CellPress

- Murayama, Y., Endo, S., Kurokawa, Y., Kurita, A., Iwasaki, S., and Araki, H. (2024). Coordination of cohesin and DNA replication observed with purified proteins. Nature 626, 653–660.
- Ochs, F., Green, C., Szczurek, A.T., Pytowski, L., Kolesnikova, S., Brown, J., Gerlich, D.W., Buckle, V., Schermelleh, L., and Nasmyth, K.A. (2024). Sister chromatid cohesion is mediated by individual cohesin complexes. Science 383, 1122–1130.
- Haering, C.H., Farcas, A.M., Arumugam, P., Metson, J., and Nasmyth, K. (2008). The cohesin ring concatenates sister DNA molecules. Nature 454, 297–301.
- Gligoris, T.G., Scheinost, J.C., Bürmann, F., Petela, N., Chan, K.L., Uluocak, P., Beckouët, F., Gruber, S., Nasmyth, K., and Löwe, J. (2014). Closing the cohesin ring: Structure and function of its Smc3-kleisin interface. Science 346, 963–967.
- Zhang, N., Kuznetsov, S.G., Sharan, S.K., Li, K., Rao, P.H., and Pati, D. (2008). A handcuff model for the cohesin complex. J. Cell Biol. 183, 1019–1031.

- Kim, Y., Shi, Z., Zhang, H., Finkelstein, I.J., and Yu, H. (2019). Human cohesin compacts DNA by loop extrusion. Science *366*, 1345–1349.
- 11. Xiang, S., and Koshland, D. (2021). Cohesin architecture and clustering in vivo. eLife 10, e62243.
- Cattoglio, C., Pustova, I., Walther, N., Ho, J.J., Hantsche-Grininger, M., Inouye, C.J., Hossain, M.J., Dailey, G.M., Ellenberg, J., and Darzacq, X. (2019). Determining cellular CTCF and cohesin abundances to constrain 3D genome models. eLife 8, e40164.
- Ladurner, R., Kreidl, E., Ivanov, M.P., Ekker, H., Idarraga-Amado, M.H., Busslinger, G.A., Wutz, G., Cisneros, D.A., and Peters, J. (2016). Sororin actively maintains sister chromatid cohesion. EMBO J. 35, 635–653.
- Rankin, S., Ayad, N.G., and Kirschner, M.W. (2005). Sororin, a substrate of the anaphasepromoting complex, is required for sister chromatid cohesion in vertebrates. Mol. Cell 18, 185–200.
- Nishiyama, T., Ladurner, R., Schmitz, J., Kreidl, E., Schleiffer, A., Bhaskara, V., Bando, M., Shirahige, K., Hyman, A.A., Mechtler, K., *et al.* (2010). Sororin mediates sister chromatid

cohesion by antagonizing Wapl. Cell *143*, 737–749.

Current Biology

Dispatches

- 16. Srinivasan, M., Fumasoni, M., Petela, N.J., Murray, A., and Nasmyth, K.A. (2020). Cohesion is established during DNA replication utilising chromosome associated cohesin rings as well as those loaded de novo onto nascent DNAs. eLife 9, e56611.
- Davidson, I.F., Bauer, B., Goetz, D., Tang, W., Wutz, G., and Peters, J.M. (2019). DNA loop extrusion by human cohesin. Science 366, 1338–1345.
- Liu, Y., and Dekker, J. (2022). CTCF–CTCF loops and intra-TAD interactions show differential dependence on cohesin ring integrity. Nat. Cell Biol. 24, 1516–1527.
- Ünal, E., Heidinger-Pauli, J.M., and Koshland, D. (2007). DNA double-strand breaks trigger genome-wide sister-chromatid cohesion through Eco1 (Ctf7). Science 317, 245–248.
- 20. Ström, L., Karlsson, C., Lindroos, H.B., Wedahl, S., Katou, Y., Shirahige, K., and Sjögren, C. (2007). Postreplicative formation of cohesion is required for repair and induced by a single DNA break. Science 317, 242–245.

Actomyosin cortex: Inherently oscillatory?

Andrew B. Goryachev* and Marcin Leda

School of Biological Sciences, Institute of Cell Biology, Centre for Engineering Biology, The University of Edinburgh, Max Born Crescent, Edinburgh EH9 3BF, UK

*Correspondence: Andrew.Goryachev@ed.ac.uk https://doi.org/10.1016/j.cub.2024.05.072

A new analysis of cytokinetic furrow ingression in the *Caenorhabditis elegans* zygote at high spatiotemporal resolution demonstrates that, rather than being a process of steady, spatially uniform constriction, furrow ingression is modulated by complex contractile oscillations that move around the furrow, possibly in the form of propagating waves.

The actomyosin cortex makes all the difference between complex, dynamically behaving animal cells and the static, spherical bags of chemicals passively floating in the surrounding fluid that cells would be without this cortex. The ability of the actomyosin cortex to actively contract, expand and dynamically remodel itself makes essential contributions to all vital cell functions, most notably to cell migration and cytokinesis¹. The contractile activity of the cortex is spatially prepatterned on the cell membrane by the activity of small GTPases of the Rho family². During cytokinesis, the furrow is induced by an

equatorial belt of active RhoA GTPase, known as the Rho zone, that directly induces both the F-actin polymerization and the activation of myosin II³. In turn, myosin contractility feeds back into the regulation of Rho in an important but as yet poorly understood manner, presumably by spatially redistributing the GTPase and its regulators. So far it has been unambiguously established that furrow constriction induces a pronounced furrow-directed flow of the actomyosin cortex (Figure 1A) that both concentrates F-actin and myosin in the furrow and induces nematic ordering of actin filaments, thus further promoting furrow

constriction by aligning myosin motors along the furrow^{4,5}. Ostensibly, nothing in the biological function of cytokinesis seems to require that furrow ingression should not be an axially symmetric process of radially uniform ingression, starting from the equatorial belt encircling the mother cell all the way to the midbody separating the two nascent sisters, as it is often pictured in the textbooks. However, in many cell types cytokinesis occurs in a highly asymmetrical manner⁶. Thus, in epithelia the furrow ingresses largely in the basal to apical direction, reflecting the highly polarized organization of these cells. Surprisingly, however, highly

R682 Current Biology *34*, R675–R696, July *22*, 2024 © 2024 Elsevier Inc. All rights are reserved, including those for text and data mining, Al training, and similar technologies.



Current Biology Dispatches

asymmetrical furrow ingression is also observed in non-adherent embryonic cells, with the first division of the *Caenorhabditis elegans* zygote being a remarkable example that has been studied genetically at a fine molecular resolution⁷. This well-described phenomenon (Figure 1B) is highly counterintuitive, given the initial axial symmetry of the zygote with the celldivision spindle acting as the axis of symmetry.

In this issue of Current Biology, Werner et al.⁸ revisit the dynamics of the cytokinetic furrow during the first division of the C. elegans zygote using a combination of experimental and theoretical approaches. To study this process, these authors developed a livecell imaging pipeline with unprecedented spatiotemporal resolution. Using an inverted resonant scanning confocal microscope, they were able to acquire z-stacks of 40 optical sections separated by 1 µm every 2.7 seconds. Together with another recent study⁹ that put more emphasis on the measurement of the cortical flow surrounding the furrow, Werner et al.⁸ provide the most complete and detailed guantitative description to date of furrow ingression in the C. elegans zygote during its first division. The authors partitioned the furrow circumference into 72 angular sections of 5° each. Their analysis, tracking the dynamics of individual angular segments, not only further confirmed the highly asymmetric nature of furrow ingression but also found stochastic oscillations of individual furrow segments, undetected in the previous studies that analyzed only the spatially averaged dynamics of the furrow diameter. Werner et al.⁸ also observed similar dynamics of furrow ingression in the consecutive divisions of smaller embryonic cells. The authors further found that the asymmetry of ingression can be decoupled from the oscillations induced by perturbations already reported to abrogate the asymmetry of ingression, such as genetic ablation of the scaffolding proteins anillin and septins⁷. To explain these oscillations, Werner et al.8 turned to the mechanobiochemical model they had previously proposed¹⁰.

These observations by Werner *et al.*⁸ are highly consistent with a growing body



Figure 1. Is the cytokinetic furrow related to waves of actomyosin contractility? (A) Diagram of cytokinetic furrow ingression. Actomyosin flow (beige arrows) concentrates and aligns actin (green) and myosin-2 (magenta) filaments. (B) Asymmetric ingression of the furrow in the *C. elegans* zygote (adapted from Werner *et al.*⁶). The position of the ingressing furrow in the plane of cytokinesis is schematically shown at the consecutive time points. (C) Biochemical regulation of the pulses and waves by an activator-inhibitor circuit (see text). (D) Cytokinetic furrow in early starfish blastomeres is patterned by the Rho zone, which emerges as a narrowing band of waves (adapted from Bernent *et al.*¹⁵). RhoA activity waves are shown in magenta.

of publications reporting actomyosin cortex dynamic activity, which is widely observed across many cell types and organisms in the form of contractile pulses¹¹ and propagating waves¹²⁻¹⁶ and is collectively referred to as cortical excitability^{2,17}. Summarizing these diverse phenomena in a nutshell, two types of spatially localized temporal peaks, closely following each other in time, are typically observed (Figure 1C). The first peak is heralded by the sharp increase in the activity of a Rho family small GTPase, most notably RhoA, Cdc42 or Rac1, while the second is that of dynamically polymerized F-actin and actin-binding proteins. Mechanistically, this dynamic pattern has been explained via the action of two feedback loops converging on a Rho GTPase. Fast positive feedback induces activation of the Rho GTPase by guanine nucleotide exchange factors (GEFs, the activators) that are recruited by the active, GTPbound form of the GTPase¹⁸. The GTPase is then inactivated by time-delayed negative feedback, most commonly traced to the F-actin-bound

GTPase-activating proteins (GAPs, the inhibitors). (For details, see a recent review² and references therein.) Mechanical stress-generating myosin contraction, preceded by its recruitment and activation, typically follows the actin polymerization peak, sometimes with a pronounced time delay¹³. In static pulses, the peaks of GTPase activity and actin polymerization are co-localized on the cortex, while, in propagating pulses and waves, these peaks are shifted in space, so that the actin-associated inhibitor follows behind the activator (active Rho GTPase). The notion of cortical excitability should be understood broadly in the sense of the underlying molecular mechanism consisting of the activator and the time-delayed inhibitor, rather than in the strict mathematical sense, because both excitable and oscillatory behaviors are always found in the adjacent domains of the system's parameters and can rarely be distinguished in experiments.

In the context of cell division, cortical excitability has been observed during the first mitotic divisions of frog and starfish

CellPress



embryonic blastomeres as turbulent wave patterns appearing at the very onset of furrow ingression within the initially broad equatorial cortical band that rapidly shrinks in width as the furrow ingresses¹⁵ (Figure 1D). Theoretical modeling, confirmed by experiment, explained this observation as a result of the progressive spatial concentration of the RhoA GEF Ect2 within the equatorial cortex by the action of the cell-division spindle¹⁵. This suggested that the Rho zone that initiates furrow formation and, at a low spatiotemporal resolution, appears as a static equatorial belt with a bell-shaped intensity profile may, in fact, be formed via the spatial focusing of an oscillatory wave pattern. The Werner et al.⁸ data (see video S3 in this paper) presenting the activity of Rho around the ingressing furrow of the C. elegans zygote strikingly resemble the earlier observations in starfish¹⁵ and suggest the broad ubiquity of cortical excitability accompanying the onset of furrowing. While the exact nature of the spatiotemporal dynamics in the center of the mature ingressing furrow remains unclear¹⁹ and the narrow, rapidly ingressing furrow is difficult to image, recent data suggest that the Rhopowered actomyosin waves persist well into this advanced phase of cytokinesis²⁰. The high-resolution data of Werner et al.⁸ seem to offer strong support for this observation. Further work will be needed to elucidate the precise mechanobiochemical dynamics in the furrow by using converging experimental and theoretical approaches.

Werner et al.8 conclude: "...contractile oscillations emerge from a system of essential, conserved biochemical and structural elements and may be considered inevitable given the biochemical and mechanical feedback intrinsic to the contractile cytoskeleton." This astute observation summarizes much of the previous work that established various specific mechanisms of actomyosin cortex regulation. From the dynamical systems theory viewpoint, these mechanisms are inherently oscillatory due to the nonlinear molecular circuits of the activator-inhibitor type that are embedded in them. The biological function of these oscillations remains an important and still poorly understood question. Werner et al.8 suggest a

functional explanation by proposing that alternating phases of contraction and relaxation promote the cortex remodeling that is needed to counteract cortex compaction, which is associated with prolonged phases of continuous cortex contraction. Future work will address this interesting hypothesis and other potential functional implications of cortical excitability.

DECLARATION OF INTERESTS

The authors declare no competing interests.

REFERENCES

- Balasubramanian, M.K., Bi, E., and Glotzer, M. (2004). Comparative analysis of cytokinesis in budding yeast, fission yeast and animal cells. Curr. Biol. 14, R806–R818. https://doi.org/10. 1016/j.cub.2004.09.022.
- Bernent, W.M., Goryachev, A.B., Miller, A.L., and von Dassow, G. (2024). Patterning of cell cortex by Rho GTPases. Nat. Rev. Mol. Cell Biol. 25, 290–308.
- Bernent, W.M., Benink, H.A., and von Dassow, G. (2005). A microtubule-dependent zone of active RhoA during cleavage plane specification. J. Cell Biol. 170, 91–101. https:// doi.org/10.1083/jcb.200501131.
- Khaliullin, R.N., Green, R.A., Shi, L.Z., Gomez-Cavazos, J.S., Berns, M.W., Desai, A., and Oegema, K. (2018). A positive-feedbackbased mechanism for constriction rate acceleration during cytokinesis in Caenorhabditis elegans. eLife 7, e36073. https://doi.org/10.7554/eLife.36073.
- Reymann, A.C., Staniscia, F., Erzberger, A., Salbreux, G., and Grill, S.W. (2016). Cortical flow aligns actin filaments to form a furrow. eLife 5, e17807. https://doi.org/10.7554/eLife. 17807.
- Thieleke-Matos, C., Osório, D.S., Carvalho, A.X., and Morais-de-Sá, E. (2017). Emerging mechanisms and roles for asymmetric cytokinesis. Int. Rev. Cell Mol. Biol. 332, 297-345. https://doi.org/10.1016/bs.ircmb. 2017.01.004.
- Maddox, A.S., Lewellyn, L., Desai, A., and Oegema, K. (2007). Anillin and the septins promote asymmetric ingression of the cytokinetic furrow. Dev. Cell 12, 827–835. https://doi.org/10.1016/j.devcel.2007.02.018.
- Werner, M.E., Ray, D.D., Breen, C., Staddon, M.F., Jug, F., Banerjee, S., and Maddox, A.S. (2024). Mechanical and biochemical feedback combine to generate complex contractile oscillations in cytokinesis. Curr. Biol. 34, 3201–3214.
- Hsu, C.R., Sangha, G., Fan, W., Zheng, J., and Sugioka, K. (2023). Contractile ring mechanosensation and its anillin-dependent tuning during early embryogenesis. Nat. Commun. 14, 8138. https://doi.org/10.1038/ s41467-023-43996-4.

 Staddon, M.F., Munro, E.M., and Banerjee, S. (2022). Pulsatile contractions and pattern formation in excitable actomyosin cortex. PLoS Comput. Biol. 18, e1009981. https://doi. org/10.1371/journal.pcbi.1009981.

Current Biology

Dispatches

- Michaux, J.B., Robin, F.B., McFadden, W.M., and Munro, E.M. (2018). Excitable RhoA dynamics drive pulsed contractions in the early C. elegans embryo. J. Cell Biol. 217, 4230– 4252. https://doi.org/10.1083/jcb.201806161.
- Xiao, S., Tong, C., Yang, Y., and Wu, M. (2017). Mitotic cortical waves predict future division sites by encoding positional and size information. Dev. Cell 43, 493–506.e3. https:// doi.org/10.1016/j.devcel.2017.10.023.
- Graessl, M., Koch, J., Calderon, A., Kamps, D., Banerjee, S., Mazel, T., Schulze, N., Jungkurth, J.K., Patwardhan, R., Solouk, D., et al. (2017). An excitable Rho GTPase signaling network generates dynamic subcellular contraction patterns. J. Cell Biol. 216, 4271–4285. https:// doi.org/10.1083/jcb.201706052.
- Michaud, A., Leda, M., Swider, Z.T., Kim, S., He, J., Landino, J., Valley, J.R., Huisken, J., Goryachev, A.B., von Dassow, G., and Bement, W.M. (2022). A versatile cortical pattern-forming circuit based on Rho, F-actin, Ect2, and RGA-3/ 4. J. Cell Biol. 221, e202203017. https://doi.org/ 10.1083/jcb.202203017.
- Bement, W.M., Leda, M., Moe, A.M., Kita, A.M., Larson, M.E., Golding, A.E., Pfeuti, C., Su, K.C., Miller, A.L., Goryachev, A.B., and von Dassow, G. (2015). Activator-inhibitor coupling between Rho signalling and actin assembly makes the cell cortex an excitable medium. Nat. Cell Biol. 17, 1471–1483. https://doi.org/ 10.1038/ncb3251.
- Jackson, J.A., Denk-Lobnig, M., Kitzinger, K.A., and Martin, A.C. (2024). Change in RhoGAP and RhoGEF availability drives transitions in cortical patterning and excitability in Drosophila. Curr. Biol. 34, 2132–2146.e5. https://doi.org/10.1016/j.cub.2024.04.021.
- Michaud, A., Swider, Z.T., Landino, J., Leda, M., Miller, A.L., von Dassow, G., Goryachev, A.B., and Bement, W.M. (2021). Cortical excitability and cell division. Curr. Biol. 31, R553–R559. https://doi.org/10.1016/j.cub.2021.02.053.
- Goryachev, A.B., and Leda, M. (2019). Autoactivation of small GTPases by the GEFeffector positive feedback modules. F1000Res. 8, 1676. https://doi.org/10.12688/ f1000research.20003.1.
- Goryachev, A.B., Leda, M., Miller, A.L., von Dassow, G., and Bement, W.M. (2016). How to make a static cytokinetic furrow out of traveling excitable waves. Small GTPases 7, 65–70. https://doi.org/10.1080/21541248.2016. 1168505.
- Swider, Z.T., Michaud, A., Leda, M., Landino, J., Goryachev, A.B., and Bement, W.M. (2022). Cell cycle and developmental control of cortical excitability in Xenopus laevis. Mol. Biol. Cell 33, ar73. https://doi.org/10.1091/ mbc.E22-01-0025.