Crosslinkers both drive and brake cytoskeletal remodeling and furrowing in cytokinesis

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Abstract

Cytokinesis and other cell shape changes are driven by the actomyosin contractile cytoskeleton. The molecular rearrangements that bring about contractility in non-muscle cells are currently debated. Specifically, both filament sliding by myosin motors, as well as cytoskeletal crosslinking by myosins and non-motor crosslinkers, are thought to promote contractility. Here, we examined how the abundance of motor and non-motor crosslinkers controls the speed of cytokinetic furrowing. We built a minimal model to simulate the contractile dynamics of the C. elegans zygote cytokinetic ring. This model predicted that intermediate levels of non-motor crosslinkers would allow maximal contraction speed, which we found to be the case for the scaffold protein anillin, in vivo. Our model also demonstrated a non-linear relationship between the abundance of motor ensembles and contraction speed. In vivo, thorough depletion of non-muscle myosin II delayed furrow initiation, slowed F-actin alignment, and reduced maximum contraction speed, but partial depletion allowed faster-than-expected kinetics. Thus, both motor and non-motor crosslinkers promote cytokinetic ring closure when present at low levels, but act as a brake when present at higher levels. Together, our findings extend the growing appreciation for the roles of crosslinkers, but reveal that they not only drive but also brake cytoskeletal remodeling.
Introduction

The actomyosin cortex powers cell shape change during diverse cellular behaviors including cell migration, tissue morphogenesis and cell division. The cortex is a heterogeneous meshwork rich in actin filaments (F-actin), cytoskeletal crosslinkers, cytoskeleton-plasma membrane linkers, and myosin motors (Clark et al., 2014). The final step of mitotic or meiotic cell division is cytokinesis, the physical division of the cell into two. During cytokinesis, cues from the anaphase spindle elicit specialization of the cortical cytoskeleton to form an actomyosin ring at the cell equator. The cytokinetic actomyosin ring is enriched with formin family actin nucleators that generate long unbranched F-actin, active non-muscle myosin II (NMM-II), and crosslinking proteins including anillin, alpha-actinin, the septins, and plastin. The ring dynamically rearranges, initially from a wide band into a tighter ring, and ultimately completely closes, generating a membrane partition between the daughter cells (Green et al., 2012).

The cytoskeletal rearrangements proposed to bring about cytokinetic ring closure include actomyosin filament sliding, F-actin depolymerization, and cytoskeletal crosslinking (Mendes Pinto et al., 2013). Sliding is thought to be driven by the motor activity of myosins including NMM-II, and loss of NMM-II function via injection of a blocking antibody, gene knock-out, protein depletion, or pharmaceutical inhibition eliminates furrowing (Schroeder, 1972; Mabuchi and Okuno, 1977; Straight et al., 2003; Matsumura et al., 2011). In some settings, the rate of cell constriction scales with the motor activity of NMM-II (Vasquez et al., 2016). However, a motor-impaired NMM-II mutant that crosslinks, but does not slide, F-actin rescued the speed of cytokinetic furrowing caused by thorough depletion or genetic deletion of NMM-II from animal cells (Ma et al., 2012). In addition, cell biological work with budding yeast and theoretical modeling demonstrated that ring closure can be powered by the thermal ratcheting of non-motor
crosslinkers along depolymerizing F-actin (Mendes Pinto et al., 2012; Oelz et al., 2015). Similarly, in fission yeast, a motor-impaired NMM-II mutant that robustly crosslinks F-actin is sufficient for ring assembly (Palani et al., 2017). Collectively, these studies suggest that F-actin crosslinking promotes cytoskeletal remodeling during cytokinesis, and ring closure in animal and fungal cells.

As introduced above, several cytoskeletal crosslinkers are abundant in the cytokinetic ring in animal cells, including NMM-II and anillin. NMM-II forms minifilaments, bipolar assemblies containing 16-56 motor subunits, each of which is bound to F-actin for 5-35% of its ATPase cycle (Burridge and Bray, 1975; Niederman and Pollard, 1975; Sinard et al., 1989; Verkhovsky et al., 1995). NMM-II minifilaments are robust F-actin crosslinkers (Vicente-Manzanares et al., 2009). Anillin is a multi-domain protein thought to coordinate both structural and regulatory elements of the cytokinetic ring. Anillin was first identified as an F-actin bundling protein, and has since been shown to bind active NMM-II, septins, the formin mDia2, RhoA, and several other proteins, as well as plasma membrane lipids (Piekny and Maddox, 2010; Liu et al., 2012; Reyes et al., 2014; Sun et al., 2015). Anillin depletion causes cytokinesis failure in cultured mammalian and Drosophila cells, but is dispensable for cytokinetic ring closure in the C. elegans zygote (Maddox et al., 2005; Straight et al., 2005; Zhao and Fang, 2005; Hickson and O'Farrell, 2008). Cortexillin crosslinks F-actin indirectly to the membrane and is important for the mechanical properties of the cortex and cytokinetic dynamics in the social amoeba Dictyostelium discoideum (Srivastava et al., 2016). Additional cytoskeletal crosslinkers that constitutively reside in the cortex, such as fimbrin/plastin, also contribute to cytokinesis (Ding et al., 2017). In sum, diverse cytoskeletal crosslinkers are abundant in the cytokinetic ring.

Interestingly, before crosslinking was implicated in driving cytokinesis, it was demonstrated that crosslinkers can block ring closure in mammalian cultured cells. The abundance
of alpha-actinin scales inversely with furrowing speed in animal cells, as overexpression slows furrowing while depletion allows faster furrowing (Mukhina et al., 2007). The picture is more complex in fission yeast, where an intermediate abundance and F-actin binding affinity of alpha-actinin are required for proper cytokinetic ring dynamics; thus this crosslinker both drives and blocks cytokinetic ring remodeling (Li et al., 2016). Similarly, in vitro reconstituted and simulated simple actomyosin rings exhibit maximal contraction speed and force generation with an intermediate amount of connectivity (Ennomani et al., 2016). Finally, an experimental increase or decrease of the abundance of plastin/fimbrin slows cytokinetic furrowing in the C. elegans zygote (Ding et al., 2017). Thus, the abundance of crosslinkers has been variously shown to scale with actomyosin ring closure speed positively, negatively, or in a complex manner (speed maximal at intermediate crosslinker levels). As such, it is currently unresolved whether cytoskeletal crosslinkers drive or attenuate remodeling in the cytokinetic ring.

Here, we tested how tuning motor- and non-motor crosslinkers influences cytokinetic ring constriction in animal cells. We used the C. elegans zygote as a model cell type since its stereotyped size, shape, and cell division kinetics, and its mechanical isolation within the eggshell are well-suited for quantitative studies of ring-intrinsic factors. To develop intuition about tuning crosslinker levels in this contractile system and guide our biological experimentation, we built an agent-based minimal model of the C. elegans zygote cytokinetic ring, depicting fibers representing F-actin, fiber crosslinkers, and motor ensembles representing NMM-II minifilaments. Tuning crosslinker abundance in silico predicted that an intermediate level of non-motor crosslinker would allow maximal ring closure speed. We then targeted the scaffold protein anillin in vivo, and generated populations of cells with a graded abundance of anillin by carrying out RNA-mediated depletion over a time-course. Partial depletion of anillin allowed faster furrowing than observed
in control cells, but in more thoroughly depleted cells, speed was normal. We next used our model to tune the abundance of motor ensembles and found a non-linear relationship between motor abundance and ring closure speed. *In vivo,* partial NMM-II depletion allowed faster furrowing than in control cells, while thorough depletion slowed ring closure. Towards defining the mechanism by which NMM-II both drives and brakes furrowing, we examined the kinetics of F-actin organization and found evidence that NMM-II also not only drives but also slows cytoskeletal remodeling. Our work demonstrates that both a motor- and a non-motor crosslinker can not only drive, but also attenuate, cytokinesis and thus extends our current understanding of the roles of cytoskeletal crosslinkers in cortical remodeling.

**Results**

*Simulated actomyosin rings with NMM-II-like motor ensembles close with in vivo kinetics*

Agent-based simulation of cytoskeletal machinery by CytoSim was recently used to tune the abundance of motors and non-motor crosslinkers in actomyosin-like patches and rings with different architectures (Ennomani *et al.*, 2016)While this approach provided the valuable insight that intermediate levels of crosslinkers allow maximal contraction speed, several features of the published models limit their relevance to cytokinesis *in vivo.* First, they employed motors modeled on myosin VI (a dimeric, pointed end-directed, highly processive motor (Rock *et al.*, 2001)), or on a generic, fast, processive barbed end-directed motor (Ding *et al.*, 2017). Furthermore, to model *in vitro* reconstituted rings with stabilized F-actin, simulated fibers were non-dynamic (Ennomani *et al.*, 2016). Here, we built on published models to depict NMM-II-like motors (see below), crosslinkers, and dynamic fibers, in a 30 micron-diameter ring representing a two-dimensional slice of the *C. elegans* zygote cytokinetic ring. The absolute and relative abundance of components
was set according to measurements of the fission yeast cytokinetic ring, scaled to a cross section of the *C. elegans* zygote division plane (Figure 1A; (Wu and Pollard, 2005); see Methods). The starting length and treadmilling dynamics of actin fibers were based on measurements from molecule counting studies, electron microscopy, as well as previously-established parameter ranges (see Supplemental Table 1) (Wu and Pollard, 2005; Kamasaki *et al.*, 2007; Davies *et al.*, 2014).

While employing many established parameters in our model, we adapted published models to simulate the behavior of NMM-II minilaments, modeling motor ensembles as rods with a motoring fiber-binding site (“hand”) at each end. The behavior of each hand exhibits the collective binding dynamics for a prescribed number of motor heads according to alterations of motor parameters that include binding rate, unbinding rate, and duty ratio (see Supplemental Table 1) (Stam *et al.*, 2015). Since NMM-II can exist as dimers or as minilaments with as many as 56 motor subunits *in vivo* (Burridge and Bray, 1975; Niederman and Pollard, 1975; Sinard *et al.*, 1989; Verkhovsky *et al.*, 1995), we kept the number of motor ensembles constant and tested how the speed of *in silico* ring closure was affected by the number of motor subunits per ensemble (the valence). Rings with motor ensembles representing 28 motor subunits closed with the most biologically relevant speeds (Figure 1B) leading us to utilize this valence in our control simulations.

We then measured the kinetics of simulated ring closure and found that our control *in silico* rings accelerated, maintained a relatively constant speed for much of closure, with maximum ring closure rates occurring 150-250 seconds after closure initiation, before gradually decelerating (Figure 1C). To compare simulation results with *in vivo* data, we acquired optical sections throughout the thickness of *C. elegans* zygotes, rotated image data sets 90 degrees to observe the
entire division plane, visualized with a fluorescently-tagged ring component, and used custom Matlab-based software to annotate the position of the cytokinetic ring over time (Figure 1D, E; (Dorn et al., 2010)). As *in silico*, the ring closed in an average of 5 minutes, accelerating until approximately half closed, and then decelerating (Figure 1F, F’; (Bourdages et al., 2014)). Thus, simulated control rings and rings visualized *in vivo* exhibited similar closure dynamics, suggesting that our *in silico* approach using bipolar motor ensembles faithfully recapitulates some aspects of *in vivo* ring dynamics.

*An intermediate amount of non-motor crosslinkers allows maximal ring closure speed* in silico and *in vivo*.

As introduced above, previous work has demonstrated that intermediate levels of cytoskeletal crosslinking maximizes constriction of acto-myosin VI networks *in vitro* and *in silico*, and the fission yeast and *C. elegans* cytokinetic rings *in vivo* (Ennomani et al., 2016; Li et al., 2016; Ding et al., 2017). To test the dependence of *in silico* ring constriction on non-motor fiber crosslinkers in our simulations, we varied the number of crosslinkers around the value set according to the measured collective abundance of two major F-actin crosslinkers (alpha-actinin and anillin (Mid1)) in the fission yeast cytokinetic ring (Wu and Pollard, 2005), scaled up to our 30-micron diameter ring. At the starting value (12,000) set from estimates of fission yeast, rings often fragmented but the maximum closure speed of those that remained intact was essentially unchanged (Figure 2A). Since ring fragmentation is not observed in control cells *in vivo*, we reasoned that our starting value of crosslinkers underestimated connectivity, potentially because cytoskeleton-membrane coupling is not accounted for in our minimal model. Therefore, we increased crosslinker abundance from our starting value and found that maximum ring closure
speed peaked at 36,000, which suggested that cytoskeletal connectivity helps drive ring closure. This gain in ring speed was lost again by further increases in crosslinker abundance, indicating that they also attenuate ring closure.

We next tested the prediction that an intermediate level of non-motor crosslinkers in vivo also allows maximum speed. The multi-domain scaffold protein anillin is implicated in providing mechanical connectivity to the ring. While Drosophila and mammalian cells fail cytokinesis following anillin depletion, C. elegans zygotes are robust to thorough depletion of anillin (encoded by the gene ani-1; (Maddox et al., 2005), allowing us to study the effects of depletion of cytokinetic dynamics. To test how the speed of cytokinetic ring constriction scales with the amount of crosslinking in animal cells, we depleted anillin over a time-course and measured residual anillin in the cytokinetic ring in embryos expressing anillin tagged at its endogenous locus with mNeonGreen (mNG::ANI-1; Figure 1D, 2B; (Rehain-Bell et al., 2017)). The abundance of residual anillin in the cytokinetic ring was estimated from the fluorescence intensity in the 180 degree arc closest to the coverslip (Figure 1D). With increasing exposure time to bacterial food expressing dsRNA directed against ani-1, zygotes contained progressively less anillin (Figure 2B, C). We calculated the maximum furrowing speed (32 ± 0.6% of the starting radius per minute for control cells (Fig. 2C and C’; occurs at ~50% closure), as a metric for cytokinetic ring performance. As the level of anillin was reduced, furrowing reached a significantly higher maximum speed (p=0.0001; Figure 2C). These results suggest that, while anillin is a highly conserved crosslinker enriched in the cytokinetic ring and thus presumed to augment ring function, wild-type levels of anillin attenuate ring closure speed.

In cells depleted of anillin beyond approximately 50%, furrowing speed could no longer be reliably tracked by visualizing residual mNG::anillin. To test how more thorough anillin
depletion changed furrowing speed, we tracked furrowing kinetics in worms expressing functional fluorescently-tagged NMM-II heavy chain (NMY-2∷GFP) under the control of an integrated exogenous locus (Nance et al., 2003). We measured residual endogenous anillin levels using western blots of whole worm extracts from worms depleted of anillin for various lengths of time, which led to a gradual reduction of anillin to 2% control levels (Figure 2F). Similar to our observation above, partial depletion of anillin to 50% of control levels lead to a significant increase in furrowing speed (p=0.0002; Figure 2E). Faster speeds at intermediate anillin levels could not be explained by an overabundance of NMM-II in the cytokinetic ring (Figure S1). In contrast, further reduction of anillin levels gradually restored furrowing speed to statistically indistinguishable from that of control cells (p=0.10 for 54 hour depletion compared to control; Figure 2G). These results suggest that, as in vitro, in silico (Ennomani et al., 2016), and in vivo for plastin (Ding et al., 2017), an intermediate amount of cytoskeletal crosslinking by anillin allows maximal contractility, and thus that crosslinking not only drives cytokinetic ring closure, but also attenuates furrowing speed. Furthermore, our in silico and in vivo results demonstrate that while alteration of crosslinker abundance can tune ring closure speed, these systems are robust, attaining control-level speed even after dramatic (50-fold) reduction of a major crosslinker. This is in contrast to the behavior of other simulated contractile networks, which fail to constrict with low crosslinker level and arrest with high crosslinker level (Ennomani et al., 2016; Ding et al., 2017). This distinction suggested that our simulated actomyosin network contained another robust crosslinking activity, namely our bipolar motors that represent NMM-II.
NMM-II both drives cytokinetic ring closure and limits its maximum speed

The crosslinking activity of NMM-II has been implicated in driving cytokinetic ring closure (Ma et al., 2012), but the effect of tuning motor-crosslinker levels on ingression dynamics has not been explored. To test if motor crosslinkers can both promote and attenuate ingression speed as described for non-motor crosslinkers, we first used our model to test how tuning the abundance of bipolar motor ensembles affected ring closure speed in silico, by performing simulations with randomly varied motor abundance between 20 and 120% of the control value (Figure 3A). Reduction of motor levels below 50% control slowed ring closure, in agreement with the idea that motors drive ring closure in silico. Furthermore, rings lacking bipolar motor arrays altogether failed to constrict (Figure 3B). However, over much of the range of motor level (between 50 and 120% control levels), ring closure speed did not appreciably vary (Figure 3A). The observation that adding more motors beyond a certain level does not increase ring closure speed supports the idea that bipolar motor arrays not only drive, but also attenuate, furrowing in silico.

To test how the level of NMM-II affects furrowing speed in vivo, we tuned ring levels of NMM-II by depleting the NMM-II heavy chain NMY-2 in worms expressing NMY-2-GFP, and measured residual NMY-2 to track ring closure. Reduction of NMY-2 levels below 50% of control levels significantly slowed ring closure (p<0.0001), in agreement with the idea that motors drive ring closure in vivo. However, partial depletion of NMY-2, to approximately 60% of control levels led to a significant increase in maximum ring closure speed (p=0.02), suggesting that NMY-2 can also attenuate closure speed in vivo. The same non-linear effect of myosin level on maximum furrowing speed was also obtained with a different C. elegans strain (Figure 3D). These results
suggest that myosin not only drives ring closure but also resists cytoskeletal remodeling during furrowing.

Does NMM-II act as a motor, a crosslinker, or both? Some insight into this question may emerge from our minimal model. If NMM-II were to act only as a motor, one might expect that the speed of contractile events would scale linearly with NMM-II abundance. If NMM-II were to act only as a crosslinker, one would expect contractility speed to peak at intermediate NMM-II levels (Ennomani et al., 2016; Li et al., 2016). We reasoned that a combination of the two effects (motor – linear, and crosslinker - quadratic) would result in a complex relationship between NMM-II and contractility. We sought mathematical evidence that NMM-II levels in vivo affect speed in a linear, quadratic, or more complex fashion (evidence that it acts as a motor, a crosslinker, or both), by fitting our data comparing NMM-II abundance and ring closure speed to polynomial curves of increasing order and monitoring the quality of the fit. Our in silico data were fit better by higher order polynomials than by simpler curves, indicating that motor abundance has a complex (non-linear) relationship with ring closure speed (Figure 4A, B). The same tests performed on in vivo data indicated that the dependence of ring closure speed on NMM-II abundance was also best fitted by higher order polynomial curves (Figure 4C and D). These findings support the idea that NMM-II functions both as a motor and a crosslinker.

Motor-impaired NMM-II is sufficient for cytokinesis in mammalian cells (Ma et al., 2012). To recapitulate this result in silico, we simulated rings in which motor ensembles had a motoring speed of zero. Rings with “motor-dead” motor ensembles constricted faster than simulated ring with control motors (Figure 3B). This result agrees with the concept that crosslinking, in concert with treadmilling actin, can drive ring closure (Mendes Pinto et al., 2012; Oelz et al., 2015), and furthermore that motoring can oppose ring closure as a brake. Importantly, for motor-dead myosin-
like ensembles to drive rapid ring closure \textit{in silico}, they must track depolymerizing filament ends (Figure 3B). In sum, this \textit{in silico} work supports the idea that the correct balance of motor and crosslinker activities and abundance is required for optimal ring dynamics.

\textit{NMM-II both drives and attenuates cytokinetic furrowing initiation and F-actin organization}

When the cytokinetic ring is at maximum speed, it is a tightly focused, diffraction limited cytoskeletal cord. In this configuration, crosslinkers could attenuate ring closure by blocking cytoskeletal sliding and remodeling. In contrast, when the cytokinetic ring first forms, cytoskeletal components are sparse, occupying a broad band of cortex (Henson \textit{et al.}, 2017); in this configuration, crosslinkers could have different effects than at maximum speed. Thus, we next examined how NMM-II level relates to the timing of furrow initiation by again depleting NMM-II over a time-course and scoring the onset of furrowing as time when the cortex first began to ingress away from the coverslip. Over most of the range of depletion time, initiation occurred later in cells more thoroughly depleted of NMM-II. However, when myosin was partially depleted to the level at which higher maximum speeds were achieved (12 hours), ingression occurred earlier than predicted by the trend exhibited by the other data (Figure 5A). These results suggest that while NMM-II drives furrow initiation, it also attenuates this early cell shape change to some degree.

Furrow initiation has been attributed to the remodeling of an initially isotropic cytoskeletal meshwork into circumferential bundles (Reymann \textit{et al.}, 2016). The effects of NMM-II levels on furrowing kinetics could relate to NMM-II’s roles in this cytoskeletal organization, but NMM-II could drive filament bundling and circumferential alignment, but also limit alignment by stabilizing isotropic filament intersections (Henson \textit{et al.}, 2017). To test how these opposing activities affect early cytoskeletal remodeling during furrow initiation, we imaged cells expressing
a GFP-tagged probe for F-actin (Jordan et al., 2016), depleted NMY-2MHC over a time-course, and measured the orientation of F-actin features, over time. As previously shown (Reymann et al., 2016), F-actin is initially poorly organized in the cell equator, and local order increased in a linear fashion, in a process we will call F-actin alignment “maturation” (Figure 5B, C). The increase in order reflected a convergence on the circumferential direction (decrease in offset angle; see Figure 5F). We plotted the initial linear rate of maturation for control cells and those depleted of NMY-2 to varying extents. The rate of alignment maturation was reduced by the mildest depletion, and more strongly reduced by the most severe depletion (Figure 5D, E). However, at the intermediate NMM-II level at which higher maximum furrowing speed and precocious initiation took place, the rate of F-actin alignment maturation was higher than expected based on the maturation rates of control cells and those depleted for 8 or 24 hours. From these results, we conclude that NMM-II not only drives but also attenuates cytoskeletal alignment. This implicates NMM-II not only in crosslinking, but specifically in promoting filament alignment, potentially by mediating filament bundling. In sum, our findings support the idea that crosslinkers not only contribute positively to, but also limit, the cytoskeletal remodeling that underlies cytokinetic ring closure.

Discussion

Speed is of the essence for cytokinesis in early embryos, since cell cycles are short, and a persistent cytoplasmic connection between daughter cells could lead to intercellular aneuploidy or defects in cell fate determination. Like other aspects of cell division in the C. elegans zygote, furrowing is exceptionally rapid and appears to have been fully optimized by evolutionary adaptation for high-fidelity, rapid early development. Therefore, it is somewhat unexpected that any experimental perturbation can increase furrowing speed. How can a depleted cytokinetic ring
function “better” than a control ring? Crosslinkers, including NMM-II, may block cytoskeletal remodeling and therefore furrowing in one or more ways, including stiffening the cortex by stabilizing interactions, suppressing actin depolymerization, or via steric hindrance. One might predict that crosslinkers in excess of the levels that allow maximal furrowing speed are incorporated into the ring where they would facilitate early remodeling. However, the same intermediate NMM-II depletion that allowed faster maximum speed also resulted in faster-than-expected cytoskeletal organization and furrow initiation (Figures 3C and D, and 5E). This lack of kinetic advantage in any of the stages we assayed demonstrates that mechanical brakes are part of the cytokinetic ring despite compromising speed, and suggests that they offer a distinct advantage, such as to make furrowing responsive to inhibitory signals for error correction.

The nature of the cytoskeletal remodeling that drives animal cytokinetic ring closure is still debated. One hypothesis is that filaments slide past one another as in muscle contraction (Schroeder, 1972). Alternatively, the new ends of depolymerizing F-actin may be ratcheted together via dynamic non-motor crosslinking (Mendes Pinto et al., 2012). Our findings that crosslinkers both drive and attenuate furrowing do not refute this latter model, but suggest that the abundance of crosslinker must be delicately balanced to optimally achieve remodeling, and thus extend our understanding of the structural mechanisms of cytokinetic ring closure.

Of similar importance is the question of how myosin motors drive constriction. Recent work has demonstrated that dynamic end-tracking crosslinking can drive constriction (Mendes Pinto et al., 2012; Oelz et al., 2015), but a role for motoring activity has not been fully discounted (Zumdieck et al., 2007; Oelz et al., 2015; Bidone et al., 2017). Our in silico findings that motor-dead myosin-like ensembles can drive ring closure as long as they can track depolymerizing actin fiber ends (Figure 3B) support the idea that dynamic crosslinking of treadmilling actin drives...
contraction. However, we also found that motoring activity slows closure of in silico rings, compared to motor-dead myosins, supporting the idea that motoring attenuates actomyosin contractile dynamics. In sum, our work suggests three contributions from motor ensembles: driving contractility via motoring and via crosslinking, as well as attenuating contractility. These in silico findings must be considered cautiously, since motor-dead NMM-II in vivo could have different biophysical properties than in silico; it may not only lack the power stroke but also bind and unbind F-actin with different kinetics. In addition, our modeling of NMM-II minifilaments may not accurately simulate some aspects of motor ensembles; our calculated multimerization of binding and unbinding dynamics of NMMII minifilaments could change the effect or magnitude of motoring activity on contractility.

We found that an intermediate amount of anillin and NMM-II allows maximal contraction speed. Similarly, maximal speed results from intermediate amounts of alpha-actinin in S. pombe (Li et al., 2016) and in vitro (Ennomani et al., 2016). Agent-based modeling of contractile networks containing generic motor dimers (Ding et al., 2017), myosin VI-like dimers (Ennomani et al., 2016), bipolar motor ensembles that represent NMM-II minifilaments (Figure 1D) also demonstrates that intermediate amounts of crosslinking allows maximal contractility. Continuum theory suggests that this behavior results from an effect on cytoskeletal mesh size and structure (Lenz et al., 2012). Together, these diverse observations suggest that the balance of positive and negative effects of motor and non-motor cytoskeletal crosslinkers, revealed here for animal cell cytokinesis, is a general principle of actomyosin contractility.
**Experimental procedures**

Strains, growth conditions and sample preparation

The following strains were used: JJ1473 (zuIs45 [nmy-2::NMY-2::GFP + unc-119(+)] V), OD95 (unc-119(ed3) III; ltIs38 [pAA1; pie-1/GFP::PH(PLC1delta1); unc-119 (+)]; ltIs37 [pAA64; pie-1/mCherry::his-58; unc-119 (+)] IV), MDX29 (ani-1(mon7[mNeonGreen^3xFlag::ani-1]) III) (Rehain-Bell et al., 2017), MDX40 (ani-1(mon7[mNeonGreen^3xFlag::ani-1], unc-119(ed3) III; nmy-2(cp52[nmy-2::mkate2 + LoxP unc-119(+) LoxP]) I), and JCC719 (mgSi3[tb-unc-119(+) pie-1>gfp:utrophin] II.; unc-119 (+)] III; ltIs37 [pAA64; pie-1/mCherry::his-58; unc-119 (+)] IV) (Jordan et al., 2016). Worms were maintained at 20°C according to standard procedures (Munro et al., 2004). Embryos were dissected from gravid hermaphrodites and mounted on coverslips on 2% agarose pads.

RNA-mediated protein depletions

Depletion of ANI-1, NMY-2, LET-502, and MEL-11 was performed by feeding worms bacteria from the Ahringer collection expressing dsRNAs directed against the targets, according to standard procedures (Min et al., 2010). The identity and sequence of all dsRNAs were confirmed by sequencing. Throughout this study, we exclusively examined perturbations that allow cytokinesis to succeed, while exhibiting quantitative defects.

**C. elegans embryo live cell imaging conditions:**

Imaging for panels 2C-E, 3C-D, 4A, 5A and S2 was performed on a DeltaVision Elite widefield microscopy system using the software Softworks (Applied Precision GE-Healthcare), equipped
with a CoolSnap HQ2 camera (Photometrics) at 2x2 binning and a 60x/1.42 plan Apo objective (Olympus). All image analysis was performed on non-deconvolved data.

Imaging for panels 2G and S1 (NMY-2::GFP embryos depleted of ANI-1\textsuperscript{nnillin}) was performed with a Nikon TE-2000 inverted microscope equipped with a swept field real-time confocal module (Prairie Instruments) and CoolSnap HQ2 CCD camera (Photometrics). The use of the 70-µm slit, 60x magnification, and a 200 ms exposure time were kept constant.

Imaging of actin alignment during furrow initiation was performed on a Nikon TE300 inverted microscope with a Plan APO 60x 1.4 NA oil objective, a Yokogawa Nipkow spinning disk, Hamamatsu ORCA-ER camera, Prior stage microcontroller, and Melles Griot ion laser power supply. Embryos were dissected, as previously described, and imaged prior to 1 cell division with 2 second intervals between each image acquisition. Image data was aligned based on disappearance of the polar concentration of actin and the onset of cortical swirling prior to furrow initiation. Images were acquired in a single cortical plane through the maturation of the furrow, which was determined based on the ingression of the contractile ring past the cortical imaging plane.

**Measurements of ring closure**

Anaphase onset was determined by observing a separation between chromatin masses visible against the background of myosin fluorescence in the spindle. Ring closure was determined using semi-automated custom software cyanRing (for CYtokinesis ANalysis of the RING) as described previously (Dorn \textit{et al.}, 2010; Bourdages \textit{et al.}, 2014). In cyanRing, the equatorial region of the embryo is cropped from the 3D image stack, rotated, and maximum-intensity projected to produce a view of the cytokinetic ring along the spindle axis as viewed from the posterior direction. The
user then defines the cell outline as well as the outline of the cytokinetic ring by selecting at least three points, through which best-fit circles are drawn. Radii are calculated from best-fit circles and used to calculate ring closure as a percentage of starting size.

Measurements of cytokinetic ring myosin levels

The intensity of myosin at maximum speed was extracted from cyanRing annotations of ring position. The integrated intensity was calculated for a 9-pixel radius torus encompassing the cytokinetic ring and normalized against a region of background outside the cell. Experimental intensity values were normalized to the average of control cell data acquired on the same day.

Quantitative immunoblotting

L4-stage hermaphrodites were injected with dsRNA directed against ani-1 (Maddox et al., 2005) and incubated at 20°C for 12-54 hours. Extracts were prepared from control worms and those depleted of ANI-1\textsuperscript{anillin} using standard protocols. Extract loaded onto the 100% loading lanes contains approximately 10 worms. Immunoblotting was performed using an anti-ANI-1 polyclonal antibody (Maddox et al., 2005) and anti-α-tubulin clone DM1α (Sigma). Protein bands from film were quantified using ImageJ software. Loading was normalized using tubulin as a control. Data presented are the relative anillin amounts as a ratio of anillin in depleted worms relative to that of control worms. The extent of depletion estimated via blotting for endogenous anillin in whole worms likely underestimates levels in embryos, since the target protein is more thoroughly depleted from the germline and embryos than other tissues.
Simulations

Agent-based modeling was performed using the Open Source software CytoSim beta for MacOS 10.6+ ((Nedelec and Foethke, 2007), www.cytosim.org). General setup is described in great detail in the included simulation file and supplemental table (Supplemental File 1; Supplemental Table 1). Motor head unbinding dynamics are calculated by the Kramer method: \( k_{\text{off}} = k_0 \times \exp(\frac{F_t}{F_0}) \); where \( k_0 \) is the unloaded unbinding rate, \( F_0 \) is the unbinding force, and \( F_t \) is the force felt by the binding motor at time \( t \). Motoring speed was calculated at each simulation frame by the formula: \( V_t = V_0 \times (1 - \frac{F_t}{F_0}) \); where \( V_0 \) is the unloaded motor speed, \( F_0 \) is the stall force, and \( F_t \) is the load force at timepoint \( t \). Myosin complexes were simulated as bipolar couples with actin-binding motoring domains attached at either end of a filament. Each actin-binding motor domain was modeled to simulate the dynamics of multiple myosin motoring heads (between 2-28) for total myosin valence of 4-56 motors. Actin dynamics were based off previous models (Mendes Pinto et al., 2012; Oelz et al., 2015) and include depolymerizing primarily at pointed ends and polymerizing primarily at barbed ends, with a net treadmilling rate of 0.04 \( \mu \text{m/s} \) and net depolymerization rate of 0.004 \( \mu \text{m/s} \). Crosslinkers were modeled after those of previous work (Ennomani et al., 2016) to represent a crosslinker like alpha actinin, bearing a single actin-binding domain at each end of a small filament. Initially, actin filaments were assembled in a tangential orientation to the circular cell space in a radius of approximately 14.5 \( \mu \text{m} \) with a ring width of 300 nm. After equilibrating in the simulation crosslinkers and motors were added to the simulation space and simulations were allowed to run for 400 seconds of simulated time. Control contractile ring simulation parameters are listed in supplemental table 1 and in the attached configuration file. Plots of in silico ring closure kinetics were smoothened with a five time-point rolling average to reduce noise.
Stepwise regression analysis

Stepwise regression analysis for our *in vivo* and *in silico* myosin depletion speed curves was performed using GraphPad Prism software (GraphPad Software Inc, La Jolla, CA). Data were normalized to control myosin levels (x axis) and control maximum speed (y axis). Polynomial regressions were fitted to the normalized experimental data and simulation data, and F-test analysis was performed to generate absolute sum of squares and adjusted R² (aR²) values for each polynomial fit. Optimal fitting was determined based on increase of the aR² to a peak value followed by plateauing or decrease as additional terms are added to the polynomial fit equation.

Acknowledgements

We are grateful to Laura Miller, Vincent Boudreau, Young Jun Yun, Xiaohu Wan, Kathryn Rehain-Bell, and Melissa Plooster for technical help. We thank Jian Liu for insightful discussions and Mark Peifer, Michael Werner, and Dan Dickinson for critical reading of this manuscript. We thank the entire Maddox labs for their thoughtful input, and Scott Williams for his support.

Figure legends

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Figure 5. The kinetics of furrow initiation and circumferential F-actin bundling respond non-linearly to NMM-II abundance. A) Furrow initiation timing in cells expressing a GFP-tagged F-actin probe, relative to time of depletion for control cells and those depleted of NMY-2 for between 8 and 24 h. Bars denote average ± SEM. B) Cortical F-actin visualized via GFP-utrophin at three timepoints with respect to polar cap disappearance. C) F-actin order in the cell equator and anterior.
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Supplemental File 1

The CytoSim configuration file is provided as a supplemental document.

Supplemental Table 1

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GFP: utrophin CH domains (F-actin)

F-actin alignment (% maximal)

Time (sec post anaphase onset)

Time of NMY-2 depetion (hr)
(Increasing NMY-2 level →)

F-actin alignment rate

Time post anaphase onset (sec)

F-actin alignment rate

Time of NMY-2 depetion (hr)
(Increasing NMY-2 level →)

Offset angle from circumferential (degrees)

Time post anaphase onset (sec)
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