Contraction of cross-linked actomyosin bundles

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Received 30 April 2012
Accepted for publication 6 June 2012
Published 11 July 2012
Online at stacks.iop.org/PhysBio/9/046004

Abstract
Cross-linked actomyosin bundles retract when severed in vivo by laser ablation, or when isolated from the cell and micromanipulated in vitro in the presence of ATP. We identify the timescale for contraction as a viscoelastic time \( \tau \), where the viscosity is due to (internal) protein friction. We obtain an estimate of the order of magnitude of the contraction time \( \tau \approx 10^{-100} \) s, consistent with available experimental data for circumferential microfilament bundles and stress fibers. Our results are supported by an exactly solvable, hydrodynamic model of a retracting bundle as a cylinder of isotropic, active matter, from which the order of magnitude of the active stress is estimated.

1. Introduction

Cells organize filamentous actin (F-actin) into complex cytoskeletal structures that play a major role in determining cell rheology and cell shape, and in generating the forces necessary for motility, cell division or tissue stability [1]. Depending on the nature of the actin-binding proteins that nucleate, help polymerize and cross-link actin filaments, the structure of F-actin networks varies widely [2, 3], from the near isotropic gels found in the cell cortex to the linear bundles that form filopodia or stereocilia [4, 5]. Passive cross-linkers, such as \( \alpha \)-actinin or fascin, contribute to the network elasticity, whereas bipolar mini-filaments of non-muscle myosin II motors that pull on neighboring actin filaments of opposite polarity are responsible for contractility.

Cross-linked actomyosin bundles include the circumferential bundles (CBs) found near apical cell junctions of epithelia [6], and the stress fibers (SFs) assembled in the cytoskeleton of non-muscle animal cells that exert substantial traction forces on their environment [7]. They are robust and stable organelles, that can be extracted from the cell while maintaining their shape, structure and contractility, over durations long enough to allow mechanical testing [8–10]. Indeed, isolated CBs [9] as well as isolated SFs [10] contract in vitro in the presence of adenosine triphosphate (ATP).

Laser photoablation stands out as a powerful and versatile tool, widely used to reveal the distribution, orientation and relative intensity of stress in living cells and tissues (see [11, 12] for recent reviews). In order to investigate the cytoskeletal basis of the mechanical properties of cells and tissues, the retraction of ablated actomyosin bundles has been studied quantitatively by several groups [13–17]. These experiments give unambiguous evidence that the bundles are under tension in vivo, since they retract once severed, and that the retraction is an active process, since it is blocked by inhibitors of contractility [15, 16, 18]. The relaxation dynamics is generally fitted by a single exponential, that defines a contraction time, whereas the initial velocity at the time of ablation gives access to (relative) measurements of the preexisting bundle tension. Interestingly, the retraction that follows laser ablation is also relevant in (unperturbed) physiological conditions since SFs spontaneously rupture in vivo [19].

We use dimensional analysis to estimate the contraction time of actomyosin bundles, and show that the main source of dissipation during contraction is protein friction (section 2). The mechanical properties of retracting SFs have so far been interpreted with the help of models [17, 18, 20, 21] that emphasize the underlying sarcomeric structure. One exception is a discrete, numerical model based on the tensegrity hypothesis that accounts for much of the observed
2. Contraction time

The relaxation of the length of a SF severed in vivo is well fitted by an exponential function of time, with a contraction time $\tau$ of the order of 1–10 s, depending on cell type [16–18], and spatial position within the cell [25]. Laser ablation of the apical CBs of epithelial cells yields a somewhat longer contraction time of the order of 10–100 s [13–15, 26, 27]. Retracting bundles were first depicted as Kelvin–Voigt bodies [16], using a simple phenomenological model consisting in a dashpot and a spring in parallel, with a viscoelastic time equal to the ratio of the viscosity coefficient to the elastic modulus. However, the origin of the viscosity remains controversial. Internal viscosity dominates according to [17], whereas an external viscous drag is preferred in [20], implying a surprisingly large cytosolic viscosity of the order of 10 Pa s. In [22], the contraction time closely follows the (microscopic) viscoelastic time of components of the fiber, a parameter of the model.

In section 2.1, we estimate the orders of magnitude of the viscosity coefficient due to internal protein friction, of the elastic modulus of the bundle, and deduce the order of magnitude of the viscoelastic contraction time due to protein friction. In section 2.2, using well-established numerical values of the cytosolic viscosity, we further show that external viscous drag is negligible, and would lead to a much shorter viscoelastic time, at variance with experiment. We next evaluate the poroelastic time that governs the permeation of the cytosol through the F-actin network, and discuss its possible relevance to the dynamics of contraction. Finally, we calculate the order of magnitude of the elastic modulus and viscosity coefficient of SFs and CBs (section 2.3). An order of magnitude is hereafter defined by the integer value, obtained by truncation, of the decimal logarithm of the quantity of interest.

2.1. Viscoelastic time

We propose that the main source of dissipation in cross-linked actomyosin bundles lies in the binding-unbinding dynamics of cross-linkers on actin filaments. This dynamics leads to an effective (protein) friction, as introduced first in the context of rubber friction [28], and later for actomyosin dynamics in muscle cells [29].

In the linear regime, the protein friction force $F_p$ exerted on one filament is proportional to its relative velocity $v$ (with respect to neighbor filaments), with a friction coefficient $\zeta_p$: $F_p = -\zeta_p v$. Since the energy dissipated after unbinding was stored as elastic energy in strained cross-linkers, an estimate of the friction coefficient is [28]

$$\zeta_p = n_X k_X \tau_X,$$

where $n_X$ is the average number of attached cross-linkers per filament, $k_X$ is the spring constant of the cross-linker and $\tau_X$ is the typical time for bond rupture. We expect that several cross-linker proteins, either passive or active, would contribute additively to the friction coefficient: $\zeta_p = \sum_X n_X k_X \tau_X$. To our knowledge, the spring constant of $\alpha$-actinin, arguably the most prevalent passive cross-linker in SFs, has not been measured. For lack of data, only protein friction due to myosin filaments will be taken into account. Using the numerical values $n_X \approx 10$, $k_X \approx 0.1$ pN nm $^{-1}$ for myosin filaments [30, 31], and equation (1), we obtain the order of magnitude of the microscopic friction coefficient $\zeta_p \approx 10^{-3} - 10^{-2}$ N s $^{-1}$.

We expect the dissipative stress $\sigma_p$ due to protein friction to scale as $\sigma_p \approx n_F \eta_p v / A$, where $n_F$ is the number of actin filaments in a section of the bundle, $A$ is the area of the section and $v$ is the velocity. In three dimensions, protein friction translates into a viscosity coefficient $\eta_p$, with $\sigma_p = \eta_p \partial v / \partial z \approx n_F \eta_p l_F / A$, where $U$ and $L$ are the contraction velocity and the length of the bundle. Assuming for simplicity a constant velocity gradient $v = \frac{U}{L}$, the local relative velocity on the scale of a filament is $v' = \frac{U}{L} v$, where $l_F$ is the typical length of an actin filament (see figure 1(B)). Note that although we have assumed that filaments are aligned in the $z$-direction, we may also consider a homogeneous, random orientation of filaments. This would modify the prefactors which arise from the average orientation of two filaments. Equating the two expressions for $\sigma_p$, we deduce the order of magnitude of the three-dimensional viscosity coefficient:

$$\eta_p \approx n_F \frac{l_F}{A} \zeta_p. \quad (2)$$

The stiffness of the bundle is dominated by cross-linkers, such as myosin filaments, known to be softer than actin filaments: $k_X \approx 0.1$ pN nm $^{-1}$ [30, 31] compared to $k_F \approx 10$ pN nm $^{-1}$ [32, 33]. The elasticity of the bundle is characterized by a network structure of actin filaments and cross-linkers with long residual time. The network has two ends at $z = 0$ and $z = L$ connected by various pathways in parallel. Each pathway has filaments and cross-linkers connected in series, and the bundle elasticity is approximated by that of a dominant pathway (figure 1(C)). When hard and soft springs are connected in series, the force acting on the ensemble of two springs for the displacement $\Delta z$ is $F \approx \Delta z / (k_F^{-1} + k_X^{-1})$, where $k_F$ is a spring constant of a hard actin filament and $k_X$ is that of a soft cross-linker. When $k_F \gg k_X$, the force is dominated by $k_X$. The elastic stress $\sigma^e$ is of the order $\sigma^e = E u_{\Delta z} \approx E \Delta Z \frac{\Delta z}{L}$, where $E$ and $\Delta Z$, respectively, denote the Young modulus, and the (macroscopic) displacement of the bundle. Denoting by $l_X$ the typical length between cross-linkers in the network, approximated by the length of a myosin filament, we expect the (microscopic) displacement of a cross-linker to scale as $\Delta z \approx \Delta Z \frac{l_X}{L}$. Since the number of cross-linkers in a section is $n_X n_F$, we find for the elastic stress $\sigma^e \approx n_X n_F k_X \Delta Z / A$. Since the two expressions for $\sigma^e$ are equal, the order of magnitude of the Young modulus reads

$$E \approx n_X n_F \frac{l_X}{A} k_X. \quad (3)$$
Using equations (1)–(3), we obtain the order of magnitude of the viscoelastic time due to protein friction:

\[
\tau = \frac{\eta_p}{E} \approx \frac{l_F}{\kappa_X} \approx \tau_{\kappa_X}, \tag{4}
\]

independent of the extension of the bundle. Indeed, experiments suggest that the contraction time is independent of the initial width \(a_0\) [16], and of the initial length \(l_0\) [34] of the ablated SF, at odds with the prediction \(\tau \propto l_0^2\) of the sarcomere-based model introduced in [20].

The typical lengths of actin and myosin filaments are, respectively, \(l_F \approx 1\ \mu m\) and \(l_X \approx 0.1\ \mu m\) [35, 36]. The association/dissociation rates of myosin light chain and \(\alpha\)-actinin have been measured in SFs in vivo in fluorescence recovery after photobleaching assays [37]. The turnover times are of the order \(\tau_{\kappa_X} \approx 1 - 10\ \text{s}\), consistent with the unbinding times measured on single actomyosin bonds under physiological loads [38, 39]. We obtain for the order of magnitude of the contraction time \(\tau\) the range

\[
\tau \approx 10^1 - 10^2\ \text{s}, \tag{5}
\]
in accord with experimental observations for contraction in vivo after laser ablation, as well as in vitro after extraction from the cell [9, 10].

2.2. Poroelastic time

One obvious alternative source of dissipation is the hydrodynamic friction, due to the viscosity of the cytosol. At small scale, the longitudinal friction coefficient due to viscous drag on an actin filament, modeled as a cylinder of length \(l_F\) and diameter \(d_F\), reads

\[
\zeta_D = 2\pi n_{\text{cytosol}} l_F / (l_F / d_F + \gamma_{\text{ij}}),
\]

where \(n_{\text{cytosol}}\) is the viscosity of the cytosol, and \(\gamma_{\text{ij}}\) is a dimensionless number of order \(10^{-1}\) [40]. Using \(l_F \approx 1\ \mu m,\ d_F \approx 10\ \text{nm}\) and well-established values for the cytosolic viscosity \(n_{\text{cytosol}} \approx 10^{-3} - 10^{-1}\ \text{Pa s}\) [41], we find \(\zeta_D \approx 10^{-9} - 10^{-7}\ \text{N m}^{-1}\ \text{s}\), negligible when compared to \(\zeta_P\). At the scale of the bundle, with \(l_B \approx 10\ \mu m, d_B \approx 0.1\ \mu m\), we obtain

\[
\zeta_D \approx 10^{-8} - 10^{-6}\ \text{N m}^{-1} \ll \zeta_P. \tag{6}
\]

Viscous drag against the cytosol may thus be neglected.

Furthermore, cytosol is squeezed out of the biopolymer network during the contraction: permeation also contributes to the dissipation. The permeation of a solvent through an elastic network has been studied in the context of chemical gels (see [42] for a recent review of stress–diffusion coupling), and has led to interesting insights into, e.g., the mechanics of the poroelastic cytoskeleton [41]. In a two-component system where fluid cytosol (the solvent) permeates an elastic polymer matrix, the total stress is expressed as the sum of the elastic stress of the polymer network, and of a pressure term for the liquid solvent: \(\sigma_{ij}^{\text{tot}} = \sigma_{ij}^\text{el} - p \delta_{ij}\), where \(\delta_{ij}\) is the identity tensor (see section 3 for a detailed calculation).

Supplementing this constitutive equation with Darcy’s law for the permeation of the solvent, one obtains a diffusion equation for the displacement field of the gel, with a diffusion constant \(D \approx \kappa E\), where \(\kappa\) is the permeability coefficient. Since \(\kappa \propto \xi^2 / n_{\text{cytosol}}\), where \(\xi\) is the mesh size of the network, the terms \(n_{\text{cytosol}}\) is the cytosolic viscosity, the timescale for relaxation over a typical distance \(a_0\) evaluated as the radius of the bundle, reads

\[
\tau_P = \frac{a_0^2}{D} \approx \left( \frac{a_0}{\xi} \right)^2 n_{\text{cytosol}} / E. \tag{6}
\]

From equation (3), and \(A \approx a_0^2\), we expect the poroelastic time to be sensitive to the width of the bundle: \(\tau_P \propto a_0^2\). The typical radius of a SF is \(a_0^\text{SF} \approx 100\ \text{nm}\) [43], whereas the cross-sectional area of a CB is of the order of \(A^{\text{CB}} \approx 1\ \mu m^2\).
We formulate a hydrodynamic description valid on large length scales compared to the typical mesh size of the underlying polymer network \(d \gg \xi \approx 10 \text{ nm} \) [8, 10]. In experiments, bundles are ablated far from their end points. We consider the retraction of one half of the severed bundle: the other tip is fixed and sets the origin of the \(z\)-axis. We consider the simplified geometry where (half-) a bundle initially adopts the shape of a cylinder of axis \(\Omega z\) (see figure 1(A)). We naturally use the cylindrical coordinates \((\rho, \theta, z)\). The bundle initially occupies the volume defined by \(0 \leq \rho \leq a_0\), \(0 \leq z \leq l_0\), where \(a_0\) and \(l_0\) respectively, denote the initial radius and length.

While this simplified geometry may seem a natural approximation for SFs spanning the ventral side of adherent cells and bound to the substrate at (fixed) focal adhesions, we believe that the following observations also justify its relevance for apical CBs. First, the ablation is generally performed along nearly straight cell junctions: the local curvature may be neglected. Second, the shape of the cell is most often preserved despite the ablation of one cell junction, while other apical bundles in the same cell remain mostly unperturbed [13, 15], perhaps due to the stabilizing influence of the surrounding epithelium. The retracting cell junction may therefore be treated as attached to an immobile cell–cell vertex and nearly independent of the remainder of the apical actin cortex.

The severed SFs do not retract when the ablation is performed in the presence of inhibitors of contractility [10, 16]. For this reason, the displacement field \(\mathbf{u}\) is defined with respect to the initial state (immediately after ablation): \(\mathbf{u}(t = 0) = \mathbf{0}\). Following [49], we postulate the following functional form for components of \(\mathbf{u}\):

\[
\mathbf{u}_e(r, \theta, z, t) = u_e(r, t) \quad (12)
\]

\[
\mathbf{u}_r(r, \theta, z, t) = 0 \quad (13)
\]

\[
\mathbf{u}_z(r, \theta, z, t) = e(t) \, z \quad (14)
\]

This ansatz is central to our calculation. The displacement field is independent of \(\theta\) due to rotational invariance about the axis \(\Omega z\). The origin is fixed, \(\mathbf{u}_c(z = 0) = 0\) at all times, and the longitudinal strain \(e(t)\) is uniform. The initial cylindrical shape is preserved by our ansatz for the displacement field, and the radius \(a(t)\) and length \(L(t)\) of the cylinder at a later
time $t > 0$ read
\[ a(t) = a_0 + u(a_0, t), \tag{15} \]
\[ L(t) = L_0 (1 + e(t)), \tag{16} \]
where $e(t)$ appears as the relative variation of length of the bundle, negative for a contraction (see figure 1(A)).

For simplicity, we assume that the bundle material properties are isotropic. In section 2, our estimates rely on the physical properties of cross-linkers, which remain approximately isotropic. In addition, the orientation of actin filaments inside actomyosin bundles shows a significant amount of disorder. The binding/unbinding kinetics of cross-linkers is taken into account by an effective, bulk viscous term with coefficient $\eta_p$, due to protein friction. We include in the constitutive equations a constant, isotropic, active stress $\sigma_{p\text{active}} = \sigma_A \delta(t)$, and $\sigma_A$ is positive since the bundle is under tension. The active stress $\sigma_A$ is assumed to be uniform, and independent of time: we neglect the banded myosin patterns that reflect the (disordered) sarcomeric organization typical of SFs [50]. Note however that not all contractile actomyosin bundles exhibit a sarcomeric organization [51, 52].

On the timescale involved, the final rest state is well defined. For SFs, the relative total retraction length $|e_\infty|$ is of the order of 10% [16, 17]: deformations are small enough for linear elasticity to hold. We denote by $E$ and $\nu$ the Young modulus and the Poisson ratio of the bundle, and by $K = \frac{E}{(1 - 2\nu)(1 + \nu)}$ and $G = \frac{E}{2(1 + \nu)}$ the bulk and shear elastic moduli. Shear strains and shear elastic stresses cancel by construction. The normal elastic stresses read
\[ \sigma_{rr} = \frac{E}{(1 + \nu)(1 - 2\nu)} \left( (1 - \nu) \frac{\partial u}{\partial r} + \nu \left( \frac{u}{r} + e \right) \right), \tag{17} \]
\[ \sigma_{\theta \theta} = \frac{E}{(1 + \nu)(1 - 2\nu)} \left( (1 - \nu) \frac{u}{r} + \nu \left( \frac{\partial u}{\partial r} + e \right) \right), \tag{18} \]
\[ \sigma_{zz} = \frac{E}{(1 + \nu)(1 - 2\nu)} \left( (1 - \nu) e + \nu \left( \frac{u}{r} + \frac{\partial u}{\partial r} \right) \right). \tag{19} \]

Like any organelle in a living cell, actomyosin bundles are highly dynamic structures: protein components constantly renew while the global organization of the bundle is preserved. For SFs, fluorescence recovery assays performed in vivo yield an association/dissociation time of the order of a few minutes for actin [37, 53]. In this model, we assume that a steady state is reached over the duration of ablation experiments, and accordingly that the material content of the bundle is constant during relaxation.

### 3.2. Active viscoelastics contraction

In this section, we study the permeation of a viscous liquid (the cytosol) through an active, elastic polymer network with transient cross-links. Active permeating gels have recently been studied in detail [54, 55]. Here, we follow a simpler approach, inspired by an exact calculation pertaining to the free swelling of a chemical gel whose initial shape is a cylinder [49], including two additional ingredients: a constant active stress, and a bulk viscous stress due to protein friction.

Since the strain field obeys the ansatz (12)–(14), shear strains and shear elastic stresses cancel. The normal stresses read
\[ \sigma_{rr} = \eta_p \frac{\partial u_r}{\partial r} + \sigma_A + \sigma_{rr}^e, \tag{20} \]
\[ \sigma_{\theta \theta} = \eta_p \frac{u_r}{r} + \sigma_A + \sigma_{\theta \theta}^e, \tag{21} \]
\[ \sigma_{zz} = \eta_p \frac{\partial u_z}{\partial z} + \sigma_A + \sigma_{zz}^e, \tag{22} \]
where $\nu = \frac{3a^2}{4\pi}$ denotes the network velocity field. For a constant active stress $\sigma_A$, force balance reads
\[ \partial_t p = \partial_r \sigma_{rr}^e + \frac{1}{r} \left( \sigma_{rr}^e - \sigma_{rr}^e \right) + \eta_p \left( \frac{1}{r} \frac{\partial}{\partial r} \left( rv_r \right) \right), \tag{23} \]
\[ \partial_t \sigma_{\theta \theta} = \partial_r \sigma_{r \theta}^e, \tag{24} \]
\[ \partial_t \sigma_{zz} = \partial_r \sigma_{z z}^e, \tag{25} \]
where $p$ is the pressure field of the cytosol. Since $\partial_t \sigma_{\theta \theta}^e = \partial_t \sigma_{zz}^e = 0$, we have $\partial_t \sigma_{rr}^e = 0$: the pressure field is a function of radius and time only, $p = p(r, t)$. The radial dependence of the pressure field is obtained from equation (23) after integration with respect to $r$, using the boundary condition $p(a, t) = p_{\text{ext}}$, where $p_{\text{ext}}$ denotes the hydrodynamic pressure in the surrounding cytosol. We find
\[ p(r, t) = p_{\text{ext}} + \eta_p \left( \frac{1}{r} \frac{\partial}{\partial r} \left( rv_r \right) \right) \frac{a}{(1 + \nu)(1 - 2\nu)} + \frac{1}{(1 + \nu)(1 - 2\nu)} \left( \frac{1}{r} \frac{\partial}{\partial r} \left( ru_u \right) \right). \tag{26} \]

Using the previous equation, we eliminate the pressure field from Darcy’s law $\nabla \cdot \vec{v} = \kappa \nabla^2 p$, where $\kappa$ is the permeability, and obtain the following equation for the displacement field:
\[ \frac{\partial u}{\partial t} + \frac{1}{2} \frac{d e}{d t} = D \frac{\partial}{\partial r} \left( \frac{1}{r} \frac{\partial}{\partial r} \left( ru_u \right) \right) + I_p^2 \frac{\partial}{\partial r} \left( \frac{1}{r} \frac{\partial}{\partial r} \left( ru_u \right) \right), \tag{27} \]
where $I_p^2 = \kappa \eta_p / D = \frac{1 - \nu}{(1 + \nu)(1 - 2\nu)} \kappa E$ is a diffusion coefficient, and their ratio
\[ I_p^2 = \frac{1}{D} = \frac{1 + \nu}{1 - 2\nu} \eta_p / E \tag{28} \]
is a viscoelastic time.

The boundary condition at $r = a, \sigma_{rr}(r = a, t) = -p_{\text{ext}}$, yields
\[ \frac{E}{(1 + \nu)(1 - 2\nu)} \left( (1 - \nu) \frac{\partial u}{\partial r} \right)_{r=a} + \nu \left( \frac{u(a)}{a} + e \right) \]
\[ + \eta_p \frac{\partial u_r}{\partial r} \bigg|_{r=a} = -\sigma_A. \tag{29} \]

In the case of free contraction, the external force applied on the tip of the cylinder at $z = L$ is equal to $\int_0^L d r \, 2\pi r \, \sigma_{zz}(r, t) = -\pi a^2 p_{\text{ext}}$. Combining the two boundary conditions, we obtain
\[ \tau_G \frac{d}{d t} \left( \frac{u(a)}{a} - e \right) = - \left( \frac{u(a)}{a} - e \right). \tag{30} \]
where $\tau_G$ is a viscoelastic time based on the shear elastic modulus:
\begin{equation}
\tau_G = \frac{\eta_p}{2G} \quad (31)
\end{equation}
which contributes to the relaxation provided that $\frac{u(a_0, t = 0)}{a_0} \neq e(t = 0)$, see also equations (A.12) and (A.13). Here, the initial strain is equal to zero $u(a_0, t = 0) = e(t = 0) = 0$, and the solution of equation (30) is for all time $t$:
\begin{equation}
e(t) = \frac{u(a, t)}{a} \simeq \frac{u(a_0, t)}{a_0} \quad (32)
\end{equation}

The length and the radius of the bundle both relax in time according to the same functional form since $\frac{e(t) - e_0}{a_0}$.

Equations (27)–(32) are solved by the expansion:
\begin{equation}
ev(t) = e_\infty + \sum_n e_n \ e^{-t/\tau_n} \quad , (33)
\end{equation}
u(r, t) = u_\infty(r) + \sum_n u_n(r) \ e^{-t/\tau_n} \quad , (34)

where $\tau_n$ are relaxation times. Equation (27) yields a differential equation obeyed by the amplitudes $u_n$ and $e_n$:
\begin{equation}
u_n + \frac{1}{2} e_\sigma r = D \left( \frac{\tau_p - \tau_n}{\tau_n} \right) \frac{d}{dr} \left( \frac{1}{r} \frac{d u_n}{dr} \right) \quad . (35)
\end{equation}

In the following, we define the lengths $l_n$ by $e_n = D \ |\tau_p - \tau_n|$. In the long time limit, the stationary solution reads
\begin{equation}
ev_\infty = -\frac{\sigma_A}{3K} \quad , (36)
u_\infty(r) = -\frac{\sigma_A}{3K} r \quad , (37)
\end{equation}
Remarkably, we predict that actomyosin bundles also contract along the radial direction ($a_\infty < a_0$), independently of the value of the Poisson ratio $\nu$, since the final radius reads
\begin{equation}
a_\infty = a_0 \left( 1 + e_\infty \right) = a_0 \left( 1 - \frac{\sigma_A}{3K} \right) \quad . (38)
\end{equation}

Indeed, electron microscopy imaging indicates that isolated SFs contract radially [10]. To our knowledge, this observation has not been confirmed by optical imaging in a live cell, due to insufficient spatial resolution.

The relaxation dynamics are solved as follows. When $\tau_p > \tau_n$, the functions $u_n(r)$ are the solutions of an inhomogeneous, modified Bessel equation:
\begin{equation}
u_n(r) = b_n \ J_1 \left( \frac{r}{l_n} \right) - \frac{1}{2} e_\sigma r \quad , (39)
\end{equation}
where the coefficient $b_n$ is an amplitude, and $J_1(x)$ is a modified Bessel function of the first kind. Since $u_n(a_0) = a_0 e_n$ (see equation (32)), we obtain $e_n = \frac{2b_n}{\ln l_n} \ J_1 \left( \frac{a_0}{a_0} \right)$ from equation (39). We deduce from equation (29) that the relaxation times $\tau_p$ are solutions of the equation:
\begin{equation}
\left( \frac{\tau_p}{\tau_n} - 1 \right) \left[ a_0 \ J_1 \left( \frac{a_0}{l_n} \right) - \frac{1}{3} J_1 \left( \frac{a_0}{l_n} \right) \right] = \frac{4}{3} \ \frac{\nu - 1}{1 - \nu} \ J_1 \left( \frac{a_0}{l_n} \right) \quad . (40)
\end{equation}

When $\tau_p > \tau_n$, equation (35) is an inhomogeneous Bessel equation. Modified Bessel functions are replaced by Bessel functions:
\begin{equation}
u_n(r) = b_n \ J_1 \left( \frac{r}{l_n} \right) - \frac{1}{2} e_\sigma r \quad , (41)
\end{equation}
where $J_1(x)$ is a Bessel function of the first kind, and $e_n = \frac{2b_n}{\ln l_n} \ J_1 \left( \frac{a_0}{a_0} \right)$. The relaxation times $\tau_n$ are solutions of the equation:
\begin{equation}
\left( \frac{\tau_p}{\tau_n} - 1 \right) \left[ a_0 \ J_1 \left( \frac{a_0}{l_n} \right) - \frac{1}{3} J_1 \left( \frac{a_0}{l_n} \right) \right] = \frac{4}{3} \ \frac{\nu - 1}{1 - \nu} \ J_1 \left( \frac{a_0}{l_n} \right) \quad , (42)
\end{equation}
which may be obtained from equation (40) upon replacing $J_1$ by $J_1$. In figure 2, we plot as a function of the parameter $\frac{\nu}{\tau_p}$ the dimensionless relaxation times $\frac{\tau_p}{\tau_n}$, at a given value of the Poisson ratio. Equation (40) admits only one solution, whereas equation (42) admits an infinity of solutions, which contribute to the expansions (33), (34).

3.3. Active poroelastic limit

In the limit where $\tau_n \gg \tau_p$, equation (42) becomes
\begin{equation}
\frac{a_0}{r_n} \ J_1 \left( \frac{a_0}{r_n} \right) + \frac{5 \nu - 1}{3(1 - \nu)} \ J_1 \left( \frac{a_0}{r_n} \right) = 0 \quad , (43)
\end{equation}
with $r_n = \sqrt{D\tau_n}$, in agreement with [49]. The largest solution of equation (43) is $\tau_p \approx \tau_n = \frac{a_0}{r_n}$; this limit is realized when $\tau_p \gg \tau_n$, as may be possible, e.g., for very thick bundles assembled in vitro, since we expect the poroelastic time to scale as the fourth power of bundle radius, see equation (6) and below.
3.4. Active viscoelastic limit

We formally define the viscoelastic limit as the regime where the permeability coefficient $\kappa$ diverges. Darcy’s law then implies that the cytosolic pressure field is homogeneous ($\nabla p = 0$). Since $a_0/l_0 \propto 1/\sqrt{\kappa}$, we may use $x_\mathrm{f}(x) \approx l_1(x)$ and $x_\mathrm{f}(x) \approx l_1(x)$ in equations (40) and (42) since $0 < x \ll 1$. For both equations, we obtain a unique solution $\tau_n \to \tau_E$:

$$\tau_E = \frac{\eta_p}{3K}. \tag{44}$$

a viscoelastic time based on the bulk modulus $K$. The expansions (33), (34) reduce to one exponential term. Given the initial conditions $u(r, t = 0) = e(t = 0) = 0$, we find the expression of the displacement fields:

$$u_r(r, t) = -\frac{\sigma_A}{3K} r (1 - e^{-t/\tau_E}), \tag{45}$$

$$u_z(z, t) = -\frac{\sigma_A}{3K} z (1 - e^{-t/\tau_E}). \tag{46}$$

The length of the ablated bundle decreases as an exponential function of time, as observed in experiments. Equation (46) also yields the initial retraction velocity $v_0$, proportional to the active stress:

$$v_0 = v_z(z = L_0, t = 0) = -L_0 \frac{\sigma_A}{\eta_p}. \tag{47}$$

We may rewrite the argument $a_0/l_0$ as a function of timescales: $\frac{a_0}{l_0} = \sqrt{\frac{\tau_p}{\tau_E}}$. We find that $\tau_E - \tau_K = \frac{2\tau_p}{\tau_E - \tau_K}$; $a_0 \ll l_0$ corresponds to $\tau_p \approx \tau_K \approx \tau_E$ and $\tau_p \gg \tau_K$. The contraction of an active viscoelastic cylinder (with protein friction) does indeed reduce to an active viscoelastic behavior, provided that the viscoelastic time is large compared to the poroelastic time. The crossover between the two regimes occurs when $\tau_p \approx \tau_K$, or $a_0^2 \approx \kappa \eta_p$; it may be controlled by the bundle radius, with a crossover radius $a_c$. Using $\kappa \approx \xi^2/\eta_{\text{cytosol}}$ and $\eta_p \approx n_F \frac{\nu}{c_p} \tau_p$ (equation (2)), we find

$$a_c \approx \left(\frac{n_F l_F \xi^2}{\eta_{\text{cytosol}}}\right)^{1/4}. \tag{48}$$

Using the same numbers as in section 2, we obtain the value $a_c \approx 10 \mu$m, which is large compared to the radius of actomyosin bundles found in cells. The separation of timescales $\tau_E \gg \tau_p$ no longer exists when $a_0 \gg a_c$, and is absent without protein friction, i.e. when cross-linkers are fixed and do not unbind over the timescale considered.

In the appendix, we solve a model of an actomyosin bundle as an active, viscoelastic material, and check that the results are identical to the limit presented in this section. In addition, we consider the case where the initial state differs from the reference state, and find that the strain, initially nonzero, relaxes as a linear combination of two exponentials with characteristic times $\tau_K$ and $\tau_G$, equations (A.12), (A.13).

4. Active stress

In experiments, the stationary longitudinal strain is of order $|\varepsilon_\infty| \approx 10^{-1}$. Assuming a value of the Poisson ratio of order $\nu = 0.4$ [56, 57], the estimates of section 2 remain relevant since $3K \approx E$. Using equation (36), we deduce the order of magnitude of the active stress $\sigma_A = 3K|\varepsilon_\infty| \approx E|\varepsilon_\infty|$:

$$\sigma_A^{\text{SF}} \approx 10^4 \text{ Pa}, \tag{49}$$

$$\sigma_A^{\text{CB}} \approx 10^2 \text{ Pa}. \tag{50}$$

Since the stall force of a myosin motor is of the order $F_S \approx 1$ pN [58], the above values agree with a naive estimate of the active stress as

$$\sigma_A \approx \frac{n_A^A n_F}{n_V} \frac{F_S}{A}, \tag{51}$$

where $n_A^A$ is the number of active myosin molecules (per filament) that generate stress, with the same order of magnitude as the total number of attached cross-linkers per filament $n_A^A \approx n_V$. Since $L_0 - L_\infty = |\varepsilon_\infty|L_0$, combining equations (3) and (51) yields

$$L_0 - L_\infty \approx \frac{F_S}{k_{x} n_V} L_0. \tag{52}$$

Experiments suggest that the total retracted length is independent of the bundle radius $a_0$ [16].

The value of the active stress obtained for CBs is close to the order of magnitude obtained for cortical actin $\sigma_A^{\text{CA}} \approx 10^4$ Pa [59]. Estimate (49) suggests that cells whose SFs pull on an area of the order of $1 \mu$m$^2$ exert locally a force of the order $F_S \approx 10$ nN. This is consistent with measurements of traction forces exerted by cells on micropatterned pillars [60]. Adherent cells assemble thicker and more robust SFs when the rigidity of the substrate is large [61]. In this case, traction forces saturate to a value independent of the external stiffness. In [62], a simple model of the cytoskeleton as an active, elastic material allowed to identify active contractility as the physical origin of the saturation traction force, yielding $10^4$ Pa as an order of magnitude of the active stress, in agreement with (49).

The values of $\varepsilon_\infty$ measured in ablation assays are similar to the values of the ‘preexisting strain’ measured in isolated SFs [43], or of the ‘preextension’ upon unloading the SFs of cells adhering on a stretchable substrate [63]. Indeed, as we have seen in (36) and (37), actomyosin contraction may be seen as equivalent to a reduction in the stress-free reference length of an elastic material [64]. Experiments show that the amplitude of the preextension correlates positively with contractility [63], in qualitative agreement with equations (36) and (37). Furthermore, the knock down of $\alpha$-actinin increases preextension [63]. Given that SFs depleted in $\alpha$-actinin are expected to be softer [65], this observation also fits with equations (36) and (37), since a smaller value of the elastic modulus at fixed active stress leads to a larger strain.

5. Conclusion

Local ablation is a widely used tool to estimate the value of the local stress in living cells, up to a (generally unknown) viscosity coefficient (see equations (47) and (A.14)). Ascribing the physical origin of the fiber’s viscosity to protein friction, itself due to the association/dissociation dynamics of cross-linkers, we obtain the order of magnitude of the viscosity
coefficient $\eta_p$. Using an independent estimate of the bundle’s elastic modulus, we deduce the order of magnitude of the contraction time $\tau \approx 10–100$ s, interpreted as a viscoelastic time. We find that the order of magnitude of the poroelastic timescales is much smaller, and study rigorously the limit where poroelasticity may be neglected thanks to an exactly solvable model of the contracting bundle. We identify a well-defined threshold, controlled for instance by the bundle width: viscoelasticity (resp. poroelasticity) dominates when the viscoelastic time is much longer (resp. much shorter) than the poroelastic time. For an isotropic material, the model predicts that contraction occurs both in the longitudinal and radial directions, irrespective of the value of the Poisson ratio. From the observed longitudinal strain, we deduce the order of magnitude of the active stress: $\sigma_{\text{CB}}^\text{A} \approx 10^4$ Pa in CBs and $\sigma_{\text{SF}}^\text{A} \approx 10^5$ Pa in SFs. Following the literature, we distinguish SFs from CBs. However, their protein constituents and macroscopic properties are identical: the differences we emphasize may in fact be superficial, and turn out to conceal a continuum of parameter values.

We expect our results to be relevant to the mechanics of other cytoskeletal structures, such as the actin purse string at the circumference of healing wounds [66], or the supra-cellular actin cable that surrounds the amnioserosa during dorsal closure of fly embryos [67]. Circular, contractile actomyosin bundles also form in adherent (single) fibroblasts during the closure of fly embryos [67], or the supra-cellular bundles from the microscopic parameters and macroscopic properties are identical: the differences we distinguish SFs from CBs. However, their protein constituents and microscopic parameters pertaining to individual constituents (filaments and cross-linkers). This important question is left for future study.

Acknowledgments

The authors thank Axel Buguin, Damien Cuvelier, François Graner, Shinji Deguchi, Jean–François Joanny, Jacques Prost and Tetsuo Yamaguchi for fruitful discussions, as well as anonymous referees for constructive criticism. NY acknowledges support by a Grant-in-Aid for Young Scientists (B) (no. 23740317). PM would like to thank Professor Masaki Sano and Professor Takao Ohta for their kind hospitality, as well as the Kavli Institute for Theoretical Physics, with partial support by the National Science Foundation under grant no. NSFPHY05-51164. This work was supported by JSPS, MAEE and MESR under the Japan–France Integrated Action Program (SAKURA).

Appendix. Active viscoelastic contraction

Using the same ansatz for the displacement field, equations (12)–(14), the constitutive equations for the active, viscoelastic contraction of a cylinder of isotropic material read

\[
\sigma_{rr} = \eta_p \frac{d u}{d r} + \sigma_A + \frac{E}{(1 + \nu)(1 - 2\nu)} \left(1 - \frac{v}{r} + e \right) \left(1 - \frac{v}{r} + e \right),
\]

(A.1)

\[
\sigma_{\theta\theta} = \eta_p \frac{v}{r} + \sigma_A + \frac{E}{(1 + \nu)(1 - 2\nu)} \left(1 - \frac{v}{r} + e \right) \left(1 - \frac{v}{r} + e \right),
\]

(A.2)

\[
\sigma_{zz} = \eta_p \frac{d e}{d r} + \sigma_A + \frac{E}{(1 + \nu)(1 - 2\nu)} \left(1 - \frac{v}{r} + e \right) \left(1 - \frac{v}{r} + e \right).
\]

(A.3)

Again, since $u$ and $e$ are independent of $\theta$ and $z$, the azimuthal and longitudinal components of the force balance equation are immediately verified. In the radial direction, we find

\[
\eta_p \frac{d u}{d r} \left(1 - \frac{v}{r} + e \right) + \frac{E}{(1 + \nu)(1 - 2\nu)} \left(1 - \frac{v}{r} + e \right) \left(1 - \frac{v}{r} + e \right) = 0.
\]

(A.4)

A radial displacement linear in $r$:

\[
u(r, t) = \frac{1}{2} A(t) r
\]

(A.5)

solves equation (A.4), provided that the dimensionless function $A(t)$ depends on time only. The stress field is then uniform (with $\sigma_{\theta\theta} = \sigma_{rr}$):

\[
\sigma_{rr} = \frac{1}{2} \eta_p \frac{d A}{d r} + \sigma_A + \frac{E}{(1 + \nu)(1 - 2\nu)} \left(1 - \frac{v}{r} + e \right) \left(1 - \frac{v}{r} + e \right),
\]

(A.6)

\[
\sigma_{zz} = \eta_p \frac{d e}{d r} + \sigma_A + \frac{E}{(1 + \nu)(1 - 2\nu)} \left(1 - \frac{v}{r} + e \right) \left(1 - \frac{v}{r} + e \right).
\]

(A.7)

and determined by the boundary conditions.

Neglecting the external, cytosolic pressure, normal stresses at the free surface are $\sigma_{nn}(r = a, t) = \sigma_{nn}(z = L, t) = 0$. We obtain a system of two coupled differential equations for $A(t)$ and $e(t)$:

\[
(1 + \nu)(1 - 2\nu) \eta_p \frac{d A}{E} = -A - 2ve - 2(1 + \nu)(1 - 2\nu) \frac{\sigma_A}{E},
\]

(A.8)
(1 + ν)(1 − 2ν) \frac{de}{E} \frac{d}{dt} = −νA + (ν − 1)e \\
+ (1 + ν)(1 − 2ν) \frac{σ_{A}}{E}, \quad (A.9)

diagonalized as
\tau_{G} \frac{d}{dt} (A + e) = −(A + e) − \frac{σ_{A}}{K}, \quad (A.10)
\tau_{G} \frac{d}{dt} (2e − A) = −(2e − A), \quad (A.11)

where \( τ_{G} \) and \( τ_{K} \) are defined in equations (31) and (44), respectively. For zero initial displacements, we find \( A(t) = 2e(t) \), and \( e(t) = −\frac{σ_{A}}{3K} (1 − e^{−t/τ_{K}}) \), in agreement with equations (45) and (46).

If we now take into account a possible difference between the initial state and the stress-free reference state of the passive bundle, the initial conditions become \( A(t = 0) = A_{0} \neq 0 \), \( e(t = 0) = e_{0} \neq 0 \). The strain relaxes as a linear combination of two exponentials with characteristic times \( τ_{G} \) and \( τ_{K} \):
\[ A(t) = −\frac{2σ_{A}}{3K} (1 − e^{−t/τ_{K}}) + \frac{2}{3} (A_{0} + e_{0}) e^{−t/τ_{K}} \]
\[ + \frac{1}{3} (A_{0} − 2e_{0}) e^{−t/τ_{G}}, \quad (A.12) \]
\[ e(t) = −\frac{σ_{A}}{3K} (1 − e^{−t/τ_{K}}) + \frac{1}{3} (A_{0} + e_{0}) e^{−t/τ_{K}} \]
\[ − \frac{1}{3} (A_{0} − 2e_{0}) e^{−t/τ_{G}}, \quad (A.13) \]

A nonzero initial elastic stress also contributes to the recoil velocity:
\[ v_{0} = −L_{0} \frac{σ_{A} + σ_{G}^{\ell}(t = 0)}{η_{p}}, \quad (A.14) \]

with \( σ_{G}^{\ell}(t = 0) = \frac{E}{(1 + ν)(1 − 2ν)} ((1 − ν)e_{0} + νA_{0}) \). Since \( ν = \frac{1}{2} \), the active contraction of bundles initially stretched or compressed may yield a measurement of the Poisson ratio. In [114], the relaxation of ablated CBs has been fitted by a sum of two exponential functions with relaxation times \( τ_{1} \) and \( τ_{2} \), with \( τ_{1} ≈ 10 \). Assuming that our model is valid, this observation suggests that, in this experiment, \( \frac{τ_{1}}{τ_{0}} \approx 10 \), or equivalently \( \frac{1}{ν} ≈ 10^{−1} \).

For completeness, we also solve the case of an incompressible material. The dynamical equations for \( A(t) \) and \( e(t) \) read
\[ \tau_{G} \frac{dA}{dt} + A = −\frac{σ_{A}}{G}, \quad (A.15) \]
\[ \tau_{G} \frac{de}{dt} + e = −\frac{σ_{A}}{2G}. \quad (A.16) \]

We find that the bundle contracts both radially and longitudinally with a characteristic time \( τ_{G} \), the viscoelastic time based on the shear elastic modulus:
\[ A(t) = −\frac{σ_{A}}{G} + (\frac{σ_{A}}{G} + A_{0}) e^{−t/τ_{G}}, \quad (A.17) \]
\[ e(t) = −\frac{σ_{A}}{2G} + (\frac{σ_{A}}{2G} + e_{0}) e^{−t/τ_{G}}. \quad (A.18) \]
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