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Divergent *Rickettsia* species exhibit distinct mechanisms of actin-based motility

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Abstract

Many *Rickettsia* species undergo actin-based motility to promote cell-cell spread during infection. Rickettsial genomes often encode two motility effectors, RickA and Sca2, which in the spotted fever group I species *R. parkeri* act by activating the host Arp2/3 complex, or by mimicking eukaryotic formins, respectively. The function of RickA and Sca2 orthologs in the distantly related species *R. bellii* was unclear. We report that *R. bellii* RickA activates the host Arp2/3 complex but has no discernable role in bacterial motility. The *R. bellii* Sca2 ortholog, Sca2/6, nucleates and elongates actin with a flexible structure and an unusual actin monomer-binding motif in a mechanism distinct from formins or other microbial actin nucleators. *R. bellii* motility is solely correlated with Sca2/6 localization and, compared with *R. parkeri* motility, is slow and meandering, generating distinctly organized actin tails. The evolutionary flexibility in the mechanism and regulation of rickettsial actin-based motility suggest similar adaptability for other microbes.

Introduction

Intracellular bacteria have evolved numerous ways to co-opt the host cell actin cytoskeleton for processes including invasion, innate immune avoidance, and cell-cell spread (Colonne et al., 2016; Lamason and Welch, 2017; Stradal and Schelhaas, 2018). Actin-based motility is one mechanism through which actin contributes to microbial cell-cell spread. This process uses the force derived from the nucleation and elongation of actin filaments at the bacterial surface to drive movement through the host cell cytoplasm, resulting in the assembly of actin comet tails (Lamason and Welch, 2017; Dowd et al., 2021). Motility positions bacteria near the host cell plasma membrane to enable entry into membrane protrusions that can be engulfed into neighboring cells (Lamason and Welch, 2017; Dowd et al., 2021).

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The mechanism of actin-based motility has been studied for a variety of pathogens including *Rickettsia* species (Lamason and Welch, 2017; Alqassim, 2022). *Rickettsia* are Gram-negative obligate intracellular alphaproteobacteria that typically reside in arthropods such as ticks, fleas, and mites (Voss and Rahman, 2021). The *Rickettsia* genus is divided into 5 distinct groups clustered by molecular phylogenomics and disease features (El Karkouri et al., 2022; Rymaszewska and Piotrowski, 2024). These groups include the spotted fever groups (SFG I/II) and typhus group (TG), which contain pathogens that cause spotted fever and typhus in humans. They also include the canadensis group (CG) and bellii group (BG), which contain species considered to be non-pathogenic tick endosymbionts. Actin-based motility has been observed for divergent species within most of the groups including the SFG I species, *R. parkeri*, and the BG species, *R. bellii* (Teysseire et al., 1992; Heinzen et al., 1993; Gouin et al., 1999; Van Kirk et al., 2000; Haglund et al., 2010; Pan et al., 2022).

Rickettsia species are distinctive amongst microbes that undergo actin-based motility in that their genomes often encode two different motility effectors, RickA and Sca2 (Kleba et al., 2010; Haglund et al., 2010; Reed et al., 2014; Lehman et al., 2024). Studies with the SFG I species, *R. parkeri*, harboring transposon mutants in *rickA* or *sca2* demonstrated that RickA and Sca2 function independently to drive two temporal phases of motility (Reed et al., 2014; Harris et al., 2018). RickA-motility occurs at early time points of infection (< 2 h post-infection (hpi)), is slower, and proceeds in more meandering trajectories, resulting in actin tails that are short and curved (Reed et al., 2014; Jeng et al., 2004). Sca2-motility occurs later (> 5 hpi), is faster, and proceeds in more linear trajectories, resulting in actin tails that are long and straight (Reed et al., 2014). Mutations in *rickA* and *sca2* lead to the formation of smaller plaques during infection of cultured cells, indicating both RickA-motility and Sca2-motility contribute to cell-cell spread (Kleba et al., 2010; Reed et al., 2014; Tran et al., 2025). In a mouse model of infection, RickA is important for eschar formation in the skin, whereas Sca2 is important for dissemination to internal organs (Burke et al., 2021; Tran et al., 2025).

In addition to differences in their roles in cell-cell spread and pathogenicity, RickA and Sca2 from SFG I species nucleate actin filaments through distinct biochemical mechanisms. RickA is secreted by bacteria through an unknown mechanism and acts as a nucleation-promoting factor (NPF) that activates the host Arp2/3 complex to form Y-branched actin filaments through conserved C-terminal WH2, central, and acidic (WCA) motifs (Gouin et al., 2004; Jeng et al., 2004). Sca2 is a type V secretion system (T5SS) or autotransporter protein, a protein family that consists of an N-terminal signal sequence that enables passage through the bacterial inner membrane, a C-terminal translocation domain consisting of a β-barrel structure that embeds in the outer membrane, and a central passenger domain that threads through the translocation domain and is displayed on the bacterial surface (Fan et al., 2016). The Sca2 passenger domain from SFG I species nucleates and processively elongates actin filaments in a profilin-dependent manner, similar to eukaryotic formin proteins (Haglund et al., 2010; Madasu et al., 2013; Alqassim et al., 2019). Within the passenger domain of SFG I Sca2, the middle domain binds to monomeric globular (G) actin, and the N-terminal domain (NTD) folds into a ring structure resembling a formin-like core that cooperatively binds two actin subunits with high affinity in conjunction with the C-terminal repeat domain (CRD) (Alqassim et al., 2019; Carman et al., 2023). Interestingly,

the passenger domain of the Sca2 ortholog from the divergent BG species, *R. bellii*, differs dramatically in sequence from SFG I Sca2 (Haglund et al., 2010). The single gene encoding the *R. bellii* Sca2 ortholog may have undergone a tandem duplication during rickettsial evolution, yielding adjacent *sca2* and *sca6* genes (Blanc et al., 2005; Ngwamidiba et al., 2005). Both genes are intact in the SFG II species, *R. akari*, whereas one gene is degraded in SFG I species, and one or both are degraded in TG species (Blanc et al., 2005; Ngwamidiba et al., 2005; Sears et al., 2012). For this reason, the *R. bellii* ortholog is referred to as Sca2/6 (Lehman et al., 2024). We do not yet know whether and how sequence or regulatory differences in RickA or Sca2 orthologs contribute to differences in the mechanism and properties of actin-based motility in diverse *Rickettsia* species.

To better understand the functions of actin-based motility proteins in divergent *Rickettsia* species, we compared the actin nucleation mechanisms, protein localization patterns, and motility characteristics between the non-pathogenic tick endosymbiont *R. bellii* and the well-studied pathogenic SFG I species *R. parkeri*. We found evidence for considerable evolutionary flexibility in actin-based motility proteins and mechanisms within the *Rickettsia* genus.

Results

RickA is conserved while Sca2/6 has diverged in *R. bellii*

To better understand how RickA and Sca2 have diverged across *Rickettsia* species, we aligned the protein sequences from representative *Rickettsia* species from the SFG I/II, TG (Sca2 only), and BG groups, including *R. parkeri* strain Portsmouth and *R. bellii* strain RML 369-C. For RickA, the overall organization of sequence motifs is conserved (Figure 1A). Alignment of RickA protein sequences from representative species from each *Rickettsia* group showed that the C-terminal WCA region exhibits 27% sequence identity and 56% similarity overall. SFG I and BG species contain a single WH2 motif, whereas SFG II species contain two WH2 motifs. This high degree of conservation suggests that the biochemical function and activities of RickA orthologs are conserved between species.

In contrast, Sca2 orthologs from divergent species differ considerably in the organization of sequence motifs in the passenger domain (Figure 1B), likely as a result of gene duplication and degradation events (Figure S1) (Blanc et al., 2005; Ngwamidiba et al., 2005; Sears et al., 2012). In comparison with Sca2 from the SFG I species *R. parkeri* (1823 amino acids), Sca2/6 from *R. bellii* is half as long (909 amino acids) and lacks the N-terminal repeats within the NTD and CRD domains that were previously shown to form a partially occluded formin-like core (Figure 1B) (Haglund et al., 2010; Madasu et al., 2013; Alqassim et al., 2019; Carman et al., 2023). The passenger domains of the Sca2 orthologs from representative *Rickettsia* species only exhibit 11% identity and 33% similarity. Moreover, algorithms such as FoldSeek (van Kempen et al., 2024) and Dali (Holm et al., 2023) did not point to proteins with similar predicted structures and only returned protein alignments with weak e-values ($> 10^{-2}$) or Z-alignment scores (< 4.9) (Holm et al., 2008). Using a combination of AlphaFold 3 (Abramson et al., 2024) and InterPro (Blum et al., 2024) protein domain predictions, we annotated the passenger domain of *R. bellii* Sca2/6 as having a signal sequence (S), a poly-proline region (P), a putative

G-actin binding motif (G) previously annotated as a WH2 motif (Haglund et al., 2010), and a C-terminal domain (CTD) (Figure 1B). As described for Sca2 from the SFG I species *R. conorii*, the previously annotated WH2 motifs in *R. bellii* Sca2/6 (Haglund et al., 2010) are predicted to have different secondary structures than canonical WH2 domains (Ducka et al., 2010; Dominguez, 2016). Nevertheless, AlphaFold 3 structure predictions suggested that an α-helix within the previously annotated WH2 motif of *R. bellii* Sca2/6 binds to one G-actin molecule at its barbed end (pLDDT > 70, Figure S2A). This updated analysis confirms that the passenger domain of the Sca2 orthologs differs substantially between *R. bellii* and the SFG I species *R. parkeri*, suggesting potential differences in biochemical activities and mechanisms of action to generate actin filaments.

We also sought to confirm that *R. bellii* expresses RickA and Sca2/6. Both proteins were detected in *R. bellii* bacterial lysates by immunoblotting with anti-RickA or anti-Sca2/6 antibodies (Figure S3A). Thus, *R. bellii* expresses both actin-based motility effector proteins.

R. bellii RickA activates the host Arp2/3 complex *in vitro*

RickA proteins from the SFG I species, *R. rickettsii* (Jeng et al., 2004), and *R. conorii* (Gouin et al., 2004) were previously shown to function as NPFs and activate the host Arp2/3 complex. To test whether RickA from *R. bellii* also possesses NPF activity, we expressed and purified glutathione S-transferase (GST) tagged RickA (GST-RickA; Figure S3B) and performed pyrene actin polymerization assays (Figure S4A). Purified GST-RickA or Arp2/3 complex individually did not accelerate actin polymerization compared with actin alone. However, when combined, GST-RickA activated the Arp2/3 complex to nucleate actin in a concentration-dependent manner. These data confirm that the NPF activity is conserved in *R. bellii* RickA.

R. bellii Sca2/6 nucleates and elongates actin filaments *in vitro*

Our sequence comparisons of Sca2 orthologs from *R. parkeri* and *R. bellii* suggested that the biochemical activity of *R. bellii* Sca2/6 may differ considerably from that of *R. parkeri* Sca2, which nucleates actin assembly and caps actin filaments in the absence of profilin (Haglund et al., 2010; Madasu et al., 2013). To determine whether *R. bellii* Sca2/6 nucleates actin assembly, we expressed and purified the maltose-binding protein (MBP) tagged passenger domain of Sca2/6 (MBP-Sca2/6; excluding the signal sequence and autotransporter domains; Figure S3C) and performed pyrene actin polymerization assays. Purified MBP-Sca2/6 alone nucleated actin assembly in a concentration-dependent manner (Figure 2A). Cleavage of the MBP tag did not significantly impact actin nucleation activity (Figure S4B). For comparison, *R. parkeri* GST-Sca2 alone also nucleated actin filament assembly, but fluorescence plateaued at a lower value due to its barbed end capping activity in the absence of profilin (Haglund et al., 2010) (Figure 2A). Thus, *R. bellii* Sca2/6 nucleates actin assembly without capping the barbed ends of actin filaments.

R. parkeri Sca2 processively associates with barbed ends and enables filament elongation in the presence of profilin (Haglund et al., 2010; Madasu et al., 2013), like eukaryotic formins (Breitsprecher and Goode, 2013; Valencia and Quinlan, 2021). For comparison, we sought

to assess whether *R. bellii* Sca2/6 stably associates with actin filaments and/or affects the rate of filament elongation using total internal reflection fluorescence (TIRF) microscopy. We fluorescently labeled the C-terminus of *R. bellii* Sca2/6 with Alexa Fluor 647 (AF647) and cleaved the MBP-tag to create Sca2/6-AF647. Sca2/6-AF647 and MBP-Sca2/6 activity were similar in pyrene actin assays (Figure S4C). Polymerization of 1 μM actin was initiated in the absence or presence of Sca2/6-AF647, and the growth of actin filaments was visualized with TIRF microscopy. We did not observe stable association of Sca2/6 puncta with polymerizing actin filaments over a range of Sca2/6-AF647 concentrations (Movie S1). However, transient interactions between Sca2/6-AF647 puncta and the sides or ends of growing filaments were sometimes spotted. The rate of barbed end growth increased modestly (~1.2-fold) but significantly in the presence of Sca2/6-AF647 when compared with actin alone (Figure 2B). The addition of 3 μM profilin to Sca2/6-AF647 diminished the elongation rate to that of actin alone (Figure 2B). Moreover, Sca2/6 was unable to compete with capping protein (CapZ, 10 nM) to uncap the barbed ends of pre-capped actin filaments (Figure 2B). Together, these data show that *R. bellii* Sca2/6 nucleates actin and modestly enhances actin elongation independent of profilin and without detectable processive association with filament ends or uncapping activity.

R. bellii Sca2/6 is monomeric and structurally flexible in solution, binds G-actin, and requires G-actin binding for nucleation activity

To determine which domains of *R. bellii* Sca2/6 contribute to its actin nucleation activity, we expressed and purified a series of truncation mutants including: MBP-Sca2/6-ΔpolyP (missing the poly-proline region), MBP-Sca2/6-NTD (missing the CTD), or MBP-Sca2/6-CTD (missing the poly-proline and predicted G-actin binding regions) (Figure 3A). We performed pyrene actin assembly assays with 70 nM of each protein and calculated the maximum slope of the polymerization curve to compare their actin nucleation activities. MBP-Sca2/6-ΔpolyP exhibited activity that was not significantly different from full-length Sca2/6 (Figure 3B). In contrast, the activities of MBP-Sca2/6-NTD or MBP-Sca2/6-CTD were significantly reduced in comparison with full-length Sca2/6 and were comparable to actin alone (Figure 3B). These data suggest that sequences outside the poly-proline motif are sufficient for full nucleation activity, and that sequences in both the N-terminus and CTD are necessary for activity.

We next tested the function of the AlphaFold 3-predicted G-actin binding motif, comprising amino acids 86–110. To this end, we expressed and purified two variants of Sca2/6, one in which two amino acids (L101 and K102) within this motif were substituted with alanine (MBP-Sca2/6-2A), and another in which six amino acids (P97 through K102) were substituted with alanine (MBP-Sca2/6-6A). For both Sca2/6-2A and Sca2/6-6A, the confidence of AlphaFold 3 predictions for actin-binding were substantially reduced (pLDDT < 70 and < 50 respectively, Figure S2). To experimentally test whether this motif contributes to G-actin binding, we measured the binding affinity by fluorescence anisotropy with HiLyte fluor 488-labeled actin monomers and MBP-Sca2/6, MBP-Sca2/6-2A, or MBP-Sca2/6-6A. For wild-type MBP-Sca2/6, the K_D for G-actin was 0.7 μM ± 0.3 μM. The K_D was significantly higher for MBP-Sca2/6-2A (2 μM ± 1 μM), and substantially higher for

MBP-Sca2/6-6A (1 mM ± 0.7 mM) (Figure S5A). These data indicate that that the region comprising amino acids 97–102 of Sca2/6 is part of a G-actin binding motif.

To further determine the stoichiometry of binding between Sca2/6 and G-actin, and examine the conformational flexibility of the bound complex, we performed small angle X-ray scattering in line with size exclusion chromatography (SEC-SAXS) with MBP-Sca2/6 alone as well as MBP-Sca2/6 or MBP-Sca2/6-2A in the presence of G-actin (and latrunculin A to prevent actin polymerization). The calculated molecular weight (MW) from SAXS (based on the volume of correlation V_c) of MBP-Sca2/6 was ~110 kDa (sequence MW, 110 kDa), consistent with Sca2/6 behaving as a monomer in solution. In the presence of G-actin, the calculated MW for MBP-Sca2/6 plus actin was ~125 kDa, consistent with a 1:1 complex of Sca2/6 and G-actin. The calculated MW for MBP-Sca2/6-2A plus actin was ~105 kDa, consistent with the lower binding affinity for G-actin.

The normalized Kratky plot shows that all measured proteins adopt a partially unfolded conformation (Figure S5B). We then calculated pair distance distribution functions (P(r)) for MBP-Sca2/6, MBP-Sca2/6 plus actin, and MBP-Sca2/6-2A plus actin. The extended P(r) “tails” at r > 170 Å in the P(r) plot indicate that in all samples, the *R. bellii* Sca2/6 protein adopts an extended conformation (Figure 4A). The peak at ~50 Å corresponds to the intra-domain distance of the globular N-terminal MBP-tag and the broad peak at ~120 Å corresponds to the flexible Sca2/6 protein (Figure 4A). The P(r) function for MBP-Sca2/6 plus actin additionally had a broad shoulder between ~70–140 Å that is absent in functions derived for both MBP-Sca2/6 alone and MBP-Sca2/6-2A plus actin. Thus, this shoulder contains both the intra-domain distance of actin and inter-domain distances with actin (Figure 4A). However, the significant broadening of the shoulder suggests that the Sca2/6 or Sca2/6-actin region is not compact and most likely adopts a flexible conformation in solution. In further support of the location of the G-actin binding motif, we visualized AlphaFold 3-derived predicted aligned errors (PAE), which measure the confidence in the relative position of two residues within the predicted structure (Figure 4B). MBP-Sca2/6 plus actin showed confidence in interactions with actin of Sca2/6 amino acids 70–110 (which includes L101 and K102). The confidence was significantly weaker for MBP-Sca2/6-2A (Figure 4B).

AlphaFold3 models were further matched to the SAXS curves (Schneidman-Duhovny et al., 2013). The single best conformer generated by BilboMD with the clustered residues mentioned above bound to actin as a rigid domain (Pelikan et al., 2009) did not match the data (χ^2=9 for MBP-Sca2/6 and χ^2=4 for MBP-Sca2/6 plus actin), indicating the conformational variability of the protein in the solution state. The 2-state fit for both MBP-Sca2/6 and MBP-Sca2/6 plus actin (Figure 4C and D) showed a good fit to the data (Figure 4C). MBP-Sca2/6-2A was not fitted because a discernible complex with actin was not observed. Consistent with the flexible and extended conformation of both proteins suggested by normalized Kratky plot and P(r) function, the 2-state model predicted a significant contribution from unfolded linkers within MBP-Sca2/6 even in the presence of G-actin (Figure 4D). Together, these data suggest that Sca2/6 lacks larger stably folded domains and exhibits high flexibility, even when bound to G-actin.

Finally, to test the functional importance of the G-actin binding motif, we assessed the actin-nucleation activity MBP-Sca2/6-2A or MBP-Sca2/6-6A using the pyrene actin assembly assay. Neither mutant protein showed nucleation activity above background levels at concentrations ranging from 10 – 250 nM, in contrast to the clear nucleation activity of MBP-Sca2/6 over the same concentration range (Figure 3B and C). These data demonstrate that the G-actin binding motif is necessary for the actin nucleation activity of Sca2/6.

R. bellii has a single phase of actin-based motility in mammalian cell lines

Although both *R. bellii* RickA and Sca2/6 are biochemically active, their roles in *R. bellii* actin-based motility have not been determined. Our prior work with *R. parkeri* showed that this species exhibits two phases of motility; an early phase (<2 hours post-infection (hpi)) driven by RickA and a late phase (>5 hpi) driven by Sca2 (Reed et al., 2014). To determine if *R. bellii* also exhibits this same biphasic motility pattern, we infected human A549 epithelial or HMEC-1 endothelial cell lines with either *R. parkeri* or *R. bellii* and quantified the frequency at which bacteria assemble actin tails between 15 min post-infection (mpi) and 24 hpi as a measure of the frequency of actin-based motility. Actin tails were observed throughout the 24 h time course in *R. parkeri*-infected cells, with two peaks in actin tail frequency corresponding to the early RickA-motility (15 – 30 mpi) and the late Sca2-motility (16 hpi - 24 hpi) phases (Figure 5A and B). In contrast, *R. bellii* actin tails were rare prior to 8 hpi in both cell lines (Figure 5A and B). The frequency of *R. bellii* actin tails increased from 8 hpi through 24 hpi. These results suggest that *R. bellii* exhibits only a single phase of actin-based motility in infected mammalian cell lines.

No role was observed for *R. bellii* RickA and host Arp2/3 complex in actin-based motility

To investigate a possible role for RickA in *R. bellii* actin-based motility at 8 and 24 hpi, we first localized surface-associated RickA and actin by fluorescence microscopy in infected A549 cells. Although actin tails were observed at both time points, we did not observe RickA on the bacterial surface (Figure 6A and B). Next, to localize intra-bacterial RickA, we permeabilized bacteria with lysozyme. A subset of bacteria showed evidence of internal RickA staining (Figure 6A and B), consistent with our immunoblotting data showing RickA is expressed by *R. bellii* (Figure S3). These data suggest that RickA is not localized to the bacterial surface under the conditions tested and therefore its surface localization is not correlated with actin-based motility.

To examine the functional importance of RickA, we leveraged the dependency of RickA-motility on the host Arp2/3 complex and the availability of small-molecule Arp2/3 complex inhibitors CK-666 and CK-869, as well as inactive control compound CK-689 (Nolen et al., 2009; Cao et al., 2024). As a positive control, we evaluated the effect of 1 h treatment with these compounds on *L. monocytogenes* actin-based motility in infected A549 cells, a process that is known to depend on the Arp2/3 complex (Welch et al., 1997). As expected, *L. monocytogenes* actin tail frequency was significantly reduced in the presence of CK-666 or CK-869 compared to the inactive control drug (Figure 6C). In contrast, for *R. bellii*-infected A549 cells at either 8 hpi or 24 hpi, actin tail frequencies were not significantly different following 1 h treatment with the Arp2/3 complex inhibitors CK-666 or CK-869 versus the inactive control compound (Figure 6C). Thus, while RickA is biochemically active, RickA-

and Arp2/3-complex-dependent actin-based motility was not observed in *R. bellii*-infected human cell lines.

Sca2/6 surface localization is correlated with *R. bellii* actin-based motility

We next investigated a role for Sca2/6 in *R. bellii* actin-based motility at 8 and 24 hpi by localizing surface-associated Sca2/6 and actin by confocal microscopy in infected A549 and HMEC-1 cells. Sca2/6 exhibited a focused localization at the poles of ~30–40% of bacteria at 8 hpi and ~80% of bacteria at 24 hpi (Figure 7). A majority of bacteria with polar Sca2/6 foci had an associated actin tail. Moreover, for all bacteria with an actin tail in this data set, the actin tail emerged from the bacterial pole with Sca2/6 (Figure 7A and B). Therefore, polar Sca2/6 localization to the surface of *R. bellii* is tightly correlated with actin-based motility in both epithelial and endothelial cell lines.

Sca2 ortholog localization and actin tail architecture differ between *Rickettsia* species

Sca2/6 localization to a discrete focus at the *R. bellii* pole seemed distinct compared with previously reported Sca2 localization in a more cup-shaped pattern at the pole of *R. parkeri* (Haglund et al., 2010; Reed et al., 2014). To directly compare differences in Sca2 ortholog localization patterns on the surface of *R. parkeri* versus *R. bellii*, we imaged *Rickettsia*-infected A549 cells at 24 hpi using a super-resolution lattice structured illumination microscope (LSIM) and further deconvolved the images to reduce image distortion. *R. parkeri* Sca2 tended to coat the bacterial pole associated with an actin tail or even the entire bacterium, while *R. bellii* Sca2/6 localized to the bacterial pole as a distinct punctum (Figure 8A). We further quantified the surface area and sphericity of the Sca2 ortholog signal, along with the overlapped volume between the Sca2 ortholog and the bacterial signals. *R. parkeri* Sca2 occupied a larger surface area (Figure 8B) and exhibited a greater overlap with the bacterium (Figure 8C) compared with *R. bellii* Sca2/6. Sca2/6 localization was significantly more spherical on *R. bellii* than Sca2 localization was on *R. parkeri* (Figure 8D). Therefore, the Sca2 ortholog exhibits a more extreme polar localization pattern on *R. bellii* compared to *R. parkeri*.

Corresponding with differences in Sca2 ortholog localization, the architecture of the actin tails in the LSIM images was distinct for *R. parkeri* and *R. bellii* at 24 hpi, when actin-based motility is predominant for both species. *R. parkeri* actin tails typically had two bands of actin emanating from the sides of the bacterial pole (Figure 8A and E), whereas *R. bellii* actin tails had a single band of actin centered on the pole in infected A549 cells (Figure 8A and E). To quantify the spatial organization of actin tails, we took a line intensity scan of actin fluorescence perpendicular to the long axis of the actin tail (0.5 μm from the bacterial pole). *R. parkeri* actin tails showed two distinct intensity peaks spaced 0.30 ± 0.09 μm apart, whereas *R. bellii* actin tails showed a single intensity peak (Figure 8F). The correlation between Sca2 ortholog localization and actin intensity profiles suggest that differences in protein localization may impact differences actin tail organization between *Rickettsia* species.

Differences in Sca2 ortholog mechanism and localization, as well as host cell type, correlate with differences in actin-based motility

We lastly looked at the functional consequences of differences in Sca2 ortholog mechanism and localization on actin-based motility parameters. We carried out live-cell imaging of *R. parkeri*- or *R. bellii*-infected A549 or HMEC-1 cells stably expressing F-tractin-TagRFPT (Johnson and Schell, 2009) at 24 hpi for 5 min and analyzed the actin-based motility speed and efficiency for each *Rickettsia* species and host cell combination. *R. parkeri* motility was significantly faster in A549 cells (mean 21 ± 5 μm/min) compared with HMEC-1 cells (mean 11 ± 4 μm/min). *R. bellii* moved more slowly than *R. parkeri* and with indistinguishable rates in A549 (mean 8 ± 3 μm/min) versus HMEC-1 cells (mean 9 ± 3 μm/min) (Figure 9A, Movie S2 and S3). We also measured the motility efficiency (defined as the straight-line distance between the starting and stopping points (Δd) in a 1 min interval, divided by the total distance traveled (D) during the interval, or Δd/D). *R. parkeri* motility efficiency was higher in A549 cells (mean 0.8 ± 0.2) than for *R. bellii* (0.6 ± 0.3) (Figure 9B, Movie S2 and S3). Traces of representative bacterial motility paths revealed more curved paths for *R. bellii* than for *R. parkeri*, particularly in A549 cells (Figure 9C). Thus, differences in Sca2/6 mechanism and localization correlate with slower *R. bellii* speed and lower motility efficiency compared with *R. parkeri*.

Notably, the organization of *R. bellii* actin tails was dramatically different in A549 versus HMEC-1 cells. In A549 cells, actin tails were consolidated, consisting of a single bundle of actin filaments (Figure 7A, 8A and 9D). In contrast, in HMEC-1 cells, *R. bellii* actin tails were disorganized, consisting of multiple bundles of actin filaments splaying from the bacterial pole (Figure 7A and 9D). As noted above, *R. parkeri* actin tails appeared similar in organization in both types (Figure 8A and 9D). Thus, differences in Sca2 mechanism and localization also correlate with cell type-specific differences in *R. bellii* actin-tail organization.

Discussion

Our results provide insight into the evolution of actin-based motility effectors within the *Rickettsia* genus. We find that RickA orthologs have maintained the ability to activate the host Arp2/3 complex to nucleate actin filaments, but RickA function in actin-based motility is not conserved between species. Sca2 paralogs, on the other hand, contribute to actin-based motility in divergent *Rickettsia* species, but their sequences and mechanisms differ substantially between species. Divergence of nucleation mechanisms between Sca2 orthologs coupled with different localization patterns on the bacterial surface contribute to differences in actin organization and motility. Our data indicate there is considerable evolutionary plasticity in actin-based motility regulation and mechanisms within the *Rickettsia* genus.

In *R. parkeri*, RickA-motility was previously shown to occur early after infection of a host cell and to function in cell-cell spread (Reed et al., 2014; Tran et al., 2025). Although we now report that *R. bellii* bacteria express a RickA ortholog that possesses Arp2/3-dependent actin nucleation activity *in vitro*, we found no evidence for RickA localization to the surface of *R. bellii* in cell culture models, or RickA and Arp2/3 complex function in *R. bellii*

actin-based motility. The conservation of RickA in divergent species (Lehman et al., 2024), despite the genus undergoing reductive genome evolution (Blanc et al., 2007), suggests that RickA performs an important function. One explanation for our observations is that the function and/or regulation of RickA is host-dependent. SFG I species, such as *R. parkeri*, have adapted to use RickA-motility in ticks and mammals, where an *R. parkeri rickA* transposon mutant showed reduced cell-cell spread (Harris et al., 2018; Tran et al. 2025) and eschar formation (Tran et al., 2025). In contrast, the tick endosymbiont *R. bellii* may only use RickA in ticks. Our observation that RickA is expressed in both *R. parkeri* and *R. bellii* but is only secreted and localized to the surface of *R. parkeri*, suggests potential differences in the regulation of RickA secretion. It also remains possible that RickA performs important functions beyond actin-based motility.

On the other hand, Sca2 orthologs are quite different between divergent *Rickettsia* species. The *R. bellii* genome contains a single *sca2/6* gene, whereas in other species this gene appears to have undergone a tandem duplication event, yielding adjacent *sca2* and *sca6* genes that are intact in some species and degraded in others (Blanc et al., 2005; Ngwamidiba et al., 2005; Sears et al., 2012). Gene duplication can contribute to more rapid evolution (Zhang, 2003) and may have contributed to the evolution of the passenger domains of Sca2 orthologs in the different *Rickettsia* groups, which differ considerably in primary sequence. Previous studies showed that Sca2 from SFG I species nucleates and caps actin in the absence of profilin, enables elongation, and processively associates with growing barbed ends in the presence of profilin, similar to eukaryotic formins (Haglund et al., 2010; Madasu et al., 2013; Alqassim et al., 2019; Carman et al., 2023). SFG I Sca2 also assumes a folded formin-like structure, with the N-terminal region forming ring-shaped structural core in conjunction with the CRD (Alqassim et al., 2019; Carman et al., 2023). In contrast, we report that *R. bellii* Sca2/6 nucleates and modestly enhances elongation in the absence of profilin and does not cap or stably associate with filament barbed ends, characteristics that differ from eukaryotic formins. Moreover, Sca2/6 is structurally dissimilar from SFG I Sca2 and eukaryotic formins, as SAXS analysis indicates that it lacks larger stably folded domains and exhibits high flexibility. Although SFG I Sca2 possesses two high-affinity G-actin binding sites (K_D = 0.2 μM and 0.02 μM) (Alqassim et al., 2019), we find *R. bellii* Sca2/6 has a single high affinity site (K_D = 0.7 μM) between amino acids 86–110, and SAXS analysis also indicates there may be lower-affinity interactions with G-actin via amino acids 110–180. Thus, motifs interacting with G-actin comprise much of the N-terminal region of the protein. Although residues within the G-actin binding domain between amino acids 97–102 are necessary for actin nucleation, the broader region of the protein between amino acids 70–180 is not sufficient, and the CTD is also required. The contribution of the CTD to biochemical activity may be through potential low affinity interactions with F-actin. Only the poly-proline motif is dispensable for nucleation activity *in vitro*, although poly-proline sequences bind profilin (Tanaka and Shibata, 1985) and thus may contribute to actin assembly in host cells, our *in vitro* assays also show profilin does not enhance the rate of filament elongation. Moreover, while SAXS analysis reveals that Sca2/6 is a monomer in solution, crowding on the bacterial surface may also affect actin nucleation and elongation activity.

The sequence and biochemical properties of *R. bellii* Sca2/6 differ from other microbial actin nucleators. Sca2/6 behaves as a monomer, possesses a single higher affinity G-actin-binding domain predicted to bind the barbed end of an actin monomer, and does not exhibit detectable association with either end of actin filaments. These properties differ from the tandem WH2-domain nucleation factors VopL/VopF from *Vibrio* species, which dimerize, have three WH2 domains spaced by linkers, and have been shown to mediate actin nucleation and elongation via association with the pointed or barbed end of an actin filament (Tam et al., 2007; Liverman et al., 2007; Yu et al., 2011; Namgoong et al., 2011; Zahm et al., 2013; Avvaru et al., 2015; Burke et al., 2017; Kudryashova et al., 2022). *R. bellii* Sca2/6 further lacks key characteristics of the host Ena/VASP-like protein BimA from *Burkholderia* species (Benanti et al., 2015), such as the ability to trimerize. Based on our current understanding, *R. bellii* Sca2/6 therefore exhibits a distinctive mechanism of actin nucleation.

Our comparison of Sca2 ortholog localization in *R. parkeri* and *R. bellii* also reveals clear differences, with Sca2/6 in *R. bellii* exhibiting a more extreme polar distribution than Sca2 in *R. parkeri*. Differences in localization may be a result of difference in protein secretion or processing. The *Shigella* actin-based motility effector IcsA is also a T5SS protein that is secreted at the bacterial pole and can diffuse across the surface, where it is cleaved by a protease (Shere et al., 1997; Steinhauer et al., 1999). When polar secretion is rapid, slower cleavage across the entire bacterial surface acts as a pruning mechanism to keep IcsA restricted to the bacterial pole (Shere et al., 1997; Steinhauer et al., 1999). *R. parkeri* Sca2 (Haglund et al., 2010; Reed et al., 2014) and *R. bellii* Sca2/6 (this study) may also be similarly cleaved. Variations in location/rates of autotransporter secretion and protease activity may explain why the Sca2 ortholog covers more of the bacterial surface of *R. parkeri* compared with *R. bellii*.

At time points when Sca2 is the predominant motility effector for both *R. parkeri* and *R. bellii*, we observed clear differences in actin filament organization and actin-based motility. In both epithelial and endothelial cell lines, *R. parkeri* actin tails are organized into two discrete bundles that emerge from the sides of the bacterial pole, similar to prior reports (Van Kirk et al., 2000; Haglund et al., 2010), and bacteria move more quickly and in straighter trajectories. In contrast, *R. bellii* move more slowly, and their actin tails exhibit distinct organizations in different host cell types. In an epithelial cell line, *R. bellii* actin tails are organized into a single bundle, and bacteria move in more meandering trajectories. In an endothelial cell line, *R. bellii* actin tails consist of multiple splayed filament bundles and bacteria move in straighter trajectories. The splayed tail architecture is reminiscent of *R. parkeri* actin tails in infected cells depleted of the actin-bundling protein fimbrin by siRNA (Serio et al., 2010). Variations in motility likely derive from differences in Sca2 ortholog mechanisms of action and localization patterns. Differences in biochemical activity may affect rates of actin elongation and/or filament capping at the bacterial surface. The fuller coverage of *R. parkeri* Sca2 on the bacterial surface and the resulting actin density that brackets the bacterial pole may steer the bacteria in straighter trajectories. In contrast, the extreme polar distribution of *R. bellii* Sca2/6 and the reduced actin density may contribute to more meandering motility and a smaller number of elongating actin filaments generating propulsive force. Thus, differences in Sca2 ortholog localization, along with differences

in the abundance and recruitment of host actin-bundling proteins or other actin-associated proteins, likely play an important role in defining actin tail organization and bacterial movement parameters.

Together, our results provide insight into the evolution of actin-based motility mechanisms in microbial pathogens. While divergent species throughout the *Rickettsia* genus maintain the ability to undergo actin-based motility, the utilization of orthologs of the two motility effectors RickA and Sca2, and the biochemical mechanisms of Sca2 ortholog-mediated actin polymerization, have diverged. This evolution likely reflects changes in both motility effector sequences and regulation. Because of the diversity of *Rickettsia* genus, these bacteria provide a unique platform to unravel how actin-based motility evolved and contributes to pathogenicity or colonization. Future studies of how actin-based motility is affected by motility effector expression and localization, actin ultrastructure and organization, and the host cell environment will provide powerful insights into both pathogen infection and host cell biology.

Materials and methods

Mammalian cell culture and cell line generation

Vero (ATCC Cat# CCL-81, RRID:CVCL_0059), HEK293T (ATCC Cat# CRL-3216, RRID:CVCL_0063), A549 (ATCC Cat# CRM-CCL-185, RRID:CVCL_0023), and HMEC-1 (ATCC Cat# CRL-3243, RRID:CVCL_0307) cells were sourced from the University of California, Berkeley, tissue culture facility. Vero cells were grown in DMEM containing 4.5 g/L D-glucose, 4 mM L-glutamine (Gibco, 11965118) and 2% fetal bovine serum (Gemini Bio-products, 100–500). HEK293T and A549 cells were grown in DMEM containing 4.5 g/L D-glucose, 4 mM L-glutamine (Gibco, 11965118), and 10% fetal bovine serum (ATLAS Biologics, FP-0500-A). HMEC-1 cells were grown in MCDB 131 (Sigma, M8537) containing 10 mM L-glutamine (Sigma, M8537-1L), 14 mM sodium bicarbonate, 10% fetal bovine serum (Hyclone, SH30071.03), 10 ng/ml EGF (BD Biosciences, 3540001), and 1 μg/ml hydrocortisone (Sigma, H0888). All cells were grown at 37°C in 5% CO_2.

A549 or HMEC-1 cells expressing F-tractin-TagRFPT were generated through retroviral transduction with SC1205 as previously described (Lamason et al., 2016). SC1205 (F-tractin-TagRFPT-pIPFCW2) was generated by subcloning the genes encoding F-tractin (flanked by NheI and XhoI restriction sites) (Johnson and Schell, 2009) and TagRFPT (flanked by XhoI and EcoRI restriction sites) (Shaner et al., 2008) into NheI- and EcoRI-digested pIRES-puro (IP)-FCW2. Transduced cells were selected with 1 μg/mL puromycin (Sigma, P8833) and sorted using the Aria Fusion Cell Sorter in the UC Berkeley Flow Cytometry Facility to select for cells that fell in the top 30% of brightness for RFP fluorescence.

Bacterial propagation and strain construction

R. parkeri strain Portsmouth was obtained from Chris Paddock at the Centers for Disease Control and prevention. *R. bellii* strain RML 369-C was obtained from Ted Hackstadt at the NIH/NIAID Rocky Mountain Laboratories. For propagation, *Rickettsia* bacteria were

allowed to infect 5 confluent T175 flasks of Vero cells for 4–7 d at 33°C until cells rounded and started to dissociate from the monolayer. Infected cells were scraped from the bottom of the flask into the growth media, pelleted, resuspended in 10 ml of K36 buffer (50 mM KH_2PO_4, 50 mM K_2HPO_4, pH 7.0, 100 mM KCl, 15 mM NaCl). Bacteria were released on ice from Vero cells by Dounce homogenization (50 strokes). Bacteria were isolated by centrifugation in a solution of 30% RenoCal-76 (Bracco Diagnostics, 04H208) in K36 buffer using a SW-32 Ti rotor (Beckman/Coulter) at 18,500 rpm for 30 min at 4°C. The bacterial pellet was resuspended in 2 mL brain heart infusion (BHI) media (BD Difco, DF0418-17-7) and aliquoted before freezing at −80°C.

Bacterial titers were determined by serially diluting the bacterial stock and performing a plaque assay in Vero cells. Briefly, serial dilutions in Vero cell media were used to infect a 6-well plate of Vero cells by centrifugation at 300 × g for 5 min at room temperature and overnight incubation at 33°C. Cells were then overlaid in DMEM with 10% FBS (Gemini Bio-products, 100–500) and 0.5% (w/v) agarose (Sigma, A9539). Once plaques appeared (5–7 d post-infection) cells were overlaid with a mixture of 1x PBS (Gibco, 10010072), 0.5% agarose, and 2.5% (v/v) neutral red (Sigma, N6264). Plaques were quantified the next day and used to calculate the plaque forming units (PFU) per mL.

Fluorescent *R. parkeri* or *R. bellii* expressing pRAM18dRGA (Burkhardt et al., 2011) or pRAM18dR-2xCoTagBFP (Figueroa-Cuilan et al., 2023) were generated by infecting a T75 flask of Vero cells with bacteria and incubating at 33°C. Infected Vero cells were scraped up, resuspended in K36 buffer, and then broken open with 1 mm beads by two 30 s rounds of vortexing and resting on ice. Cell debris was pelleted, and the supernatant was washed 3x with 250 mM sucrose (ThermoFisher, S5). Washed bacteria were resuspended in 100 µL BHI and incubated on ice for 20 min with 10 µg of the plasmid. Bacteria were then electroporated in a 0.2 cm cuvette (Bio-Rad, 165-2086) at 2.5 kV, 200 Ω, 25 µF. Electroporated bacteria were resuspended in 1.2 mL BHI and aliquoted onto Vero cells in 6-well plate (200 uL per well). The plate was centrifuged at 300 × g for 5 min at room temperature, and then incubated at 33°C. The next day, 500 ng/mL rifampicin (Sigma, R3501; resuspended to 1 mg/mL in methanol and filter sterilized) was added to each well of infected Vero cells. After clear signs of infection were observed, *Rickettsia* were harvested by adding cold sterile water to each well for 2 min to break bacteria out of Vero cells. An equal amount of 2x BHI was added to each well and bacteria were frozen at −80°C. After visually confirming fluorescent protein expression, bacteria were propagated as described above.

L. monocytogenes strain 10403S::dasherGFP was obtained from Daniel A. Portnoy at the University of California, Berkeley. *L monocytogenes* was streaked from frozen stocks onto BHI agar plates with 200 µg/mL spectinomycin (Sigma, S4014) and grown overnight at 37°C. For infections, single colonies were used to seed overnight cultures in BHI with 200 µg/mL spectinomycin and were grown at 30°C at a slant with no shaking.

Generating plasmids for protein expression

To generate plasmids pET-GST-RickA and pET-MBP-RickA to express *R. bellii* RickA tagged with glutathione-S transferase (GST) or maltose binding

protein (MBP), the *R. bellii rickA* gene was amplified from boiled bacteria by PCR (primers: 5'-CTGTACTTCCAATCCAATGCAAAGATAACTGAGCTT-3' and 5'-CCGTTATCCACTTCCAATCTACCTTTGTTGAGATTGTT-3'). To generate the plasmid pET-MBP-Sca2/6 to express *R. bellii* Sca2/6 tagged with MBP, the sequence encoding the Sca2/6 passenger domain (aa 43–630) excluding the secretion signal sequence and autotransporter domain was amplified from plasmid DNA by touchdown PCR (Korbie and Mattick, 2008) (primers: 5'-ACCTGTACTTCCAATCCAATGCACCACCTCCACCACCC_3' and 5'-ATCCGTTATCCACTTCCAATTCATTCATCACCACCAGTAATCGCAG-3'). The primers used to amplify the *rickA* and *sca2/6* genes included homology arms that facilitated Gibson cloning (New England Biolabs, E2611S) into SspI-cut plasmids pET His6 MBP TEV LIC (RRID:Addgene_29656) or pET His6 GST TEV LIC (RRID:Addgene_29655) obtained from University of California, Berkeley, QB3 MacroLab.

To generate plasmids pET-MBP-Sca2/6-NTD, pET-MBP-Sca2/6-ΔpolyP, and pET-MBP-Sca2/6-CTD to express Sca2/6 truncation derivatives, desired regions of the plasmid pET-MBP-Sca2/6 were amplified by PCR (primers: pET-MBP-Sca2/6-NTD: 5'-TGGATTAAAATTAGAAATATAAGATG-3' and 5'-TTTGCACTTGCTTCCCCCAC-3'; pET-MBP-Sca2/6-ΔpolyP, 5'-GTTGATCCTAAATCAGCAGC-3' and 5'-CATGAACTATATCTCCTTCTTAAAG-3'; pET-MBP-Sca2/6-CTD, 5'-AATTATAAGTATATAATTTCGTATAGTACG-3' and 5'-CATGAACTATATCTCCTTCTTAAAG-3'). To generate plasmid pET-MBP-Sca2/6-2A, pET-MBP-Sca2/6 was amplified with primers encoding the L101A/K102A mutations (primers: 5'-TTATGATACAGCGGCGAAAAATAGGAAAAATATAAAAAATAAAAAG-3' and 5'-GGATTAAATGTTGGACCTAATTC-3'). To generate plasmid pET-MBP-Sca2/6-6A, pET-MBP-Sca2/6-2A was amplified with primers encoding the 6A mutations (primers: 5'-GCAGCTGCGGCGAAAAATAGG-3' and 5'-AGCTGCATTAAATGTTGGACCTAATTCAG-3'). To generate pET-MBP-Sca2/6-KCK, pET-MBP-Sca2/6 was amplified by PCR with primers encoding a C-terminal GGS linker and KCK motif (primers: 5'-AGCAAGTGCAAATGAATTGGAAGTGGATAAC-3' and 5'-TCCCCCACCGCTTCCACCGCCTTCATCACCACCAGTAATC-3'). The resulting PCR products where ligated using the KLD reaction mix (New England Biolabs, M0554S).

To generate plasmids pGEX-GST-Sca2/6–44 (aa 44–175) and pGEX-GST-Sca2/6–357 (and aa 357–464) for anti-Sca2/6 antibody production, gene sequences encoding the *R. bellii* Sca2/6 truncations were subcloned into pGEX-6P-3 (GE Healthcare, 28-9546-51).

Protein purification and fluorescent labeling

To express *R. bellii* GST-RickA and MBP-RickA, BL21-CodonPlus (DE3)-RIL *E. coli* (Agilent Technologies, 230245) were transformed with plasmid pET-GST-RickA or pET-MBP-RickA. For protein expression, bacteria were grown overnight at 37°C in LB media. The overnight culture was then diluted 1:100 into 3 L of 2xYT media and grown to an OD_{600} of 0.5–0.8. Protein expression was induced by adding IPTG (Gold Biotechnology, 20–109) to 0.3 mM and bacteria were grown at 37°C for an additional 2 h. Cells were pelleted at 4000 rpm for 20 min at 4°C, resuspended in 30 mL either GST lysis buffer (50

mM Tris, pH 7.5, 250 mM KCl, 1 mM EDTA) or MBP lysis buffer (20 mM HEPES, pH 8, 200 mM NaCl, 1 mM EDTA) with 1 mg/mL lysozyme (Sigma, L4919) and protease inhibitors (10 μg/mL leupeptin, pepstatin, chymostatin (LPC) and 1 mM PMSF), and lysed by sonication (8–25 × 10s pulses, 30% amplitude). The lysate was centrifuged at 13,000 rpm in a Sorvall SS-34 rotor for 30 min at 4°C. Lysate supernatant was run over Glutathione Sepharose 4B resin (GE Healthcare, 17-0756-01) or Amylose resin (New England Biolabs, E8021), washed with MBP or GST column buffer (the respective lysis buffer with 0.5 mM DTT), and eluted in GST column buffer with 10 mM glutathione (Sigma, G4251) or MBP column buffer with 10 mM maltose (Fisherbrand, M75). MBP-RickA was used for antibody affinity purification as described below. GST-RickA was further purified by gel filtration chromatography on a Superdex 200 Increase 10/300 GL column (Cytiva, 28-9909-44) equilibrated with Buffer A (20 mM HEPES, pH 7.5, 200 mM KCl, 2 mM EGTA, 2 mM EDTA, 0.5 mM DTT, 10% glycerol), then flash frozen in liquid N_2 and stored at −80°C.

To express GST-Sca2/6–44 and GST-Sca2/6–357 for *R. bellii* Sca2/6 antibody generation, BL21-CodonPlus(DE3)-RIPL (Agilent Technologies, 230280) transformed with pGEX-GST-Sca2/6–44 or pGEX-GST-Sca2/6. Bacteria were grown overnight at 37°C in 2xYT media, diluted 1:100 into 3 L of 2xYT media, and then grown again to an OD600 of 0.5–0.8. Protein expression was induced with 0.3–1 mM IPTG at 16°C overnight. Cells were pelleted, resuspended in lysis buffer (50 mM Tris, 200 mM KCl, 1 mM EDTA, pH 7.5) with 1 mg/mL lysozyme and protease inhibitors (10 μg/mL LPC and 1 mM PMSF), and lysed by sonication. Lysate was run over Glutathione Sepharose 4B and washed with wash buffer (lysis buffer plus 0.5 mM DTT). PreScision Protease was added to the wash buffer for 16–18 h at 4°C to cleave the GST tag, and cleaved protein was eluted with 1 column volume of wash buffer. Elutions were run over a Superdex 75 10/300 GL column (GE Healthcare, 29–1487-21) in 20 mM Tris, pH 7.5, 100 mM KCl, 1 mM EGTA, 2 mM EDTA, 0.5 mM DTT, 10% glycerol, then flash frozen and stored at −80°C.

To express the *R. bellii* MPB-Sca2/6 proteins for use in actin assembly assays, BL21-CodonPlus (DE3)-RIPL *E. coli* cells (Agilent Technologies, 230280) transformed with expression plasmids pET-MBP-Sca2/6, pET-MBP-Sca2/6-ΔpolyP, pET-MBP-Sca2/6-2A, pET-MBP-Sca2/6-6A, pET-MBP-Sca2/6-NTD, or pET-MBP-Sca2/6-CTD. Growth and expression conditions were as described above for expression at 16°C. Cells were pelleted, lysed with lysis buffer (50 mM HEPES, pH 7.5, 500 mM KCl, 10 mM imidazole, 10 % glycerol) with 1 mg/mL lysozyme and protease inhibitors (GoldBio ProBlock Gold Bacterial Protease Inhibitor Cocktail, GB-108-2, Roche cOmplete EDTA-free Protease Inhibitor Cocktail, 4693159001, or APEX Protease Inhbitor Cocktail EDTA-free, K1007) followed by sonication (8–25 × 5–10s pulses, 20–30% amplitude). Lysate was run over an Ni-NTA resin (Qiagen, 30210), washed with column buffer (50 mM HEPES, pH 7.5, 500 mM KCl, 20 mM imidazole, 1 mM DTT, 10% glycerol), and eluted in elution buffer (50 mM HEPES, pH 7.5, 500 mM KCl, 250 mM imidazole, 1mM DTT, 10% glycerol). Elutions were run over a HiTrapQ HP column (Cytiva, 17-1153-01) with a 100 – 800 mM KCl gradient in anion exchange buffer (20 mM Tris, pH 7.5, 10% glycerol, 0.5 mM DTT) and then a Sephacryl S300 (Cytiva) or Superdex 200 Increase 10/300 GL column equilibrated with Buffer A or Buffer B (20 mM HEPES, pH 7.5, 500 mM KCl, 2 mM EGTA, 2 mM EDTA, 0.5 mM DTT,

10% glycerol). Anion exchange was not used when prepping the MBP-Sca2/6-NTD protein. Proteins were flash frozen in liquid N_2 and stored at −80°C.

To fluorescently label *R. bellii* Sca2/6 (Sca2/6-AF647), MBP-Sca2/6-KCK was expressed as described for MBP-Sca2/6 proteins and purified as described for MBP-RickA. Post-purification, the MBP-tag was cleaved with His-TEV protease for 1 h at room temperature and separated on a Superdex 200 Increase 10/300 GL column equilibrated with Buffer A. Sca2/6-KCK was dialyzed overnight into Buffer A with 1 mM TCEP (Sigma, 646547) instead of DTT. Equimolar amounts of Sca2/6-KCK (35 μg) and AlexaFluor 647-maleimide (Invitrogen, A23047) were mixed and the maleimide reaction was allowed to proceed overnight at 4°C. Excess dye was removed by dialysis into Buffer A before Sca2/6-AF647 was flash frozen in liquid N_2 and stored at −80°C.

Antibody production, purification, and immunoblotting

To generate antiserum to *R. bellii* Sca2/6 (anti-RbSca2/6), Sca2/6-44-175 and Sca2/6-357-464 were expressed and purified as described above, mixed in equimolar amounts, and used to immunize two rabbits (Pocono Rabbit Farm & Laboratory, Inc). The generation of antiserum to *R. parkeri* Sca2 (anti-RpSca2; (Haglund et al., 2010)) and antiserum to *R. rickettsii* RickA (anti-RrRickA; (Jeng et al., 2004)) were described previously. To affinity purify anti-RbSca2/6 or anti-RickA antibodies, 2.5 mg of *R. bellii* Sca2/6 truncations (equimolar amounts) or 500 μg of *R. bellii* MBP-RickA were conjugated to 1 ml of NHS-activated Sepharose 4 Fast Flow in ligand-coupling buffer (200 mM $NaHCO_3$, pH 8.3, 500 mM NaCl) for 30 min at room temperature or overnight at 4°C. Ligand-coupled resin was incubated with 10 ml of anti-RbSca2/6 serum or anti-RrRickA serum (*R. rickettsii* RickA is similar in sequence to *R. bellii* RickA). Serum was diluted in 10 ml binding buffer (20 mM Tris, pH 7.5) for 1 h at room temperature or overnight at 4°C. Antibodies were eluted using 100 mM glycine, pH 2.5, and fractions were pooled and dialyzed overnight at 4°C against PBS (137 mM NaCl, 2.7 mM KCl, 10 mM Na_2HPO_4, 1.8 mM KH_2PO_4, pH 7.4) for anti-RickA or TBS (150 mM NaCl, 50 mM Tris-Cl, pH 7.6) for anti-RbSca2/6. Antibodies were concentrated to 0.72 mg/mL (anti-RbRickA) and 2 mg/mL (anti-RbSca2/6) before flash freezing and storage at −80°C, or mixed with 50% glycerol and stored at −20°C.

For immunoblotting, 5×10^6 of WT *R. bellii* from a 30% prep was diluted 1:1 with 2x Laemmli buffer (Bio-Rad, 1610737) and boiled for 10 min. The samples were run on a 10% SDS-PAGE gel and transferred to a PVDF membrane (Millipore, IPFL00010). The membrane was blocked in TBS-T (20 mM Tris, pH 8, 150 mM NaCl, 0.1% Tween 20) with 5% non-fat dry milk (Apex, 20–241) for 1 h. The membrane was then incubated with 1:1000 anti-RbSca2/6 or anti-RbRickA in TBS-T with 5% milk, washed 3x in TBS-T, and incubated for 1 h with 1:5000 mouse anti-rabbit HRP secondary antibody (Santa Cruz Biotechnology, sc-2357, RRID:628497) in TBS-T with 5% milk, and washed again 3x with TBS-T. Following developing with the ECL HRP substrate kit (Advasta, K-12045-D20) for 45 s, bands were imaged on a ChemiDoc MB Imaging System (Bio-Rad).

Actin assembly and binding assays

Rabbit skeletal muscle actin (Cytoskeleton, AKL99), pyrene labeled actin (Cytoskeleton, AP05), rhodamine actin (Cytoskeleton, AR05), and HiLyte fluor 488-labeled actin (Cytoskeleton, AR06) were dialyzed for 2–3 d in G-buffer (5 mM Tris, pH 7.5, 0.2 mM $CaCl_2$, 0.2 mM ATP, 0.5 mM DTT). The dialyzed actin was centrifuged at 100,000 × g in a TLA100 rotor (Beckman Coulter) using an Optima TLX Ultracentrifuge (Beckman Coulter) for 2 h at 4°C. The top 3/4 of the supernatant was collected and run over a Superdex 200 Increase 10/300 GL column equilibrated with G-buffer. The fractions corresponding to the latter half of the actin peak (the smaller Stokes radius) were combined and used. Purified Arp2/3 complex (Cytoskeleton, RP01P) was resuspended in milliQ water according to the manufacturer instructions.

Pyrene actin assembly assays were performed by combining 1 μM G-actin mix (10% pyrene labeled) with purified proteins, Buffer A, 10x initiation buffer (10 mM $MgCl_2$, 10 mM EGTA, 5 mM ATP, 500 mM KCl) with a final KCl concentration of 96 mM. Fluorescence was measured in two replicates per reaction condition, in three independent experiments, using a Tecan Infinite F200 Pro plate reader and Magellan software v7.1 at 20 s intervals with a 365 nm excitation and 405 nm emission filters. Each curve was baseline-corrected using an average of the first 3 values and graphed in Prism 10.3.1 (GraphPad Software, Inc, RRID:SCR_002798).

For maximum slope calculations, the first derivative was calculated after smoothing (4 neighbors on each side, 0^{th} order polynomial) and averaging raw fluorescence values of two biological replicates for each sample condition using Prism 10.3.1. *R. bellii* Sca2/6 maximum slope values were then normalized to the maximum slope value of actin alone for 3 separate experiments in Microsoft Excel and plotted in Prism 10.3.1.

For anisotropy assays, MBP-Sca2/6 or MBP-Sca2/6-2A in Buffer A were serially diluted into G-buffer and added as 40% of the total volume of each reaction containing 200 nM HiLyte fluor 488-labeled G-actin in G-buffer. MBP-Sca2/6-6A in G-buffer + 5% glycerol was added as 66% of the total volume of each reaction. Fluorescence anisotropy was measured in low volume, low binding, 348-well plates (Corning, 3676) using a Tecan Infinite F200 Pro plate reader with 485 nm excitation filter, 535 nm emission filter, and gain of 100, with Magellan software (v7.1) 5 m after mixing. 3 anisotropy values taken at 1 min intervals were averaged and binding curves for 2–4 independent titrations were normalized and fit using the Hill-equation in Prism 11 and the mean K_D values are reported. The graphed values were baseline corrected using the grouped Bmax value for each condition in Prism 11.

TIRF imaging of actin filaments

To make NEM-myosin for immobilizing actin filaments, myosin (Cytoskeleton Inc., MY02) was resuspended in 10 mM imidazole, pH 7 and 0.5 M KCl. NEM (Sigma, E3876) was added at >10-fold molar excess to myosin and allowed to react at room temperature for 1 h before dialyzing overnight at 4°C into 2x HS-TBS (100 mM Tris-HCl, pH 7.5, 1.2 M KCl).

Glycerol was added to 50%, sodium azide to 0.02%, and aliquots were stored at −20°C. Actin for TIRF studies was prepared as described above.

Flow cells were prepared using 22×22 mm No. 1.5 coverslips (VWR, 48366-227), which were washed for 15 min 0.02% Hellmanex III (Hellma Analytics, 9-307-011-4-507), 3x with MilliQ water, 15 min in 0.5 M NaOH, 3x with MilliQ water, then dried with a light stream of air. Double-sided Scotch tape was placed on ethanol-cleaned microscope slides to create 2 chambers. Cleaned coverslips were placed on top of the tape and pressed with a pipette tip to seal. A solution of 10 nM NEM-myosin in HS-TBS (50 mM Tris-HCl, pH 7.5, 600 mM NaCl) was flowed into chambers for 1 m, then chambers were washed twice with HS-BSA (50 mM Tris-HCl, pH 7.5, 600 mM NaCl, 1% BSA), twice with 2x LS-BSA (50 mM Tris-HCl, pH 7.5, 150 mM NaCl, 1% BSA), and once with 1x TIRF buffer (10 mM imidazole, pH 7, 50 mM KCl, 1 mM $MgCl_2$, 1 mM EGTA, 50 mM DTT, 0.2 mM ATP, 50 mM $CaCl_2$, 15 mM glucose, 20 μg/mL catalase, 100 μg/mL glucose oxidase, 0.4% methylcellulose).

For TIRF reactions, a solution of 2 μM actin monomers (33% rhodamine-labeled) was supplemented with $MgCl_2$ to 50 μM and EDTA to 0.2 mM for 5 min to exchange Ca^{2+} for Mg^{2+}. When relevant, 0.5 or 5 nM Sca2/6-AF647 and 3 μM profilin (purified as previously described; (Fedorov et al., 1994)), or an equivalent volume of Buffer A was added. 5 min before imaging, 2x TIRF buffer was added at a 1:1 ratio to the actin and proteins of interest and the mix was flowed into the flow cell.

Imaging was carried out on a Nikon Ti Eclipse Ti2 (RRID:SCR_021068) inverted microscope equipped with a Nikon 60x/1.49 NA CFI Apo TIRF objective and temperature chamber set to 25°C (Oko labs). Single-plane TIRF images were illuminated with a LUNF 4-line laser launch and iLas2 TIRF/FRAP module (Gataca Systems) and a 512 × 512 px area was captured with an Orca Fusion Gen III sCMOS camera (Hamamatsu) every 5 s for 15–20 m with NIS Elements software (Nikon, RRID:SCR_002776) and 561 and 640 nm excitation lasers using Nikon Cy3 and Cy5 filter cubes. The 561 nm (50% power) and 640 nm (40% power) channels were captured with 500 and 300 ms exposures. For each reaction, the growth of 5 actin filaments in 3 separate movies were measured. Elongation rate was determined over the course of 300 s by manually tracing the barbed ends (fast growing end with visually stable attachment point) of each filament 60 frames apart in ImageJ2/Fiji (v2.9.0/1.53t, RRID:SCR_002285) and graphed in Prism 10.3.1.

Protein alignments, motif identification, and structure prediction

Protein alignments and trees were generated using Geneious (2025.0.3 or 2026.0.1, RRID:SCR_010519). *Rickettsia* RickA and Sca2 sequences were aligned using the Geneious global alignment MUSCLE alignment algorithms. *R. parkeri* strain Portsmouth and *R. bellii* strain RML 369-C RickA and Sca2/6 sequences were submitted to InterPro (RRID:SCR_006695) for sequence motif analysis (Blum et al., 2024). Protein sequences were submitted to the AlphaFold3 server (RRID:SCR_025454) for structure prediction (Abramson et al., 2024).

SEC-SAXS measurements and analysis

SEC-SAXS studies were performed at the SIBYLS beamline 12.3.1 at the Advanced Light Source (Rosenberg et al., 2022; Classen et al., 2013). 60 µL of 3–8 mg/mL MBP-Sca2/6 or MBP-Sca2/6-2A was suspended in SEC running buffer (5 mM Tris, pH 7.5, 1 mM EGTA, 1 mM EDTA, 0.2 mM ATP, 0.5 mM DTT, 150 mM KCl, 1% glycerol). An equimolar amount of actin and 10x molar latrunculin A (Sigma, 428021) were included when indicated. The X-ray wavelength was set to 1.24 Å and the sample-to-detector distance to 2080 mm, generating scattering vectors ($q = 4\pi\sin\theta/\lambda$, where 2θ is the scattering angle) ranging from 0.01 $Å^{-1}$ to 0.45 $Å^{-1}$. Samples were run over a 1260 Infinity HPLC system (Agilent) connected to a Shodex 803 column equilibrated with SEC running buffer. The eluent was subject to multi-angle light scattering (MALS) and the SAXS.

The radius of gyration (Rg) was calculated for each of the subtracted frames using the Guinier approximation: $I(q) = I(0)\exp(-q^2 Rg^{2/3})$ with the limits $qRg < 1.3$. The elution peak was compared to the integral of ratios to background and Rg relative to the recorded frame using the program RAW (Hopkins et al., 2017). Final merged SAXS profiles, derived by integrating multiple frames at the elution peak, were used for further analyses. The Guinier plot and pair distribution function (P(r)) were respectively calculated to determine the volume of correlation (Vc) (Rambo and Tainer, 2013) and the maximal inter-particle dimension (Svergun, 1992).

Protein models were generated using AlphaFold3 (Abramson et al., 2024). The conformational variability of proteins was performed by BilboMD restrained by PAE values from AlphaFold 3 with low values PAE (< 0.2) grouped as rigid bodies (Pelikan et al., 2009). The generated models were fitted to the SAXS curves using FoXS (Schneidman-Duhovny et al., 2013). The 2-state ensemble model was selected by MultiFoXS (Schneidman-Duhovny et al., 2016). Regions with low PAE (< 0.2) were grouped together as rigid bodies in the const.inp files. Residues 70–180 of Sca2 were bound to actin as a rigid domain based on the PAE matrices.

Fixed cell imaging

For fixed-cell imaging of cells infected with *R. parkeri* or *R. bellii*, bacteria (WT, pRAM18dRGA, or pRAM18dR-2xCoTagBFP) from 30% prep frozen stocks were added to tissue culture media at an MOI of 0.6–10 (based on PFU measurements described above), aliquoted onto 12 mm circle No. 1.5 coverslips (Fisherbrand, 12541001) pre-seeded with 2×10^5 A549 or HMEC-1 cells, and centrifuged at 300 × g for 5 min at room temperature to facilitate infection. Infected cells were incubated at 33°C for 1 h, washed 2x with PBS (Gibco, 10010072) to remove excess bacteria, and tissue culture media was replaced. Infections were allowed to proceed for 15 m - 24 h at 33°C before cells were fixed with 4% paraformaldehyde (Ted Pella Inc, 18505) in PBS for 10 min at room temperature. For fixed-cell imaging of cells infected with *L. monocytogenes,* the cells were diluted into the relevant tissue culture media at an MOI of 5 (based on OD_{600} of $1.0 = 1\times10^9$ CFU/ml *L. monocytogenes*; (Ghosh and Higgins, 2018)), and incubated at 37°C for 15 min. A549 cells were infected as described above, and infections were allowed to proceed at for a total of 8 h before they were fixed as described above. For Arp2/3 inhibitor studies, coverslips were

infected with *R. bellii* for 8 h and 24 h or *L. monocytogenes* for 8 h, as described above. At 1 h prior to fixation, coverslips were treated with 200 μM CK689 (Sigma, 182517), CK666 (Sigma, 182515), or CK869 (Sigma, C9124) dissolved in DMSO.

After fixation, coverslips were permeabilized with 0.5% Triton-X 100 (Sigma, T9284) in PBS (Gibco, 10010-023) for 5 min. For localization of surface RickA or Sca2 orthologs, coverslips were blocked for 1 h with 2% BSA (Sigma, A4503) in PBS and then incubated with 1:1000 affinity purified anti-RbSca2/6, anti-RpSca2, or anti-RbRickA in PBS with 2% BSA for 1 h at room temperature. For localization of internal (total) RickA, after blocking, bacteria were permeabilized with lysozyme buffer (PBS, 50 mM glucose, 5 mM EDTA, 5 mg/ml lysozyme (Sigma), and 0.1% Triton X-100) in a humidified chamber for 20 min at 37°C. For quantifying bacteria in Figure 5, coverslips were incubated with 1:500 rabbit anti-I7 (obtained from Ted Hackstadt at the NIH/NIAID Rocky Mountain Laboratories) in PBS with 2% BSA for 30 min at room temperature. All coverslips were incubated with 1:500 568-phalloidin (Molecular Probes, A12380) and 1:500 anti-rabbit 488 (Invitrogen, A-11008) in PBS with 2% BSA for 30 min at room temperature. Coverslips were mounted in ProLong Gold Antifade (Invitrogen, P36930), allowed to cure overnight, and sealed with clear nail polish the next day.

Standard confocal imaging of bacteria, RickA, Sca2/6, and actin was carried out using a Nikon Ti Eclipse (RRID:SCR_021242) microscope equipped with a Yokogawa CSU-XI spinning disc confocal system running MetaMorph 7.8.2.0 (Molecular Devices LLC, RRID:002368) using the 100x VC (1.4 NA) Plan Apo objective, a Clara Interline CCD Camera (Andor Technology), and 405, 488, and 561 nm excitation lasers with the following emission filters; 445/45 nm, 525/50 nm, and 607/70 nm. Bacteria were used to localize regions of interest for imaging and 3.5–4.5 μm image stacks were taken with a step size of 0.15 μm to capture all actin tails present in the field of view. The 405 nm channel (100% power) was captured with a 500 ms exposure, the 488 nm channel (100% power) was captured with a 200 ms exposure, the 561 nm channel (100% power) was captured with a 300 ms exposure. Images were imported into ImageJ2/Fiji v2.9.0/1.53t (Schindelin et al., 2012) and Z Projection with max intensity was used to collapse the stack. Bacteria, actin tails, and RickA or Sca2/6 puncta were manually quantified and plotted in Prism 10.3.1.

Lattice structured illumination microscopy images of Sca2 ortholog localization on *R. parkeri* and *R. bellii* were collected at the Rausser College of Natural Resources Biological Imaging Facility at the University of California, Berkeley, using a Zeiss Elyra 7 Lattice Structured Illumination Microscope system (RRID:SCR_025701) running Zen Black (RRID:SCR_018163) using the 63x/1.4NA objective and the system SCMOS cameras, using the following emission filters; 420–480nm, 495–550nm, and 570–620nm. The 405 nm channel (50% power) was captured with a 500 nm exposure, the 488 nm (3–12% power) channel was captured with a 30 ms exposure, and the 561 channel (5–15% power) was captured with a 100 ms exposure. Bacteria with actin tails were used to localize regions of interest for imaging 3–5.6 μm image stacks with a step size of 0.091 μm. Raw 3D image stacks were processed using the SIM function of Zen Black. SIM files were imported into Huygens Professional (Scientific Volume Imaging, v24.10, RRID:SCR_014237) and image restoration (deconvolution) was performed using CMLE to 0.01% confidence.

To quantify and compare Sca2 ortholog localization and coverage of the *R. parkeri* versus *R. bellii* surface, deconvolved images stacks were analyzed using Imaris 10.2 (Oxford Instruments, RRID:SCR_007370). Separate surfaces were created for bacteria and Sca2 ortholog to generate area (sum of triangle surfaces for Sca2 ortholog), sphericity (surface area of a sphere with the same volume as the Sca2 ortholog surface/surface area of the Sca2 ortholog surface) and overlapped volume (volume of the overlap between the bacteria and Sca2 ortholog defined surfaces) values used for quantifying Sca2 ortholog coverage of *Rickettsia*. Results were plotted in Prism 10.3.1. For actin tail intensity line scans, deconvolved images were imported into ImageJ2/Fiji v2.9.0/1.53t and a max intensity projection was made for the actin channel of each image. A 1.25 μm line segment was drawn perpendicular to the actin tail 0.5 μm from the base of the bacterium and the intensity values across the perpendicular line segment were saved for one actin tail per image. The intensity values were normalized to the smallest and largest value across individual actin tails and plotted in Prism 10.3.1. The *R. parkeri* actin tail width was calculated from the distance between the two peak fluorescence values.

Live cell imaging

For live cell imaging, 1×10^6 A549 or HMEC-1 cells stably expressing RFP-F-tractin (generated as described above) were plated in a MatTek dish with a No. 1.5 coverslip (MatTek, P35G-1.5-20-C) and incubated at 37°C overnight. Mammalian cells were infected with *R. parkeri* pRAM18dRGA or *R. bellii* pRAM18dRGA at an MOI of 1, as described above. Immediately before imaging, media was changed to live cell imaging media (Live Cell Imaging Solution (Molecular Probes, A59688DJ), 10% FBS (ATLAS Biologics, FP-0500-A), 10 mM glucose (Fisher, D16), and 0.01% oxyrase (v/v) (Oxyrase Inc, OF-0005)). Dishes were imaged in an environmental chamber set to 33°C on the Nikon Ti Eclipse confocal microscope described above. The 488 nm (20% power) and 561 nm (30% power) channels were each captured with a 500 ms exposure. Images were taken at 5 s intervals for 5 min in cells where actin tails were clearly observed.

Images were imported into ImageJ2/Fiji v2.9.0/1.53t (Schindelin et al., 2012). To calculate motility speed, the Manual Tracking Plug-In was used to track individual bacteria with actin tails over the course of 1 m in 5 s intervals, with the total distance traveled in μm representing the speed μm/min. Motility efficiency was calculated by recording the X and Y pixel coordinates from t = 0 m and t = 1 m timepoints and then using the distance formula in Microsoft Excel to determine the straight-line distance in μm between the 0 m and 1 m coordinates. This value was divided by the total distance traveled over 1 m to obtain a motility efficiency value. Results were plotted in Prism 10.3.1.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Data availability statement

Data are underlying Figures 2, 3, 5, 6, 7, 8, 9, and S5 are included in Supplementary Dataset S1.

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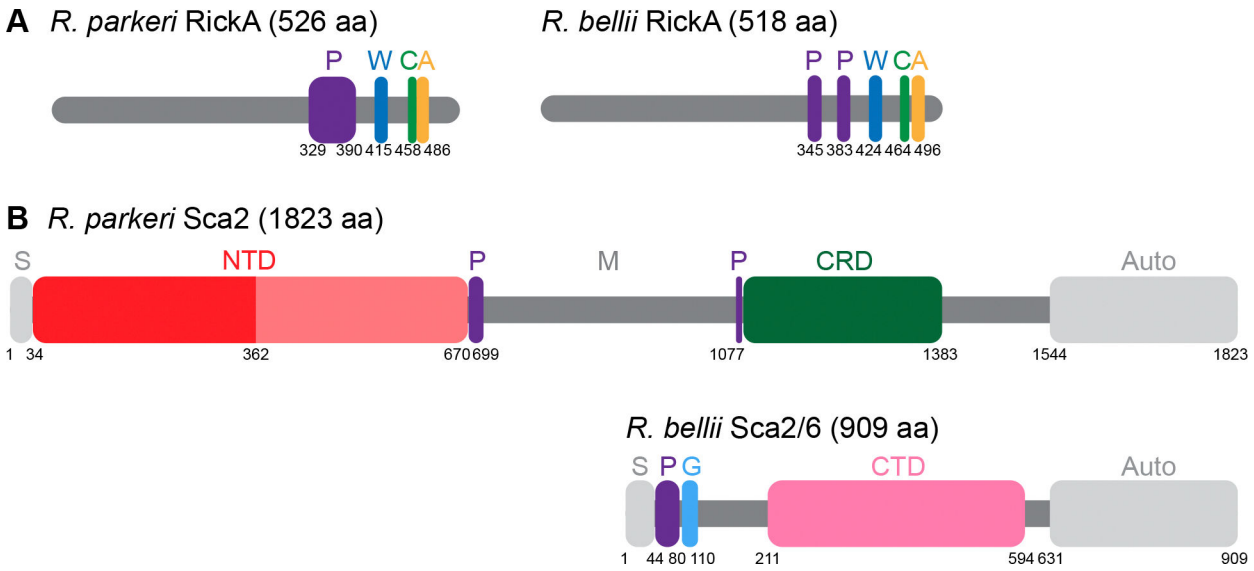

FIGURE 1.

RickA domain organization is conserved, whereas Sca2 ortholog domain organization is more variable. (A) RickA from *R. parkeri* and *R. bellii* share a common domain architecture. (B) Sca2 from *R. parkeri* and Sca2/6 *R. bellii* proteins differ considerably in their domain architecture. Abbreviations in (A) and (B): P = poly-proline or proline-rich domain, W = WASP homology-2 (WH2) motif, C = central motif, A = acidic motif, S = signal sequence, NTD = N-terminal domain (the darker half denotes the location of helical N-terminal repeats), M = middle domain, G = G-actin binding domain, CRD = C-terminal repeat domain, CTD = C-terminal domain, Auto = autotransporter domain.

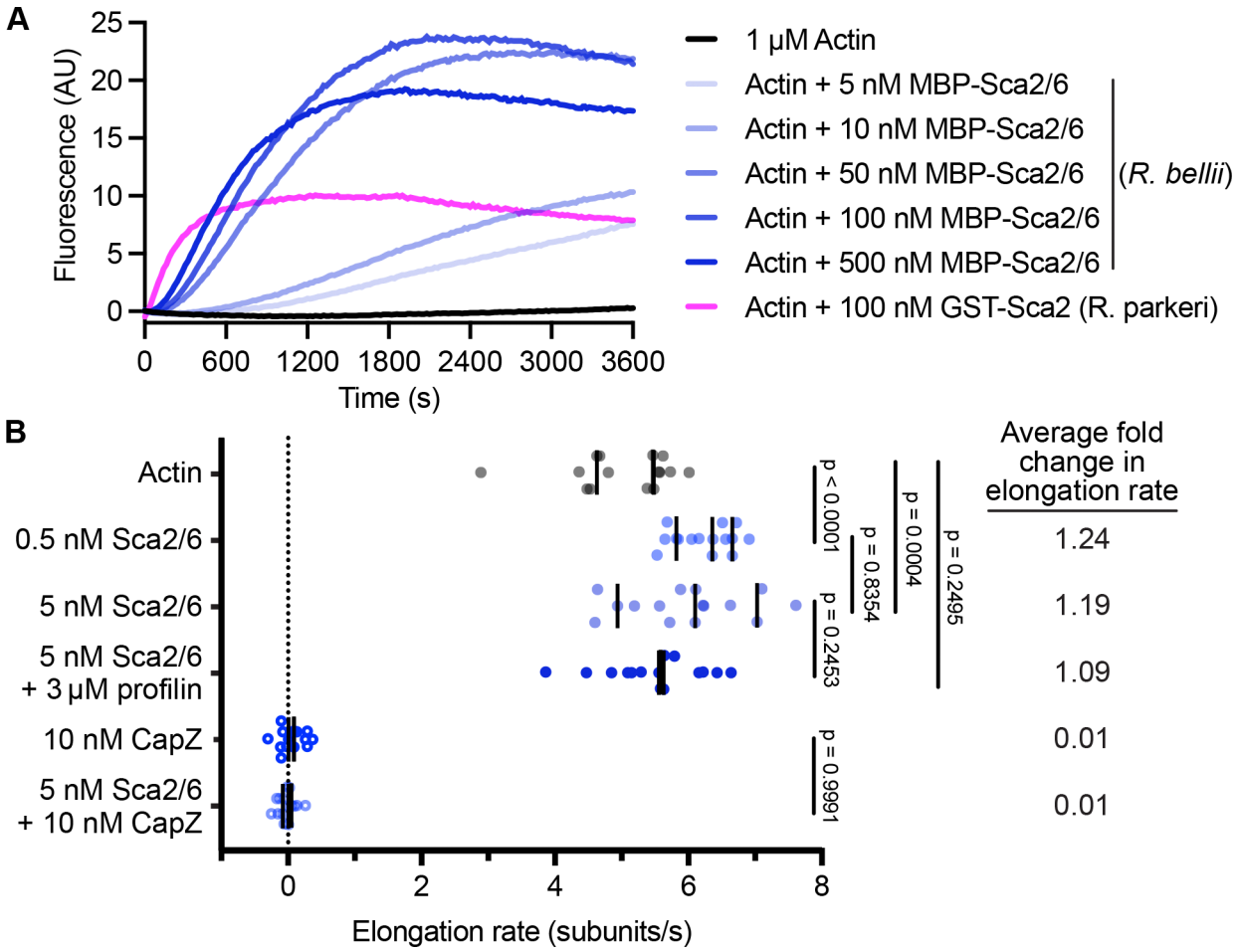

FIGURE 2.

R. bellii Sca2/6 nucleates actin filaments and promotes filament elongation. (A) Kinetics of assembly of 1 µM actin (10% pyrene-labeled) with the indicated concentrations of the *R. bellii* MBP-Sca2/6 or *R. parkeri* GST-Sca2 passenger domains. Reported fluorescence values correspond to the measured AU/1000. (B) Quantification of actin filament barbed-end elongation rates in TIRF assays performed with 1 µM actin (33% rhodamine-labeled) without or with the indicated concentrations of *R. bellii* Sca2/6-AF647, 3 µM profilin, and 10 nM CapZ. Black lines indicate the median values for each of N = 3 independent experiments. For each experiment, n = 5 filaments were analyzed. Significance was determined using a two-way ANOVA with a Tukey's multiple comparison post-test to compare the means of each replicate. Average fold changes in barbed end actin filament elongation rates are also included for the indicated concentrations of Sca2/6-AF647, profilin, and CapZ, all relative to actin alone.

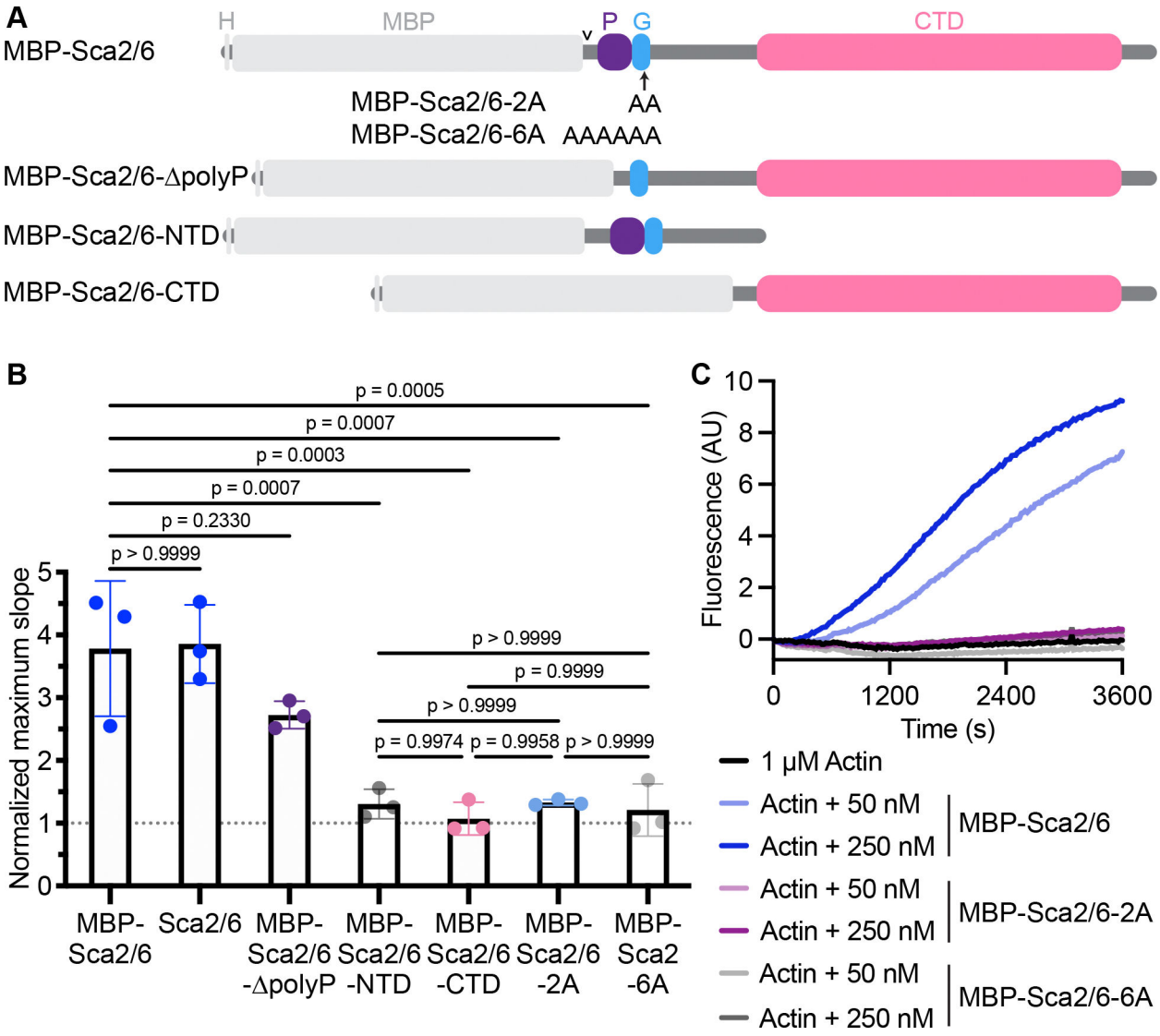

FIGURE 3.

Actin nucleation activity of *R. bellli* Sca2/6 truncations and mutants. (A) Diagram of truncated and mutated derivatives of *R. bellii* Sca2/6. H = 6x-His tag, MBP = maltose-binding protein tag, P = poly-proline domain, G = G-actin binding domain, CTD = C-terminal domain, arrowhead = TEV protease cleavage site. The MBP-Sca2/6-2A and MBP-Sca2/6-6A proteins contain 2 and 6 point mutations, respectively, in the G-actin binding motif. (B) Calculated maximum slope from pyrene-actin polymerization assays, normalized to actin alone (gray dotted line), for the indicated *R. bellii* Sca2/6 variants at 70 nM with mean values noted in the bars. N = 3 experiments for each protein, n = 2 replicates per experiment. Error bars indicate SD. Significance was determined using a one-way ANOVA with a Tukey's multiple comparisons test. (C) Kinetics of assembly of 1 μM actin (10% pyrene-labeled) with the indicated concentrations of *R. bellii* MBP-Sca2/6, MBP-Sca2/6-2A, or MBP-Sca2/6-6A. Reported fluorescence values correspond to the measured AU/1000.

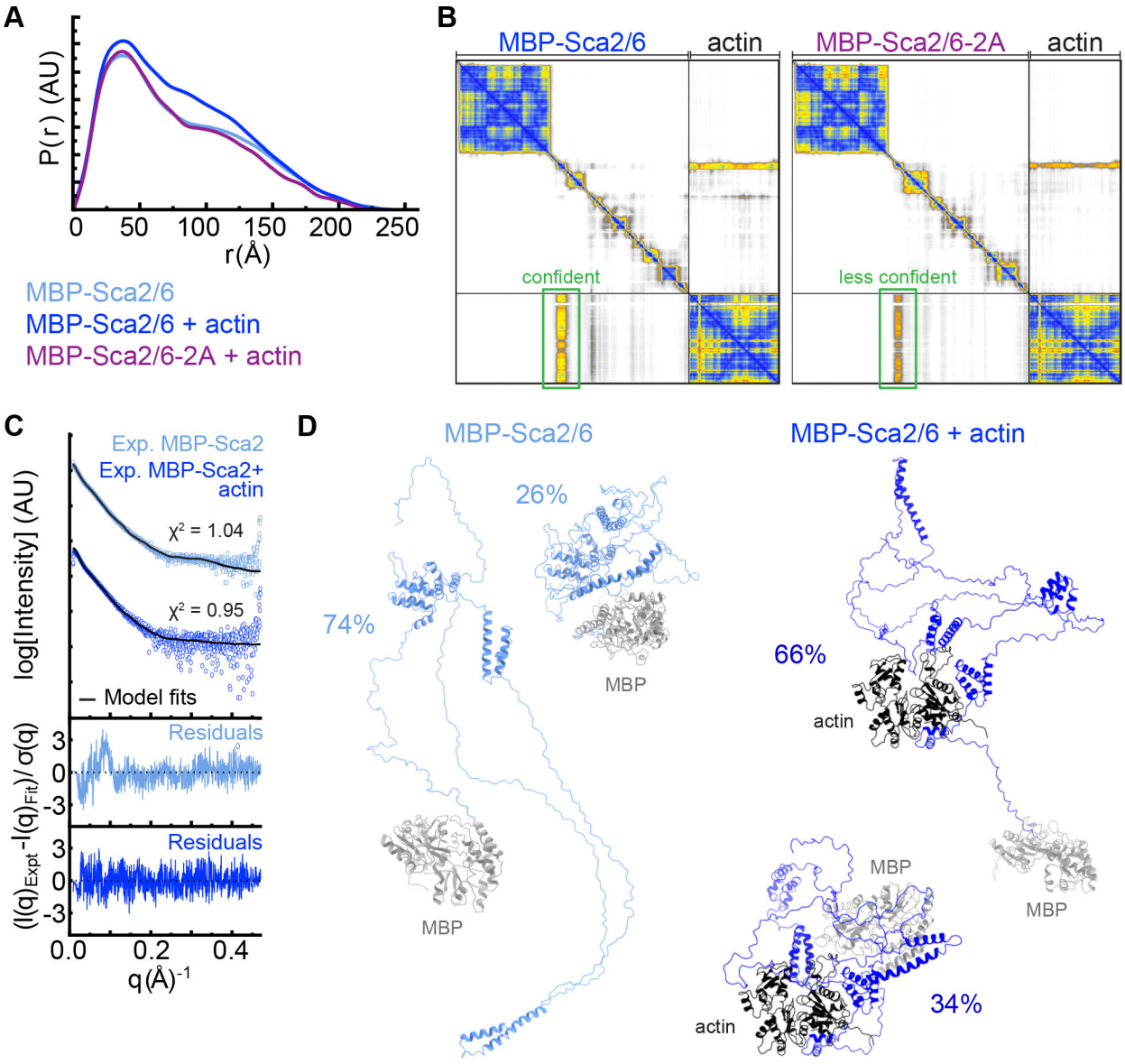

FIGURE 4.

R. bellii Sca2/6 is a structurally flexible protein that binds one molecule of G-actin through an unusual G-actin binding motif in the N-terminus. (A) Pair distance distribution functions (P(r)) calculated from SAXS data for MBP-Sca2/6, MBP-Sca2/6 plus G-actin, and MBP-Sca2/6-2A plus G-actin. Area under P(r) curves is proportional to the theoretical MW calculated from SAXS. (B) AlphaFold3 PAE matrices of MBP-Sca2/6 plus G-actin and MBP-Sca2/6-2A plus G-actin. Green boxes highlight the clusters of higher or lower confidence values that indicate interactions between MBP-Sca2/6 or MBP-Sca2/6-2A and G-actin. (C) Plot of SAXS experimental data (open circles and squares), BilboMD 2-state ensemble fits (black curves), and residuals. (D) BilboMD ensemble structures of MBP-Sca2/6 and MBP-Sca2/6 plus G-actin, labeled with the percentage of each structure in the ensemble. MBP = gray, actin = black.

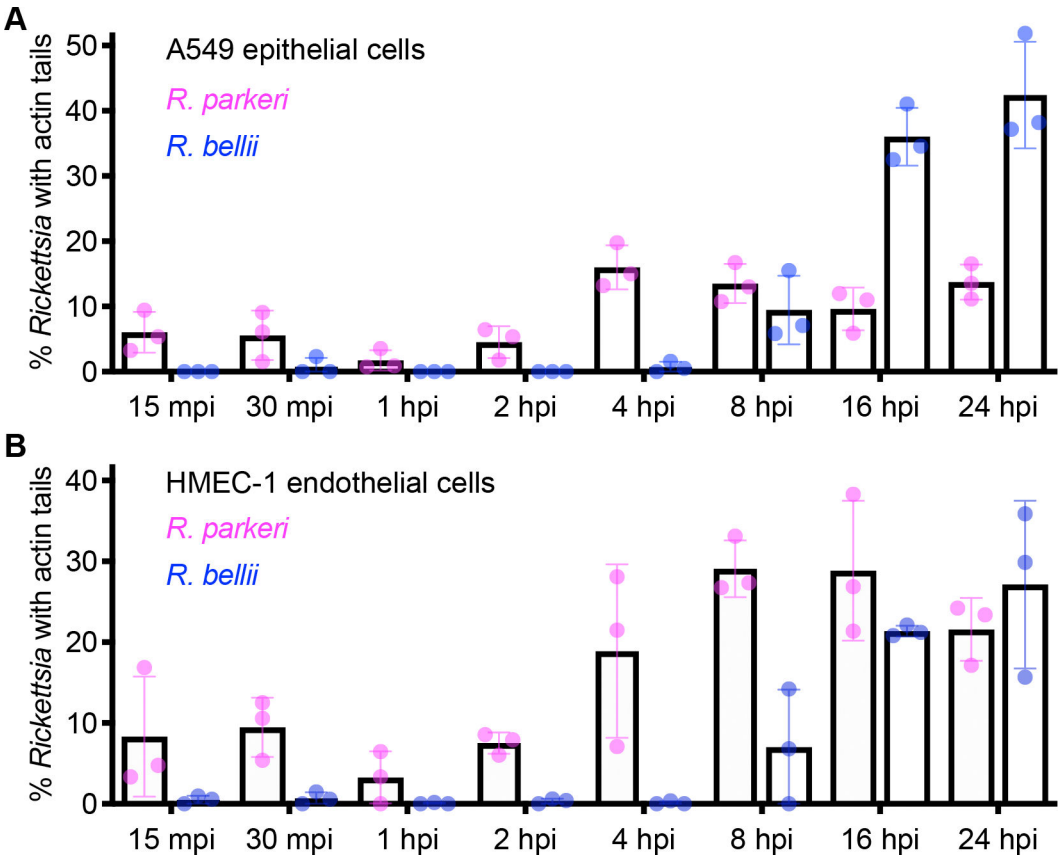

FIGURE 5.

R. bellii has a single phase of actin-based motility. Quantification of the percentage of *R. parkeri* (magenta) and *R. bellii* (blue) actin tails in infected (A) A549 human epithelial cells and (B) HMEC-1 human endothelial cells from 15 mpi to 24 h hpi. Bars indicate mean values, error bars indicate SD. N = 3 independent experiments, n ≥ 51 bacteria per experiment per time point.

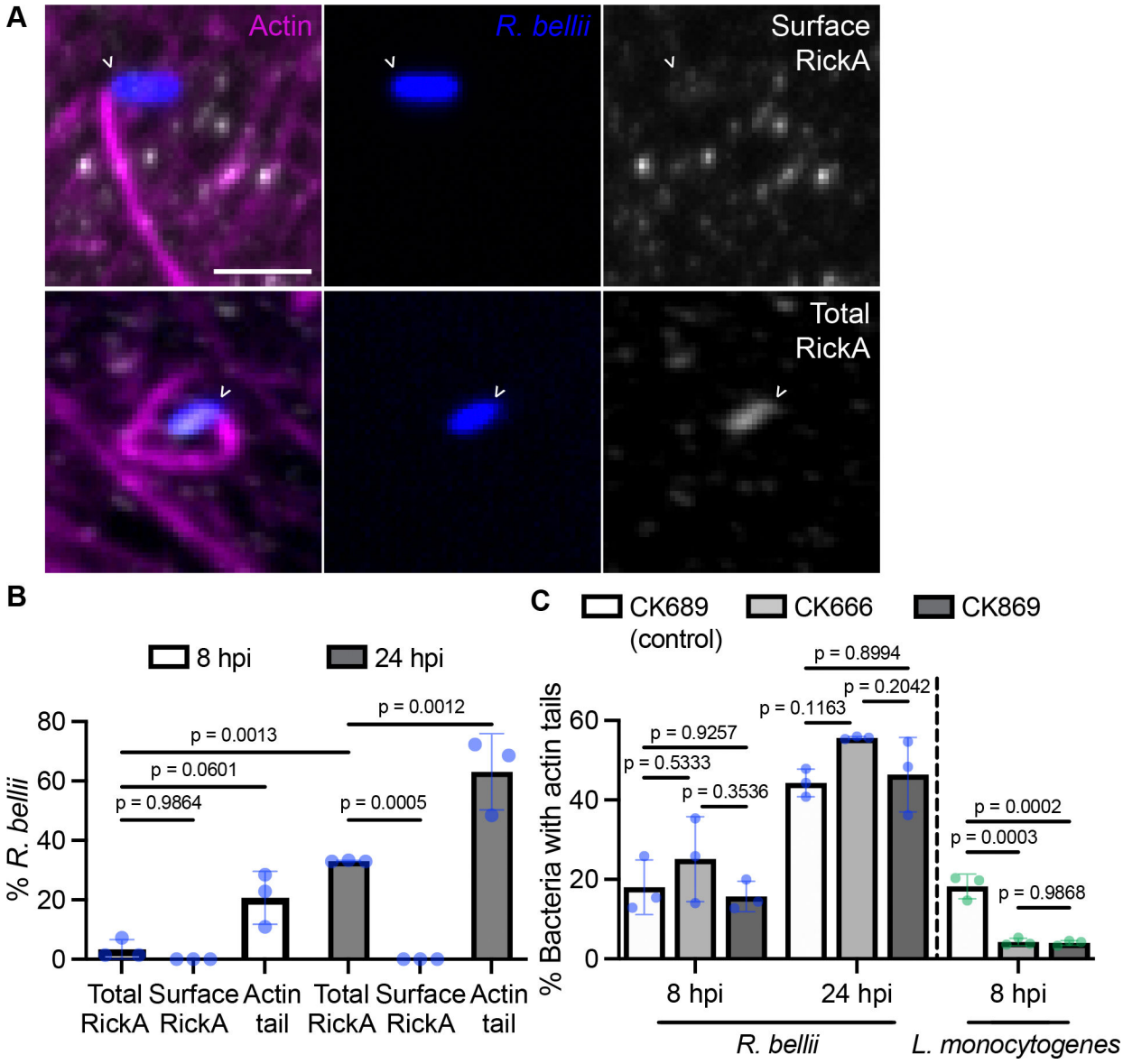

FIGURE 6.

RickA was not observed on the *R. bellii* surface and Arp2/3 complex inhibition did not impact *R. bellii* motility. (A) Representative maximum-projection images of *R. bellii* (blue, cytoplasmic BFP) in infected A549 cells immuno-stained for surface-localized and total RickA (white) and actin filaments (magenta) at 24 hpi. The bacterial pole associated with an actin tail is indicated with open arrowheads. Scale bar = 1 μm. (B) Percentage of *R. bellii* with total and surface-localized RickA at 8 and 24 hpi. N = 3 independent experiments, n ≥ 95 bacteria per experiment per time point. Significance was determined using a two-way ANOVA with a Tukey's multiple comparisons post-test. (C) Percentage of *L. monocytogenes* and *R. bellii* with actin tails at 8 and/or 24 hpi in the presence of Arp2/3 complex-inhibitors CK666 or CK869, or inactive control compound CK689. N = 3 independent experiments, n ≥ 139 bacteria per experiment per time point. Significance was

determined using a one-way ANOVA with a Tukey's multiple comparisons post-test. For (A) and (B), bars indicate mean values, error bars indicate SD.

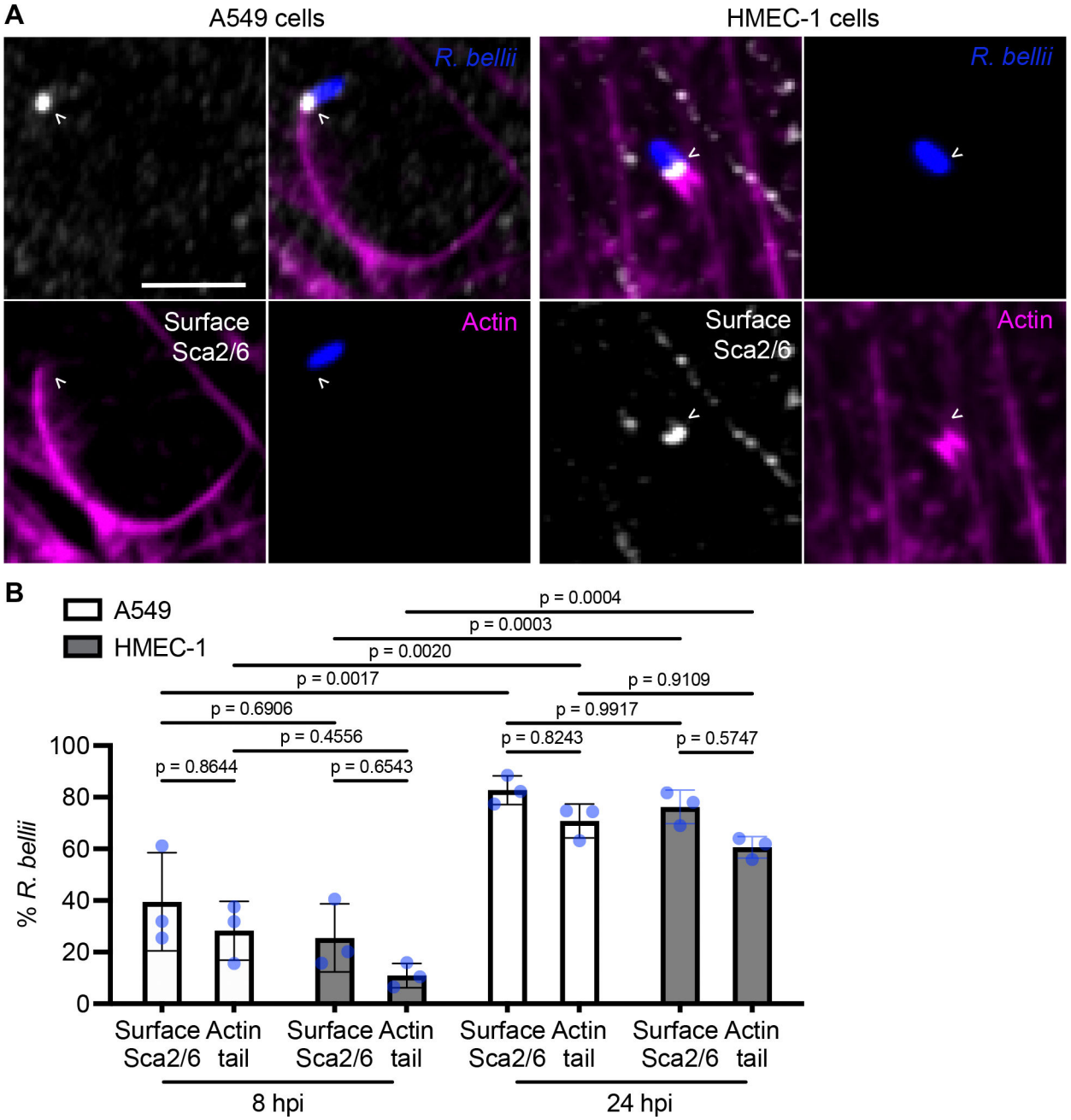

FIGURE 7.

Sca2/6 localizes to the surface of *R. bellii* in correlation with the formation of actin tails. (A) Representative confocal maximum-intensity projection image of *R. bellii* (blue, cytoplasmic BFP) with actin filaments (magenta) and Sca2/6 (white) in infected A549 at 8 hpi and HMEC-1 cells at 24 hpi. The bacterial pole associated with an actin tail is indicated with open arrowheads. Scale bar = 2 μm. (B) Percentage of *R. bellii* (cytoplasmic BFP) with polar Sca2/6 and frequency of actin tails in A549 (white bars) and HMEC-1 cells (gray bars). N = 3 independent experiments, n ≥ 42 bacteria experiment per time point. Bars indicate mean

values, error bars indicate SD. Significance was determined using a two-way ANOVA with a Tukey's multiple comparisons post-test.

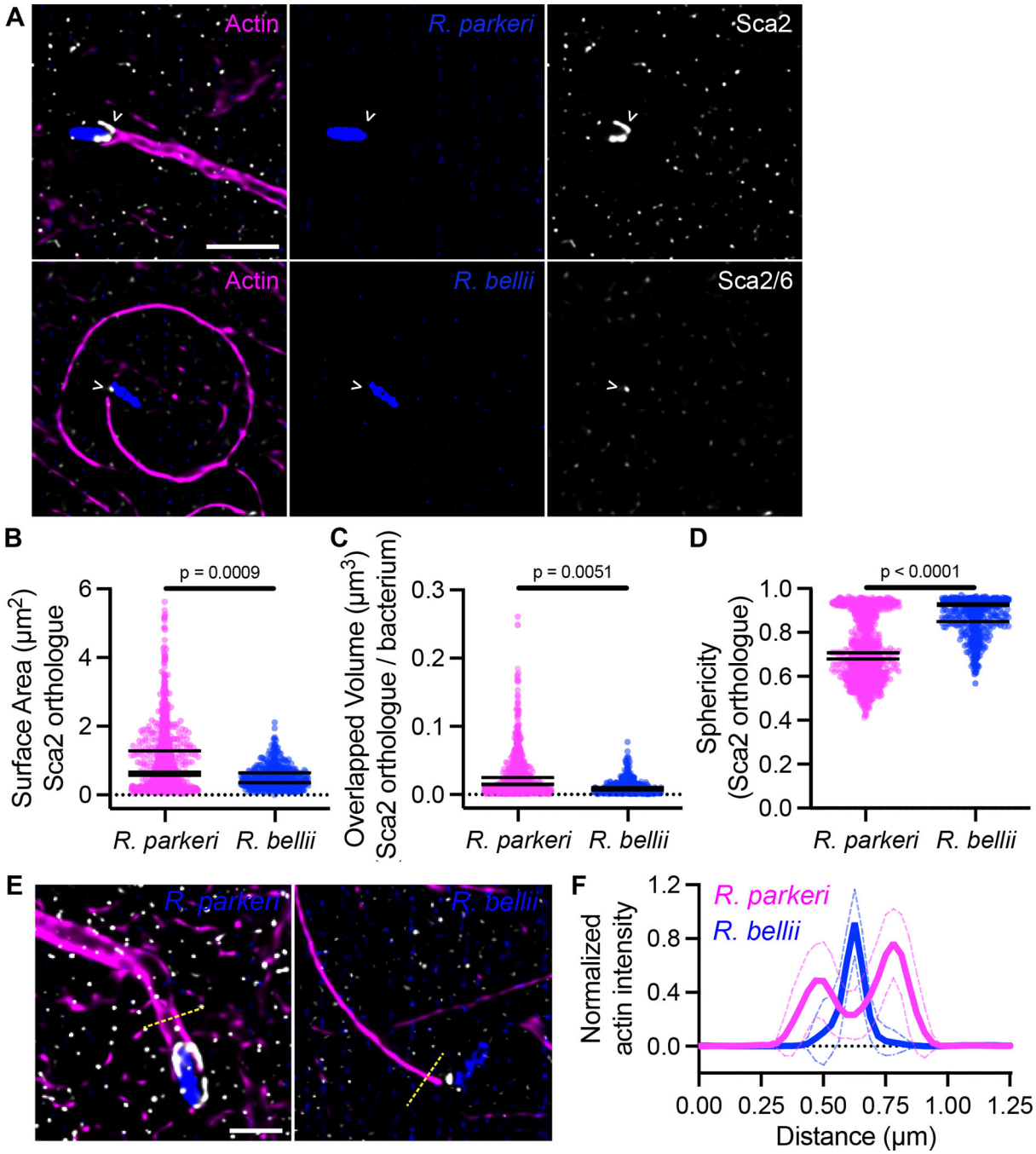

FIGURE 8.

Sca2 ortholog morphology and actin tail organization differs between *R. bellii* and *R. parkeri*. (A) Deconvolved lattice structured illumination (LSIM) maximum projections of A549 cells infected for 24 h with *R. parkeri* (blue, cytoplasmic BFP), and stained for actin filaments (magenta) and the Sca2 ortholog (white). Scale bars = 2 µm. Quantification of *R. parkeri* Sca2 and *R. bellii* Sca2/6 (B) surface area and (C) overlapped volume, and (D) sphericity. N = 3 independent replicates, n ≥ 229 bacteria per species per replicate. Significance was determined using a Welch's t test on the mean values of 6 images per

replicate. The median values of each replicate are indicated by black lines. (E) Maximum projections of deconvolved LSIM micrographs showing representative actin tail (magenta) intensity traces (dashed yellow line) positioned 0.5 μm from the start of the actin tail at the pole of the bacterium (blue) with Sca2 ortholog fluorescence (white) in infected A549 cells. Scale bar = 1 μm. (F) Plot of cumulative *R. parkeri* and *R. bellii* actin tail intensity traces. Dashed lines indicate SD. N = 3 independent experiments, n = 18 traces per *Rickettsia* species.

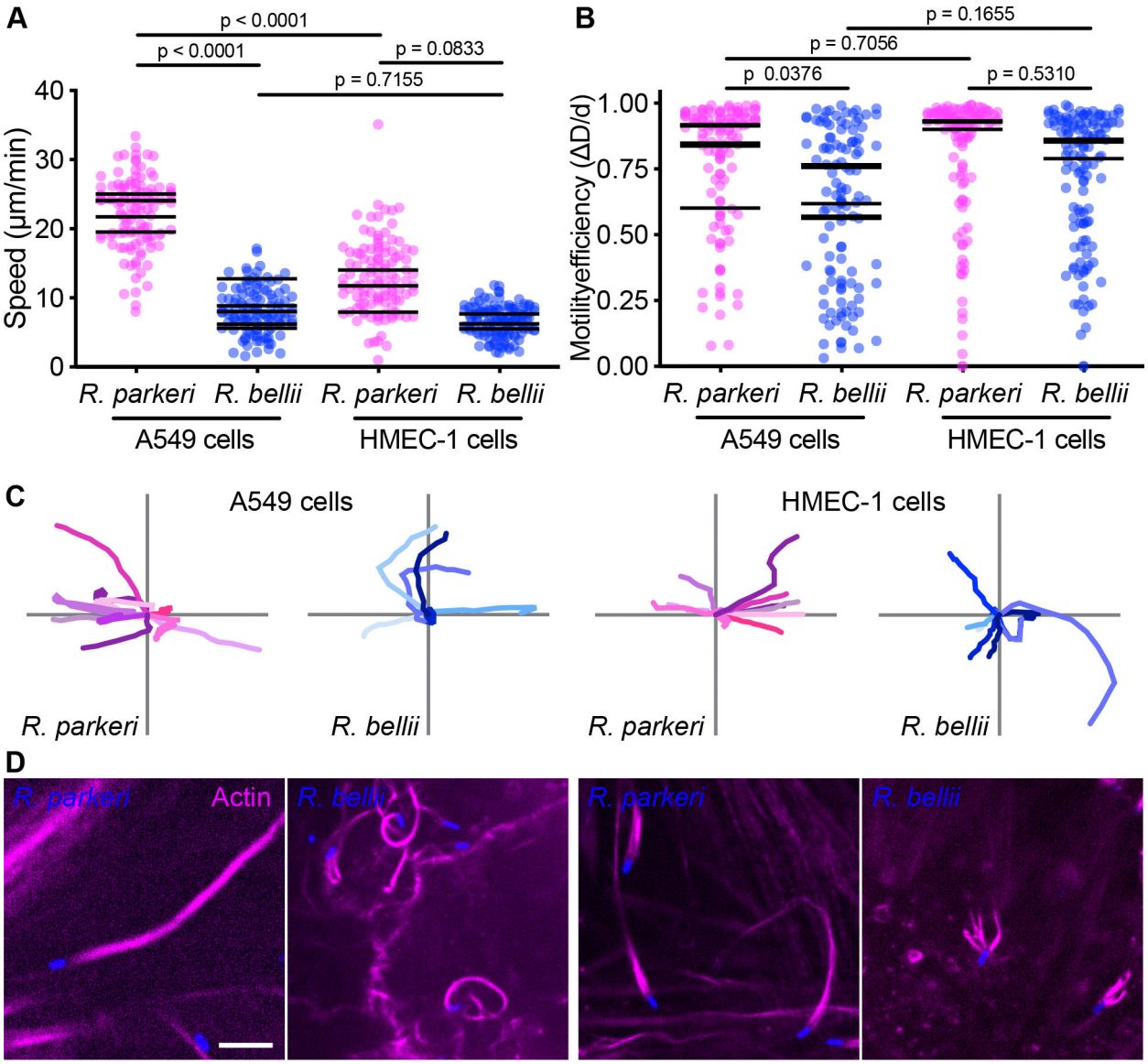

FIGURE 9.

Actin-based motility parameters and actin tail organization differ between *R. bellii* and *R. parkeri* as well as host cell lines. (A) Speed of *R. parkeri* (cytoplasmic GFP and *R. bellii* (cytoplasmic GFP) at 24 hpi in A549 and HMEC-1 cell lines. (B) Motility efficiency (ΔD/d) of *R. parkeri* (cytoplasmic GFP) and *R. bellii* (cytoplasmic GFP) at 24 hpi in A549 and HMEC-1 cell lines in 1 min intervals. N = 3 – 5 independent replicates per *Rickettsia* species and host cell line, n ≥ 110 bacteria per *Rickettsia* species and host cell line. Significance was determined using a one-way ANOVA with a (A) Tukey's multiple comparisons or (B) Kruskal-Wallis post-test on the mean values of the of each replicate. The median values of each replicate are indicated by black lines. (C) Motility traces of 10 representative *R. parkeri* (magenta) and *R. bellii* (blue) in infected A549 or HMEC-1 cell lines. Some traces are not clearly visible due to overlapping tracks. (D) Representative still

images of *R. parkeri* (blue, cytoplasmic GFP) and *R. bellii* (blue, cytoplasmic GFP) with actin tails (magenta), showing differences in actin organization. Scale bar = 5 μm.