) that show homogeneity with the respect of having two molecules of h-ADF bound per actin subunit (Fig. 7 a). The second ADF bound was also present in other subsets. Because of the greater homogeneity of this set, both the second ADF and actin are more clearly defined than in the reconstruction of the whole set (Fig. 5 f). Using this volume, it was possible to determine the approximate binding site for the second ADF on actin, and the resulting atomic model is shown in Fig. 7 b. According to our rigid body fitting (assuming no conformational changes in either G-actin or ADF), we predict that residues 22–25, 139–148, and 340–355 of the upper actin subunit and residues 28–29, 44–
tacts with actin, although there are near contacts with the second ADF molecule does not exhibit strong con-
part in the interaction with the primary ADF molecule.

50, and 88–101 of the lower actin subunit (Fig. 7 c) take part in the interaction with the primary ADF molecule.

actin COOH terminus at helix 359–364 and with helix 112–126 (Fig. 7 b and c). One possibility is that even after sorting images by twist to obtain a homogeneous population, these images had a partial second ADF occupancy that caused a weakening of the density of the second ADF molecule in the reconstruction. It has been suggested that the actin COOH terminus is flexible (Owen and DeRosier, 1993; Orlova and Egelman, 1995), and it is conceivable that small conformational changes of exposed loops and side chains help mediate the contacts between the second bound ADF and F-actin.

Discussion

Variable Twist of F-Actin

It has long been noted that F-actin exhibits a natural variation in crossover spacing (Hanson, 1967). An angular disorder model for this variability was proposed, where the possibility that actin monomers could rotate $\sim 10^\circ$ from their ideal helical positions was predicted (Egelman et al., 1982). McGough and colleagues (1997) showed that a protein of the ADF/cofilin family changed the mean twist of actin filaments by $\sim 5^\circ$ per subunit. Initially, it was suggested that changing the twist of actin might cause depolymerization of filaments via a weakening of the longitudinal bonds within the filament, specifically a breaking of the contact between subdomain 2 of the lower subunit with subdomain 1 of the upper subunit in the same long-pitch helix (McGough et al., 1997). It was subsequently shown that, in certain conditions, cofilin disrupted lateral contacts in the actin filament (McGough and Chiu, 1999). Most recently, using a mutant cofilin that changes the twist of actin filaments and fragments them, but does not depolymerize it, it was proposed that the change of twist by itself is not responsible for the enhanced rate of actin subunit dissociation (Pope et al., 2000). So the relationship between the change of twist induced by ADF/cofilin and filament destabilization remains unclear.

In the this work, we used a single particle approach for the analysis of helical structures (Egelman, 2000). The main advantage of this method is the ability to analyze short F-actin segments containing $\sim 12$ subunits, without needing to impose a uniform helical symmetry on a long filament. This has allowed us to address many issues of heterogeneity in both the twist of F-actin and the binding by ADF that have not been possible using conventional methods. We found that segments of F-actin by itself, without ADF/cofilin proteins, could exist in the state of $162^\circ$ twist observed for cofilin-decorated F-actin. Remarkably, we were able to find $\sim 8\%$ of the segments that had a mean twist of $158^\circ$, a change by $\sim 8^\circ$ per subunit from the mean twist of the whole set. We have suggested that the variability in twist within actin filaments is not continuous, but rather that subunits might exist in only a few discrete states (Orlova and Egelman, 2000). This model predicts a relatively static disorder, rather than the thermal torsional motions predicted by a continuous variability of twist. Although at this point we do not have any information about the number of such discrete states, or their distribution, our observation of many segments having a mean twist of $\sim 158^\circ$ suggests several points. It is likely that one state of twist is $\sim 158^\circ$. Another conclusion is that there must be a

Figure 6. Reconstructions of naked actin from h- and p-ADF–actin complexes at pH 6.5 and 7.7. Within actin filaments decorated with ADF, many segments can be found that appear to contain very little or no ADF. The rendered surfaces generated by IHRSR for such naked actin from p-ADF complex pH 6.5 (a), h-ADF complex, pH 6.5 (b), p-ADF complex, pH 7.7 (c), and h-ADF complex, pH 7.7 (d) are shown. Subdomains 1, 2, 3, and 4 of the actin subunit are labeled, and these domains are labeled as 1', 2', 3', and 4' on the next subunit along the same long-pitch helical strand. The normal density between subdomain 4 of one subunit and subdomain 3 on an adjacent actin monomer is present at pH 6.5 (a, red arrow), but absent at pH 7.7 (d, red arrow). G-actin subunits were fit (Materials and Methods) to naked F-actin densities from h-ADF set at pH 6.5 (e) and from h-ADF set at pH 7.7 (f). Two adjacent subunits from the symmetry-corrected model of F-actin (Holmes et al., 1990) are shown in cyan as a reference, whereas the fitted structures are shown in brown. Black arrows indicate the tilt of actin subunits away from the position in the Holmes model. The models (e and f) were visualized with the molecular graphics program VMD (Humphrey et al., 1996).
cooperativity in twist within the filament, so that the probability of a subunit having a particular twist is dependent on the twist of adjacent subunits. If twist states were randomly distributed, we would expect to see a nearly Gaussian distribution for the mean twist of 12 subunits (from the central limit theorem), and we clearly do not (Fig. 1b). Attempting to describe the actin filament in terms of a Markov model of twist probabilities dependent on the twist of adjacent subunits must still wait for more detailed information.

When the IHRSR method is applied to ADF–actin complexes, we observe a large reduction in the variability of twist of these filaments when compared with pure F-actin filaments. Consistent with what we observe for pure F-actin, we suggest that ADF/cofilin proteins stabilize an already existing state of twist of the actin filament rather than imposing a new one.

Two Molecules of ADF per Actin Subunit

Also, we have been able to see that one component of variability in the binding of ADF to actin is due to whether one ADF molecule or two bind per actin subunit. The distribution of these two possibilities is different between the h- and p-ADF. Under similar conditions at pH 7.7, the h-ADF–actin complex segments are more likely to be found in the 2:1 stoichiometry of binding than the p-ADF–actin complex.

ADF/cofilin proteins from different sources have different depolymerizing activities and for the majority of these proteins this activity is pH dependent (Yonezawa et al., 1985). The rate of actin depolymerization also depends on the isoform of actin. It was reported that UNC-60B from Caenorhabditis elegans disrupted C. elegans F-actin more efficiently than it disrupted rabbit muscle actin (Ono et al.,...
1999). On the other hand, *Acanthamoeba* actophorin depolymerizes rabbit F-actin faster than it depolymerizes *Acanthamoeba* actin (Maciver et al., 1998). h-ADF is more efficient in disrupting rabbit muscle actin filaments than is p-ADF (Ressad et al., 1998). To look at the structural basis for these differences, as well as to understand the mechanism of filament destabilization, we investigated h- and p-ADF–actin complexes with F-actin at high and low pH. One of the most important observations was the presence of a second ADF molecule bound to actin filaments. This can be easily observed with h-ADF at pH 7.7, when ADF is active in filament destabilization, but is also present more weakly with p-ADF at the same pH. We suggest that the greater efficiency observed for h-ADF compared with p-ADF in depolymerizing actin (Ressad et al., 1998) is due to the higher affinity of h-ADF for occupying the second binding site on actin. We were able to sort filament images containing the second ADF bound at the level of the raw micrographs, due to the different staining of these filaments (Fig. 3, d and f). The absence of filaments containing long regions with both light and dark staining suggests a large cooperativity in the binding of the second ADF molecule that extends over an entire filament. This is similar to what has previously been observed in the binding of heavy meromyosin to actin (Orlova and Engelman, 1997).

Although the binding of two ADF molecules per actin subunit has not been previously described, it is not inconsistent with previous observations. A stoichiometry of 1:3:1 for the interaction of h-ADF with rabbit F-actin at pH 6.5 was observed (Hawkins et al., 1993). This is consistent with our reconstruction for this complex in which only traces of the second ADF can be seen (Fig. 5 d). It was postulated (Hawkins et al., 1993) that there is no interaction between h-ADF and F-actin at pH higher than 7.5, where we can observe the 2:1 stoichiometry of binding more fully. But this is also consistent with our EM observations, since after 10 min of incubation there is no F-actin left because of the high depolymerizing activity of ADF at this pH. Even during a short incubation time (4 min on the grid) at pH 7.7, ADF was able to depolymerize approximately half of the F-actin (with a total actin concentration of 2 μM), and only short fully occupied filaments were observed by EM.

The second binding site for ADF is also in agreement with biochemical observations, even though many of the molecular details of the ADF–cofilin interaction with actin are still unknown. Using biochemical and genetic approaches, several sites on actin were predicted to be important for the interaction between these proteins. Chemical cross-linking was used to propose that residues 1–12 on actin’s NH2 terminus and residues 357–375 on the COOH terminus were involved in the interaction with the homologous starfish protein depactin (Sutoh and Mabuchi, 1986, 1989). It was shown that residues 334–336, 290–292, 326, and 328 of actin could be involved in the interaction with cofilin in yeast (Rodal et al., 1999). It was also suggested that residues 75–105 and 112–125 of rabbit muscle actin might interact with human cofilin (Renoult et al., 1999). The previously determined low resolution structure of the actin–cofilin filament displayed only general agreement with these data and predicted that residues 143–149, 345–346, 349–351, and 354 of the actin upper monomer and residues 21, 28, 36–38, 40–43, 49–54, 57, 61, 87–88, 90–96, and 101 of the lower monomer were involved in the interaction with cofilin. Since the helix containing residues 112–125 in actin is on the opposite side of the actin subunit from the position of the bound cofilin observed by McGough et al. (1997), a model of “intercalated” binding was proposed by Renoult et al. (1999). The COOH terminus of actin, suggested to be involved in the binding of ADF/cofilin proteins (Sutoh and Mabuchi, 1986), is also on the opposite side of the actin subunit. Our visualization of a second ADF bound to actin in the region of both helix 112–125 and the COOH terminus reconciles these observations, without needing to greatly change the mode of binding of the first ADF molecule from that described by McGough et al. (1997).

We suggest several reasons why a second cofilin molecule was not seen in previous EM studies of actin–cofilin complexes (McGough et al., 1997; McGough and Chiu, 1999; Pope et al., 2000). First, platelet F-actin was used in those studies, whereas we used rabbit muscle actin. As mentioned above, the isoform of actin can strongly influence the biochemical characteristics of the ADF–actin interaction. Platelet F-actin is more resistant to the depolymerization activity of human cofilin than rabbit F-actin. When rabbit F-actin was used after 30–90-min incubation on ice, they observed only short actin filaments that were useless in helical approaches (McGough et al., 1997). Second, the model for the cofilin–F-actin complex proposed by McGough et al. (1997) was based on experiments performed at pH 6.5, when this complex is stable. We observed the second molecule predominantly at pH 7.7, where actin is more easily depolymerized. Third, human cofilin shares only 70% homology with h-ADF (Bamburg, 1999) and could have a lower affinity for the second binding site.

**Variable Tilt of Actin Subunits**

Under conditions where F-actin is readily destabilized by h-ADF (pH 7.7), we can observe segments of naked actin where the subunits have undergone a large (~12°) tilt from their position in normal F-actin. This tilt appears to break the longitudinal bounds in the long-pitch helices. Since this tilt is much more striking in these naked segments than in the fully decorated F-actin, either this conformation occurs after ADF binds and dissociates from these regions or is induced by the binding of ADF to neighboring subunits. The possibility of a variable tilt of the actin subunit within the filament has been raised previously (Engelman and DeRosier, 1983; Tilney et al., 1983). In stereocilia of the inner ear, it was suggested that the ability of actin subunits to tilt by ~10° could explain the tilting of cross-bridges between actin filaments observed when these bundles bend (Tilney et al., 1983). Although actin filaments in muscle only undergo an extension of ~0.08 Å per subunit on average when full tension is induced (Huxley et al., 1994; Wakabayashi et al., 1994), relatively large axial perturbations of mass within F-actin can be seen by both x-ray diffraction (Lednev and Popp, 1990) and EM (Engelman and DeRosier, 1983) when filaments are packed into bundles. It was estimated that these displacements in axially projected mass could be roughly ±3 Å (Engelman and DeRosier, 1983), and the suggestion was made that a variable tilt of the subunits could recon-
cile such displacements with the relatively fixed average axial spacing. A comparison between our model for a subunit with a 12° tilt and the Holmes model (Holmes et al., 1990) shows that the axially projected mass distribution would shift by ~4 Å between the two. It is striking that the magnitude of the tilt previously predicted, in both angular range and projected axial shift, is quite similar to what we now observe.

It was proposed that the untwisting of actin by cofilin could disrupt the contacts between subdomain 2 of the lower subunit and subdomain 1 of the upper one, thus destabilizing the actin filament (McGough et al., 1997). The large tilt of the actin subunits is induced by ADF under conditions where filaments are readily depolymerized, and this tilt appears to make even greater changes in actin subunit–subunit contacts within the filament. Specifically, a large contact between subdomain 4 of one subunit and subdomain 3 of the subunit above is broken. We think it likely that this disruption of the normal structure of F-actin could be responsible for the destabilization of the filament and lead to either filament breakage, if it occurs, within filaments or subunit dissociation, if it occurs, at the ends of filaments.

Conclusions

The variable twist of F-actin allows segments of filaments to randomly exist in the same state of twist induced by ADF/cofilin in the absence of these proteins. The binding of ADF to actin causes cooperative changes in both F-actin tilt and twist to be propagated to actin subunits that are undecorated. The binding of two molecules of ADF per actin subunit reconciles previous biochemical observations with structural models. The depolymerization activity of ADF/cofilin may be due to both changes in the tilt and twist of actin subunits, and this may occur mainly after two molecules of ADF are bound per actin.

This work was supported by National Institutes of Health grants R01-AR42023 (E.H. Egelman) and P41-RR12255 (W. Wrighers).

Submitted: 8 December 2000
Reviewed: 1 February 2001
Accepted: 5 February 2001

References

Published April 6, 2001
Downloaded from on June 6, 2017


