Reconstitution of Actin-based Motility by Vasodilator-stimulated Phosphoprotein (VASP) Depends on the Recruitment of F-actin Seeds from the Solution Produced by Cofilin

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Vasodilator-stimulated phosphoprotein (VASP) is active in many filopodium-based and cytoskeleton reorganization processes. It is not fully understood how VASP directly functions in actin-based motility and how regulatory proteins affect its function. Here, we combine bead motility assay and single filament experiments. In the presence of a bundling component, actin bundles that grow from the surface of WT-VASP-coated beads induced movement of the beads. VASP promotes actin-based movement alone, in the absence of other actin nucleators. We propose that at physiological salt conditions VASP nucleation activity is too weak to promote motility and bundle formation. Rather, VASP recruits F-actin seeds from the solution and promotes their elongation. Cofilin has a crucial role in the nucleation of these F-actin seeds, notably under conditions of unfavorable spontaneous actin nucleation. We explored the role of multiple VASP variants. We found that the VASP-F-actin binding domain is required for the recruitment of F-actin seeds from the solution. We also found that the interaction of profilin-actin complexes with the VASP-proline-rich domain and the binding of the VASP-F-actin binding domain to the side of growing filaments is critical for transforming actin polymerization into motion. At the single filament level, profilin mediates both filament elongation rate and VASP anti-capping activity. Binding of profilin-actin complexes increases the polymerization efficiency by VASP but decreases its efficiency as an anti-capper; binding of free profilin creates the opposite effect. Finally, we found that an additional component such as methylcellulose or fascin is required for actin bundle formation and motility mediated by VASP.

Ena/VASP<sup>2</sup> proteins play important roles in many cellular processes, including actin-based movement of cells and the bacterial pathogen <i>Listeria monocytogenes</i> (1–3), fibroblast migration (4), filopodia formation (5, 6) (in conjunction with the actin-bundling protein fascin), axon growth and guidance (7–9), and cell shape and morphology changes (10). Ena/VASP contains an N-terminal EVH1, a proline-rich domain, and a C-terminal EVH2 domain. The EVH1 domain is required for recruiting Ena/VASP proteins to their sites of action. The proline-rich domain binds profilin or profilin-actin complexes. The EVH2 domain binds actin monomers (actin) and filaments (F-actin) via its GAB- and FAB-binding sites, respectively, and terminates with a coiled-coil region that mediates Ena/VASP tetramerization. Because the major pool of actin polymerization components is profilin-actin complexes (11), filament elongation by VASP depends on its ability to recruit and incorporate the complexes onto the filament barbed end (12–14). Numerous in vivo and in vitro studies were conducted to uncover the role of Ena/VASP proteins in actin-based processes, notably actin-based motility. Contradictory results were obtained both in vivo (4) and in vitro (15–20). The main objective of previous in vitro studies was to investigate how VASP mediates Arp2/3 complex-dependent actin polymerization (2, 15–18), yet none of these assays investigated how VASP functions alone in actin-based motility. Moreover, how actin polymerization mediated by VASP is translated into directed motion and the role of the actin regulatory proteins, profilin, capping proteins (CPs), and cofilin in these processes were not investigated. The effect of profilin on filament elongation by VASP was shown previously, yet contradictory results were observed (12, 21–23). VASP anti-capping (AC) activity is associated with the ability of VASP to compete with CPs for barbed end attachment and delay capping (12, 21, 22, 24). Profilin was suggested to have a positive effect on VASP AC activity (21, 22),

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<sup>†</sup>This article contains supplemental Movies 1–10.

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2 The abbreviations used are: Ena/VASP, enabled/vasodilator-stimulated phosphoprotein; AC, anti-capping; F-actin, actin filament; CP, capping protein; FAB, F-actin binding domain; FRAP, fluorescent recovery after photo-bleaching; TIRF, total internal reflection fluorescence; NEM, N-ethylmaleimide; MC, methylcellullose; cryo-TEM, cryo-transmission electron microscopy; TIRFM, total internal reflection fluorescence microscopy; tBu4, thymosin-β4.

31274 JOURNAL OF BIOLOGICAL CHEMISTRY
although the dependence of VASP AC activity on profilin concentration was measured in pyrene assays (21) and not directly at the individual filament level. Finally, the effect of cofilin on VASP function was not addressed in the past, despite the fact that both proteins are implicated in the formation and turnover of actin networks in cells (4, 10, 25–28). Although VASP and cofilin have been shown to be implicated in neuronal outgrowth and guidance (7, 29–36), the impact of cofilin on VASP activity has never been studied explicitly in vivo or in vitro.

By combining single filament experiment and bead motility assay, we show that VASP promotes actin-based movement alone, in the absence of any other actin nucleators. VASP functions as an actin recruiter, where its functionality relies on its ability to recruit preformed F-actin seeds via the FAB domain from the bulk solution and processively elongate them into long filaments. We find that cofilin promotes the nucleation of numerous F-actin seeds recruited by VASP, also under conditions where spontaneous actin nucleation is unfavorable, i.e. elevated profilin concentrations. VASP promotes filament elongation while competing with CPs, with an efficiency that depends on profilin concentration. Finally, the addition of an additional component such as methylcellulose or fascin is required for actin bundle formation and motility mediated by VASP.

EXPERIMENTAL PROCEDURES

**Protein Purification**—Actin was purified from rabbit skeletal muscle acetone powder (37) with a gel filtration step, stored on ice, and used within 2 weeks. His-VASPs (and constructs of VASP mutants) were produced as N-terminal His fusions as beads coupled to poly-L-proline and removed by urea followed by refolding and size exclusion. Human cofilin was purified by ammonium sulfate precipitation followed by size exclusion and by refolding and size exclusion. Recombinant GST-fascin was prepared by a modification of the method of Ono et al. (38). Human profilin was purified in the initial stage by capture to beads coupled to poly-L-proline and removed by urea followed by refolding and size exclusion. Human cofilin was purified by ammonium sulfate precipitation followed by size exclusion and ion exchange chromatography. Actin was labeled on Cys-374 with Alexa-Fluor 488 (Invitrogen) or Cy3 (Molecular Probes), according to standard protocols.

**Cryo-transmission Electron Microscopy (Cryo-TEM)**—Cryo-TEM was used to obtain high resolution information on the homogeneity of VASP distribution on the surface of the beads (Polysciences). Specimens for cryo-TEM were prepared according to a standard procedure (39). Samples were stored under liquid nitrogen before transfer to a TEM (Tecnai 12, FEI) operated at 120 kV in low-dose mode, with underfocus at a few micrometers to increase phase contrast. Images were recorded on a Gatan 794 or Gatan 791 CCD camera with Digital Micrograph software.

**Bead Motility Assay**—Polystyrene beads (Polysciences) (2.06 μm in diameter) were incubated in a solution consisting of 15 μM His-VASP constructs (WT VASP, VASP-ΔPro, or VASP-ΔFAB) for 30 min at room temperature. The surface of the beads was then passivated with a solution of 10% BSA according to the protocol detailed previously (40). All beads were used within 24 h. VASP-coated beads were immersed in a motility medium containing 10 mM Tris-HCl, pH 7.6, 1.7 mM Mg-ATP, 5.5 mM DTT, 15 μM glucose, 0.1 mg/ml glucose oxidase, 0.018 mg/ml catalase, 0.2 mM EGTA, 50 or 100 mM KCl, 1 mM MgCl₂, 1.1–1.65 μM Ca-ATP-actin (9.1% labeled with Alexa Fluor 488 and preincubated with profilin, when profilin is added), 0 or 20 nM CPs, 0–8 μM profilin, 0 or 2.5 μM human cofilin, and an actin bundling component, such as methylcellulose (MC) or fascin (55 nM). Replacing actin monomers with F-actin gave the same general behavior, i.e. growth of bundles and propulsion of beads. Yet quantitative analysis was only performed in assays done with actin monomers for which the concentration is known. For bead motility assays done in the presence of thymosin-β4 (tβ4) (ProSpecBio Ltd.), we used 1.1 μM Ca-ATP-actin (9.1% labeled with Alexa Fluor 488), 1 μM profilin, and 5 μM tβ4.

Samples were imaged within 10 min after mixing, by phase contrast and fluorescence microscopy using an Olympus IX-71 inverted microscope with a ×60 oil objective. The images and time-lapse were acquired using an Andor back illuminated DU-897 EMCCD camera controlled by Metamorph software (Molecular Devices).

FRAP Experiments—Fluorescent recovery after photo-bleaching (FRAP) experiments was used to measure the dynamics of actin at the tip of the bundle, in the vicinity of the bead, and along the bundle, away from the bead surface. FRAP experiments were done on a spinning disc confocal microscope (UltraView ERS FRET-H-System, PerkinElmer Life Sciences), based on an Axiovert-200 M microscope (Zeiss, Germany) equipped with a Plan-Neofluar ×63/1.4 oil objective and a Hamamatsu interline CCD camera (Hamamatsu C9100-50) driven by ImageSuite ERS. For the experiments, a spot area (spot size) of ~3 μm² was bleached (300 iterations at full laser power at 488 nm, argon source). Two pre-bleached frames were acquired at time intervals of 0.1 s between frames. Immediately after bleaching, the entire field was acquired at a scanning rate of 0.2 s per frame typically for 15 s and then at a rate of 30 s per frame. The two scanning rates were optimized for measuring the dynamics at short times (which is rapid and dominated by the diffusion of actin monomers into the bleached region) and at longer times (which is relatively slow and results from continuous polymerization of actin on the bead surface). The intensity of fluorescence recovery signal I(t) was normalized according to I(t) = I(t) / I(0) max - I(0) / max and I(0) are the intensities immediately before and after photo-bleaching, respectively.

Data Analysis, Bead Propulsion Velocity, and Bundle’s Elongation Rate—The rate at which bundles grow from the surface of the beads is designated ν_p, and the velocity of beads propelled by the action of a comet tail is designated as ν. Measurement of the beads’ propulsion velocity ν was carried out on beads propelled by the action of a single actin tail. ν_p and ν were extracted by measuring the changes in the total length of the growing bundles or propelling tail with time. Typically, 5–10 beads (with 5–10 bundles per bead) were analyzed for each experimental condition. For the analysis, we manually measured changes in the actin bundle total length (dL) from the bead surface to the end of the bundle for a time interval (dt). The detailed analysis is based on Ref. 41. The error bars are standard deviations. Student’s t tests were also applied (p values are indicated for values smaller than 0.05). Analysis of the experimental data
were performed using METAMORPH (Molecular Devices), Excel, and Origin (OriginLab Corp.).

Bundle Cross-section Intensity—The simplest way to estimate the number of filaments per bundle is to measure the bundle thickness. Yet most bundles are very thin (i.e. equal to or below resolution limits), such that measuring their thickness from fluorescence or phase contrast images is highly inaccurate. In contrast, the cross-section fluorescence can be measured accurately. For given illumination settings, camera gain, and percentage of labeled actin, the total fluorescence reflects the total number of filaments in that cross-section. Practically, the total fluorescence intensity is measured at a well defined distance from the bead surface (~5 μm). Thelogic for choosing this distance relies on the fact that it is, on one hand, far enough from the bead surface so that the measured fluorescence is the one emanating from the filaments, without being biased by the intensity emitted from the bead surface. On the other hand, this distance is sufficiently close to the bead surface to ensure that the measured fluorescence reflects the actual density of actin filaments that polymerize at the bead surface. Measuring the intensity farther away from the surface may give erroneous (lower) values due to possible disassembly of the actin bundle. For each experimental condition, we measured the cross-section intensity of 30–50 bundles. Measurements and analysis of the elongation rate, cross-section intensity, and bead velocity were done using METAMORPH (Molecular Devices), Excel, and Origin (OriginLab Corp.).

Single Actin Filament TIRF Assays—The protocol for total internal reflection fluorescence (TIRF) assay is based on Ref. 42. In experiments testing the effect of profilin and CPs, Ca-ATP-actin was first incubated with various concentrations of profilin (0–16.5 μM) in G-buffer (5 mM Tris-HCl, pH 7.8, 0.01% NaN₃, 0.1 mM CaCl₂, 0.2 mM ATP, 1 mM DTT) for 10 min at room temperature. In a following step, Ca-ATP-actin (15% labeled with Alexa Fluor 488 or Cy3) was converted to Mg-ATP-actin and incubated on beads, 1 volume (10 μl) of 10 mM EDTA, 1 mM MgCl₂, to give the appropriate factor of the final actin concentration, and incubated on room temperature for 15 min. In a following step, Ca-ATP-actin (15% labeled with rhodamine (Invitrogen)) and incubating them at room temperature for 30 min. For experiments using VASP-capped F-actin seeds, we initially incubated 40 nm phalloidin-stabilized F-actin seeds with 40 nm VASP in F-buffer (5 mM Tris-HCl, pH 7.8, 0.01% NaN₃, 100 mM KCl, 1 mM MgCl₂, and 0.2 mM EGTA) for 15 min at room temperature. 15 μl of the solution was flowed into a NEM-myosin-coated chamber and incubated for additional 2 min.

For experiments done in the absence of CPs, 1 volume (10 μl) of 2 × Mg-ATP-actin (1.5 μM, 15% labeled with Alexa Fluor 488) preincubated with 2 × profilin (0–18 μM), 100 mM KCl, and 50 nM VASP was mixed with 1 volume (10 μl) of 2 × TIRF buffer. Control experiments were carried out in the absence of VASP to measure bare filament elongation rates at the same profilin concentration. In the assays done with CPs, 1 volume (10 μl) of 4 × Mg-ATP-actin (3 μM, 15% labeled with Alexa Fluor 488) preincubated with 4 × profilin (0–36 μM) was mixed with 1 volume (10 μl) of 4 × solution composed of 200 mM KCl, 4 nm CPs, 100 nM VASP, and 2 volumes (20 μl) of 2 × TIRF buffer. For experiments done in the absence of CPs, 1 volume (10 μl) of 2 × Mg-ATP-actin (2.2 μM, 15% labeled with Cy3) preincubated with 2 × profilin (0–33 μM) was mixed with 1 volume (10 μl) of 2 × TIRF buffer (20 mM imidazole, pH 7.0, 100 mM KCl, 2 mM MgCl₂, 2 mM EGTA, 200 mM DTT, 0.4 mM ATP, 1% methylcellulose, 30 mM glucose, 40 μg/ml catalase, 200 μg/ml glucose oxidase). In these experiments, we used 0.5% (v/v) 2,06-μm diameter polystyrene microspheres (Polysciences) coated with 15 μM VASP according to the procedure used for the bead motility assays. 30 μl of the final solution was immediately loaded into a NEM-myosin-coated chamber and placed on the microscope.

Actin Nucleation in the Bulk Solution, Combined Effect of Cofilin and Profilin—We tested the effect of cofilin (0 or 2.5 μM) on actin nucleation in the absence (0 μM) and in the presence of 6 μM profilin. One volume (10 μl) of 2 × Mg-ATP-actin (2.2 μM, 15% labeled with Alexa Fluor 488) preincubated with 2 × profilin (0–12 μM), 100 mM KCl, and cofilin (0 or 5 μM) was mixed with 1 volume (10 μl) of 2 × TIRF buffer. 30 μl of the final solution was immediately loaded into a NEM-myosin-coated chamber and placed on the microscope. For each experimental condition, images were taken every 10 s. Actin nucleation was determined by counting the number of actin filaments present at short (5 min) and long (25 min) times, using ImageJ software.

Actin Polymerization from Phalloidin-stabilized F-actin Seeds—Phalloidin-stabilized F-actin seeds were prepared by mixing (1:1 molar ratio) actin filaments with phalloidin (9.1% labeled with rhodamine (Invitrogen)) and incubating them at room temperature for 30 min. For experiments using VASP-capped F-actin seeds, we initially incubated 40 nm phalloidin-stabilized F-actin seeds with 40 nm VASP in F-buffer (5 mM Tris-HCl, pH 7.8, 0.01% NaN₃, 100 mM KCl, 1 mM MgCl₂, and 0.2 mM EGTA) for 15 min at room temperature. 15 μl of the solution was flowed into a NEM-myosin-coated chamber and incubated for additional 2 min.

For experiments done in the absence of CPs, 1 volume (10 μl) of 2 × Mg-ATP-actin (1.5 μM, 15% labeled with Alexa Fluor 488) preincubated with 2 × profilin (0–18 μM), 100 mM KCl, and 50 nM VASP was mixed with 1 volume (10 μl) of 2 × TIRF buffer. Control experiments were carried out in the absence of VASP to measure bare filament elongation rates at the same profilin concentration. In the assays done with CPs, 1 volume (10 μl) of 4 × Mg-ATP-actin (3 μM, 15% labeled with Alexa Fluor 488) preincubated with 4 × profilin (0–36 μM) was mixed with 1 volume (10 μl) of 4 × solution composed of 200 mM KCl, 4 nm CPs, 100 nM VASP, and 2 volumes (20 μl) of 2 × TIRF buffer. The final solution was immediately loaded into the NEM-myosin-coated chamber containing phalloidin stabilized F-actin seeds and placed onto the microscope.

For each experimental condition, we followed the elongation of individual actin filaments growing from beads or F-actin seeds every 10 s, until overlapping between filaments was observed. When using F-actin seeds, for each profilin concentration the total length of typically 15 filaments was automatically tracked, using length measurements of the filament two-dimensional algorithm as plug-ins for ImageJ. The elongation rate vₑ was extracted from the linear part of the total length versus time curve (41).

Total internal reflection fluorescence microscopy (TIRFM) experiments were carried out on a Leica DMi6000 B microscope. Samples were excited by total internal reflection illumination at 488 and 568 nm, and images were captured with an Andor back-illuminated DU-897 EMCCD camera controlled by Leica software (LAS-AF-6000, Leica Microsystems CMS GmbH, Germany).

RESULTS

VASP Promotes Actin-based Motility—Micron-sized beads were coated with 15 μM WT VASP molecules homogeneously distributed over the surface as confirmed by cryo-TEM (data not shown). The beads were added to a mixture of purified proteins consisting of actin, profilin, cofilin, CPs, and MC, which promote actin filament bundling (see under “Experimental Procedures”) (43). 5–25 min after mixing (depending on experimental conditions), we observed the growth of numerous actin bundles from the surface of the beads (Fig. 1A and supplemental Movie 1), which sometimes fused to form thicker bun-
Bundle formation also in the presence of fascin, the characteristic bundling protein in filopodia (6). Numerous bundles grew from the surface of the beads, generating a dense array of straight bundles (Fig. 1B). In contrast to MC, we did not observe fusion of fascin bundles or motility, although the two phenomena are related because fusion promotes the breaking of the spherical symmetry, which is essential for motility (Fig. 1C and supplemental Movie 3).

Several observations led us to conclude that the barbed ends of the filaments in the bundles point toward the surface of the beads. The first observation is based on the fact that bundles that grew from the surface of the beads promoted the propul-
VASP Is an F-actin Seed Recruiter

FIGURE 2. Actin-based motility by VASP. A, initial stage of the separation of a three-bead cluster mediated by the polymerization of actin on the surface of the beads. The arrows mark the direction of motion of the beads. Conditions used are as follows: 1.65 μM Mg-ATP-actin (9.1% Alexa Fluor 488-labeled), 6 μM profilin, 2.5 μM cofilin, and 0.3% MC. Time between frames from left to right is Δt = 4, 5, and 13 min. Scale bar, 10 μm. B, time-lapse (phase contrast) images of 15 μM WT VASP-coated beads at late stages, originally part of a four-bead cluster. The beads are propelled by the action of an actin tail polymerizing at the rear. The arrows mark the direction of movement. Conditions used are as follows: 7 μM actin, 5 μM profilin, 200 nM CPs, 5 μM cofilin, and 0.3% MC. Time between frames from left to right is Δt = 3.5, 5.5, and 7.67 min. Scale bar, 20 μm.

Fission of beads (Fig. 1C and supplemental Movie 3). The second observation comes from FRAP experiments performed at different locations along the bundle (Fig. 1D), notably in the vicinity of the beads (Fig. 1D, left panel) and along the bundle, away from the bead surface (Fig. 1D, right panel). In the vicinity of the surface, the recovery of the fluorescence signal is initially fast and partial and is attributed to the diffusion of actin monomers into the bleached region (Fig. 1D, inset in left panel). It was followed by a slow recovery that grows linearly with time (Fig. 1D, inset in left panel), reflecting the continuous polymerization of actin at the bead surface. Full recovery was observed at the end of the process. A similar linear growth was observed for beads propelled by a branched actin tail, where the increase in fluorescence reflected the continuous polymerization of new actin branches at the bead surface (41). Along the bundle core, the recovery signal is partial and is attributed to the fraction of mobile actin monomers that diffuse inside the bleached region (Fig. 1D, right panel). Finally, the fact that the bundles are thinner at the extremity that points away from the bead surface suggests actin disassembly. We therefore conclude that the filaments’ barbed ends are associated with the VASP molecules at the bead surface.

Beads coated with VASP tend to stick and form clusters. The size of the clusters can vary, from a few (Fig. 2, A and B) to tens of beads. As time elapsed, the beads that were initially in contact started to separate and moved away from each other (see for example the three-bead cluster in Fig. 2A and supplemental Movie 4). Eventually, beads that originated from small clusters (≤3 beads) were propelled by the action of a single comet tail and moved at constant velocity v for ~1 h (Fig. 2B and supplemental Movie 5). The motion of clusters consisting of numerous beads (>3) was more complex, as in these cases the beads were propelled by several comets simultaneously (supplemental Movie 6). We compared the velocity v of moving beads with the growth rate of bundles v_g and found that they have very similar values (data not shown). This led us to conclude that a propelling tail and a growing bundle are equivalent objects such that the conclusions deduced from the analysis of growth of the bundles can be used for bead propulsion and vice versa.

Finally, we found that the VASP-driven motility described above is essentially dependent on the formation of actin bundles, which is the first required step toward breaking the spherical symmetry of the actin coat needed for motility. In Fig. 3, we demonstrated that there is a minimal concentration of MC below which there are no bundles. Moreover, we also show that the elongation rate of bundles is insensitive to the concentration of added MC. From that point on, all experiments were carried out at 0.3% MC.

VASP-coated Beads, Role of Profilin, Capping Proteins, and Cofilin on Bundle Formation, Growth, and Motility—The motility medium contained actin and accessory proteins implicated in actin nucleation and turnover, including profilin, CPs, and cofilin. The experiments were done at a physiological salt condition (100 mM KCl) for which VASP has no actin nucleation activity (21, 44). We investigated how each individual protein affected bundle formation and growth, as well as motility. The results are summarized in Fig. 4A. Our data show that bundles form and elongate from VASP-coated beads in the presence of actin alone, which suggests that neither profilin nor cofilin nor CPs are necessary for bundle formation and growth (Fig. 4, A and B).

We started by investigating the effect of profilin. Increasing the concentration of profilin did not significantly affect the formation of actin bundles up to 4 μM (Fig. 4B, upper row), whereas their ability to elongate was reduced at high profilin concentrations (>4 μM). The effect was even more significant when the concentration of profilin was further increased to 6 μM. At this concentration, the bundle formation was strongly suppressed. The system was now composed of short and diffuse bundles. Also, no motility of beads was observed.

We then investigated the combined effect of profilin and CPs. In the absence of profilin, numerous bundles formed in the presence of CPs (Fig. 4B, middle row), indicating that VASP efficiently competes with CPs for the barbed ends binding filaments, in accordance with previous studies (12, 21, 22, 24). The addition of profilin was found to affect bundle formation (Fig. 4B, middle row). For low concentrations of profilin, actin bundles formed without significant differences compared with the case where no profilin was added. However, the addition of 3 μM profilin totally inhibited bundle formation (instead, a diffuse layer of actin was formed), except for very rare cases (~5%) where thin bundles formed (data not shown). The total intensity of the actin layer gradually decreased with a further increase in profilin concentration; for 8 μM profilin, actin fluorescence was ~10-fold lower compared with the case with no profilin.

The strong reduction in system activity at high profilin concentrations was further investigated. At such a large molar excess of profilin over actin, the observed reduction in system activity may result from the binding to VASP of free profilin instead of profilin-actin complexes (13). At such large profilin concentrations, the spontaneous actin nucleation is also strongly suppressed (45). To discriminate between these two possible effects, we replaced profilin with tβ4, which is known
to prevent spontaneous actin nucleation and sequester actin monomers (46) but not to interact with VASP. We used 1 μM profilin and added 5 μM tβ4. Because tβ4 and profilin can exchange monomers (47), polymerization of profilin-actin complexes would still proceed with low profilin concentrations yet nucleation in the bulk could still be prevented. The experiments were done in the absence of CPs to prevent any blocking of actin polymerization at the bead surface. The addition of tβ4

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suppressed system activity (Fig. 4C). Only very weak fluorescence was observed on the bead surface, and no bundles were formed. Our data thus show that even under conditions that favor filament elongation, bundle formation and motility are lost when actin nucleation is prevented in the bulk solution. From these experiments, we also conclude that a large molar excess of profilin strongly reduces de novo nucleation of F-actin seeds in the bulk, which is needed to initiate bundle formation rather than blocking the proline-rich domain of VASP.

In contrast to profilin, the addition of micromolar cofilin concentration (2.5 μM) to the motility medium had a positive effect on system activity. First, regardless of the motility medium composition, the beads were motile in the presence of cofilin (Fig. 4A). Second, the addition of cofilin to a pure actin solution or to a solution of actin and CPs (Fig. 4B, bottom row) induced the formation of more bundles (approximately twice) in comparison with a system lacking cofilin (Fig. 4B, upper row). The bundles were thinner (i.e. had lower cross-section intensity) and elongated faster (Fig. 4D, blue brace). The faster velocity may arise from two possible mechanisms as follows: (i) lower depletion of actin monomers due to lower overall number of filaments (more bundles but much thinner), or (ii) binding of cofilin along the backbone of the filaments, proposed to occur at micromolar concentrations (48), reduces the binding strength of the VASP molecules to the side of the growing filaments, overall promoting faster elongation rates. A similar argument was used to explain the increase in velocity of beads propelled by the action of a branched actin tail (41, 49).

Finally, against the negative effects observed at high profilin concentrations, the addition of cofilin rescued motility and bundle formation, with or without CPs (Fig. 4B, green and red asterisks, respectively and Fig. 4D, green brace). Repeating the experiments at 50 mM KCl showed a certain improvement in the ability of the system to generate actin bundles (~15% of the beads formed 1–2 bundles, whereas 85% of the beads generated diffused actin bundles similarly to those formed with 100 mM KCl), which is in accord with the fact that VASP nucleates actin at nonphysiological salt concentrations (44, 50). Nevertheless, none of the beads were motile. Moreover, and similarly to the results observed at physiological salt conditions, the addition of cofilin rescued bundle formation and motility. Our data suggest that actin nucleation efficiency of VASP at high profilin concentrations is too low to support bead motility and bundle formation, regardless of salt concentration. The fact that the beads are motile and grow numerous bundles in the presence of micromolar concentrations of cofilin suggests that cofilin enables actin nucleation even at high profilin concentrations, whereas spontaneous actin nucleation is strongly suppressed.

To correlate between bundle formation by VASP and cofilin-mediated F-actin seed formation in the bulk, we examined the ability of cofilin to promote actin nucleation in the absence and in the presence of high concentrations of profilin using TIRF microscopy. The concentrations of profilin and cofilin were the same as those used in the bead motility assay. In the absence of profilin, the addition of micromolar concentrations of cofilin (2.5 μM) increased the number of F-actin seeds nucleated in the bulk (Fig. 4E), in accord with a previous study (48). Numerous F-actin seeds were nucleated within a few minutes (~5 min), which also corresponded to the time when bundles started to form on the beads (Fig. 4B, upper row). We also examined the ability of cofilin to nucleate actin at high concentrations of profilin (6 μM). At short times, cofilin increased the number of F-actin seeds nucleated in the bulk but not significantly in comparison with a solution lacking cofilin (Fig. 4E). However, after 20–25 min, which corresponds to the time when bundles started to form on the beads, we measured an ~6-fold increase in the number of F-actin seeds, which is similar to the number of F-actin seeds produced after ~5 min in the system lacking profilin (Fig. 4E). This means that in the presence of high concentrations of profilin, F-actin seed nucleation by cofilin is delayed but not inhibited. Overall, our data show that there is a tight correlation between F-actin seed production in the solution and bundle formation by VASP. Bundle formation by VASP is regulated by the concentration of F-actin seeds produced in the bulk such that bundles start to form when the concentration of seeds exceeds a concentration threshold.

**VASP Mutants Coated on Beads, FAB Domain Is Indispensable for Actin-based Activity by VASP**—Our data suggest that bundle growth and motility by VASP are initiated by the recruitment of F-actin seeds from the solution to the bead surface and their subsequent elongation by the recruitment and transfer of profilin-actin complexes to the filament barbed end.

To reveal the importance of the FAB and proline-rich domains for VASP function, we used two mutants as follows: VASP-ΔFAB that lacks the F-actin-binding motif and VASP-ΔPro that lacks the proline-rich domain responsible for recruiting profilin-actin complexes. The experiments were done in the presence of 6 μM profilin and 2.5 μM cofilin but in the absence of CPs to prevent the blocking of filament growth. Under these conditions, WT VASP induced the growth of numerous bundles from the surface of the beads (Fig. 5). The deletion of the
FAB or the proline-rich domains led to dramatic effects. Replacing WT VASP with VASP-ΔPro rendered most of the beads (>95%) inactive. The very few beads that grew bundles did so very inefficiently with $v_{p, \text{VASP-ΔPro}}/v_{p, \text{WT VASP}} = 0.075$; also, VASP-ΔFAB did not produce any bead movement. Replacing WT VASP with VASP-ΔFAB was even more dramatic, abolishing motility and the formation and growth of actin bundles. Overall, the data show that both the FAB and the proline-rich domains are essential for the activity of VASP, although the deletion of the FAB domain is much more significant, rendering VASP essentially inactive.

**Polymerization of Individual Actin Filaments from VASP-coated Beads in the Presence of Increasing Concentrations of Profilin**—Our bead assay experiments have shown that the recruitment of the profilin-actin complex via the proline-rich domain is important for VASP function. Our next goal was to investigate how profilin influences bundle elongation rate. However, because bundles did not form at high concentrations of profilin, we could not measure the elongation rate of bundles under such conditions.

We overcame this problem by employing TIRF microscopy. This technique is extremely sensitive and allows the visualization of individual actin filaments growing from the surface of beads. It is also optimal for conditions where actin nucleation is very weak and only a few filaments grow from the surface. We followed the growth of individual actin filaments from the surface of the beads for a wide profilin concentration range (0–16.5 μM) (Fig. 6 and supplemental Movies 7–10). The elongation rates never exceeded the value measured with no profilin and decreased with the increase in profilin concentration (data not shown). The fact that we did not see any improvement, even at low profilin concentrations, was surprising. Generally, the formation of actin filaments in the bulk preceded the growth of filaments on the surface of the beads. Increasing profilin concentration gradually decreased the number of filaments that nucleated in the bulk and that grew from the surface of the beads (Fig. 6, A–D). The decrease in actin nucleation in the bulk with the increase in profilin concentration is in accord with our results (Fig. 4E) and biochemical assays (45). Thus, even though we could follow the growth of individual filaments from the surface of the beads and measure their elongation precisely, we could not compare the elongation rates measured at different profilin concentrations. The main reason for this comes from the fact that actin nucleation and growth in the bulk solution compete with that on the surface of the beads. Moreover, their relative importance depends on the concentration of added profilin. At low profilin concentrations, spontaneous actin nucleation in the bulk was very efficient, and numerous filaments elongated there before filament growth was observed on the surfaces of the beads, such that the concentration of actin monomers available for polymerization on the surface was reduced. This can explain the decrease in the elongation rates observed at low profilin concentrations. In contrast, at high profilin concentrations spontaneous nucleation of actin in the bulk was strongly reduced, and only a very few filaments grew in the bulk before filaments grew on the surface such that the concentration of free monomers available for polymerization on the surface was higher in comparison with that at low profilin concentrations. Because the elongation rate is controlled by the concentration of free monomers, comparing the elongation rates obtained at different profilin concentrations was not possible.

**Effect of Profilin on the Polymerization of Actin from Phalloidin-stabilized F-actin Seeds**—To eliminate the problem of filament nucleation, we decided to use F-actin seeds. The use of F-actin seeds enabled us to compare quantitatively the effect of profilin concentration on individual filament elongation rates $v_p$ (Fig. 7). Several previous TIRF studies observed contradictory results regarding the effect of profilin on VASP-mediated elongation of individual filaments. One report reached the conclusion that profilin has no effect on the rate of filament elongation (23). Hansen and Mullins (12) found that profilin increases filament elongation rate, whereas Pasic et al. (22) observed the opposite effect. To shed light on the profilin effect on VASP function, we extended the concentration range studied from 75 nM to 9 μM profilin. We used TIRFM to measure the growth of actin (Alexa Fluor 488-labeled) from phalloidin-stabilized F-actin seeds (rhodamine-labeled) in the presence of 25 nM WT VASP, with different quantities of profilin (Fig. 7A). As a control, we used bare F-actin seeds and measured their elongation rate in the absence of VASP. In the absence of profilin, the elongation rate of VASP-capped seeds $v_{p, \text{bare F-actin seeds}} = 0.86 \pm 0.08 \, \mu m/min$ is the same as that of bare F-actin seeds $v_{p, \text{bare F-actin seeds}} = 0.88 \pm 0.08 \, \mu m/min$, in accord with previous results (22). Considering a rate constant of $8 \, \mu M^{-1} \, s^{-1}$ and unlabeled actin concentration (51), we estimate the elongation rate to be 0.89 μm/min, as we find experimentally. Except for very low concentrations of profilin (<375 nm profilin), filaments elongated up to 50% faster in the presence of VASP than without it (bare F-actin seeds), suggesting that VASP positively influences filament elongation rate (Fig. 7A). Also, in the presence of VASP, we observed a nontrivial variation of the elongation rate on profilin concen-
Anti-capping is associated with the ability of VASP molecules to compete with CPs for barbed end attachment and delay capping, overall resulting in a higher total amount of polymerized actin (21, 24) and longer filaments (12, 22). At the single filament level, the increase in filament length can result from the following: (i) the ability of VASP to compete with CPs for barbed end attachment and delay the time until capping (which is a measure of VASP AC activity); (ii) enhanced filament elongation rate \( v_p \), or (iii) both. The effect of profilin concentration has not been studied at the single filament level, only in bulk pyrene assays (21).

We use TIRFM to measure the growth of actin (Alexa Fluor 488) from rhodamine phalloidin-stabilized F-actin seeds in the presence of WT VASP (25 nM), CPs (1 nM), and increasing amounts of profilin (0–9 \( \mu \)M). Bare F-actin seeds do not elongate in the presence of CPs (data not shown), even if VASP molecules are in the solution. This suggests that the affinity of CPs for free barbed ends is much greater than that of WT VASP (52, 53). VASP-capped F-actin seeds elongated continuously in the absence of CPs (data not shown), but in the presence of CPs the elongation plateaued after a certain time \( t_b \) (see image in Fig. 7B). This suggests that the binding of CPs is delayed in the presence of VASP, in accord with previous studies (12, 22, 24). The time it takes for the filaments to get capped and stop elongating is characterized by \( \tau_p = t_b - t_i \), where \( t_i \) is the initial time of elongation. Under our experimental condition, \( \tau_p \) is of the order of several minutes (Fig. 7B, upper plot). VASP AC activity is the ability of VASP molecules to compete with CPs for barbed end attachment, and it reflects the number of VASP molecules that associate/dissociate reversibly from the filament barbed end before a CP molecule binds irreversibly and terminates the elongation process. We can calculate this number by dividing \( \tau_p \) by \( k_{off}^{-1} \), the association time of a single WT VASP tetramer to the filament barbed end. Because VASP barbed end association time is independent of profilin concentration (12), the same value of \( k_{off}^{-1} = 1.45 \) s was used for all concentrations of profilin tested. For our experimental conditions, there are hundreds of VASP binding/unbinding events before capping occurs (Fig. 7B, bottom plot). The effect of profilin on \( \tau_p \) and VASP AC shows that up to 3 \( \mu \)M profilin, profilin has a negative effect on VASP AC. We observed an \( \sim 40\% \) decrease in \( \tau_p \) (and VASP AC) compared with a solution lacking profilin. A positive effect of profilin on VASP AC was observed above 3 \( \mu \)M. In that case, \( \tau_p \) and VASP AC were larger by \( \sim 50\% \) in comparison with a solution lacking profilin.

**DISCUSSION**

The mechanism by which VASP mediates actin-based movement is addressed in this work for the first time. Using a biomimetic bead assay, we show that VASP can promote actin-driven motility without the need of any additional (potent) actin nucleators. In this study, we combine bead motility and single filament TIRF assays to investigate VASP function in actin nucleation, filament growth, bundle formation and elongation, and motility in the presence of different actin regulatory proteins implicated in actin turnover. We systematically investigate the role of profilin, CPs, and cofilin alone and in admixture.
to study their individual and combined effects on VASP function.

Our data show that at physiological salt conditions VASP nucleation activity is too weak to support motility and bundle formation. Rather, VASP functions as an actin recruiter, where its functionality relies on its ability to recruit F-actin seeds from the bulk solution via VASP FAB domain to the surface of the beads. At low profilin concentrations, F-actin seed formation in the bulk solution occurs via spontaneous actin nucleation and cofilin-mediated actin nucleation. High profilin concentrations inhibit the spontaneous nucleation of actin in the bulk, thereby the majority of the F-actin seeds are produced by cofilin. B, filament elongation and anti-capping activity by VASP. VASP molecules promote processive elongation of unbranched actin filaments by association of profilin-actin complexes to the proline-rich domain, which are then transferred to the filament barbed end via VASP GAB domain, while remaining attached to the filament’s side via VASP FAB domain. Enhanced (reduced) elongation rates and reduced (enhanced) VASP AC activity are observed for low (high) profilin concentrations, respectively. C, bundle formation depends on filament length. Transition from individual filaments to bundles occurs above a certain filament length for which the energy penalty associated with filament bending is compensated by the energy gain associated with their bundling.

Our data show that VASP promotes motility and bundle formation only if sufficient F-actin seeds are produced in the bulk solution. We find that high concentrations of cofilin...
promote the nucleation of numerous F-actin seeds even at high concentrations of profilin, which is needed in cells to minimize uncontrolled spontaneous nucleation in the bulk. Our data are consistent with in vivo studies demonstrating that high concentrations of active cofilin at the leading edge stimulate actin assembly and motility in carcinoma cells (57). The necessity for seeds for the initiation of branched network formation by the Arp2/3 complex was also shown in vitro both experimentally and theoretically (56, 58), and it is consistent with the fact that freshly polymerized actin is preferred for dendritic nucleation by the Wiskott-Aldrich syndrome protein-Arp2/3 complex (59). We thus suggest that cofilin functions at the cell’s leading edge as an F-actin seed supplier by nucleating fresh polymerized actin recruited by VASP and Wiskott-Aldrich syndrome protein-Arp2/3 complex at the cell’s leading edge of motile cells (24, 29, 57, 59, 60) and in neuronal systems (33, 36). We argue that the production of F-actin seeds in the bulk solution in cells does not contradict the requirement that uncontrolled filament assembly should be minimized. In fact, F-actin seeds that are not recruited at the cell leading edge are rapidly capped by CPs (which also localize to the cell leading edge (28)) and are depolymerized to refill the pool of actin monomers. In that way, network formation is regulated, and uncontrolled filament growth is minimized.

Following the recruitment of F-actin seeds, VASP promotes the elongation of filaments, while competing with CPs for barbed end attachment. Here, we show that the ability of VASP to compete with CPs depends on the concentration of profilin. At low/intermediate profilin concentrations, profilin enhances the elongation rate and reduces VASP anti-capping activity, while at high concentrations of profilin, we observe the opposite effects. This behavior can be explained as follows: at low/intermediate profilin concentrations, profilin-actin complexes are the major components in solution, whereas at high profilin concentration there is free profilin. We found that profilin concentration determines the affinity of VASP to actin filaments. At low/intermediate profilin concentrations, this affinity is weak, which allows both actin monomers and CPs to have easier access to the filament’s barbed ends, thereby resulting in a higher elongation rate and reduced AC activity. However, at high profilin concentrations, the affinity of VASP to the filament barbed ends is high, resulting in lower accessibility of actin monomers and CPs to the barbed ends, thereby giving lower elongation rates and higher AC activity. In light of these results, and because the concentration of profilin in cells is elevated, we conclude that it is likely that in vivo VASP functions as a good anti-capper at the expense of reduced elongation rates. Therefore, VASP provides cells with the ability to grow persistent extensions, which grow continuously (but at a moderate rate) and do not undergo erratic movements and retractions. Such extensions are useful for many cell types and can explain the observed accumulation of Ena/VASP proteins in protruding lamellipodia (28) and at the tips of filopodia (5, 61, 62), where they efficiently compete with CPs.

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