

Investigation of peristaltic pumping as a cellular motility mechanism

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ABSTRACT

The slime mold *Physarum polycephalum* has been shown to migrate while exhibiting rhythmic contractions that drive an intracellular flow similar to classical peristalsis. In this work, we investigate the feasibility of using the peristaltic pumping of intracellular cytoplasm as a mechanism to drive cellular motility. Stresses associated with peristaltic flows of cytoplasm are quantified. We also use two different models to quantify the spatio-temporal relationship between deformation and flow waves in peristaltic pumping. The relationship predicted by our models is then compared to experimental measurements of *Physarum*. This work was presented at PhysNet 2015.

Categories and Subject Descriptors

I.6 [Simulation and Modeling]: [Miscellaneous]

Keywords

Physarum, peristalsis, motility

The true slime mold *Physarum polycephalum* exhibits a vast array of sophisticated manipulations of its intracellular cytoplasm. The large size of individual specimens and the relative ease with which it may be imaged has made *Physarum* a popular model organism for cellular investigations. Removing a small sample of the organism results in a so-called microplasmodium. Initially after segregation, microplasmodia adopt a round shape and begin to reorganize their disrupted cytoskeleton [4]. As they grow past a critical size (approx 100 μm), the microplasmodia spontaneously elongate [1]. A tadpole-like shape develops, with a flow channel of non-gelated cytoplasm along the cell longitudinal axis. The cell begins to rhythmically contract in a fashion similar to peristaltic pumping. This results in a drastic increase in intracellular fluid velocity as a distinct back-and-forth pattern of cytoplasmic flow develops. The onset of this behavior has been observed to coincide with a drastic increase in the

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locomotion speed of growing *Physarum*. It has naturally been hypothesized that the flow of cytoplasm is therefore a driving phenomenon in this particular example of amoeboid motility.

Previous authors have used Particle Image Velocimetry (PIV) to measure the spatio-temporal flow of cytoplasm within migrating *Physarum* microplasmodia [3]. The flow profile was visualized as a function of the cell longitudinal axis (which the authors call the Anterior-Posterior (AP) axis and we call the cell axis). This revealed a distinct and regular traveling wave pattern, as regions of forward cytoplasmic flow develop at the posterior of the cell and propagate to the anterior, followed by regions of backward cytoplasmic flow. Furthermore, the authors showed that the flow wave is of the same wavelength and period as the wave of peristaltic contraction on the cell exterior. The two waves have a well-defined phase relative to one another (See Figure 1). The authors argue that this phase relationship, in addition to the anterograde propagation of the peristaltic wave, results in a net forward displacement of the cells center of mass, and thus cellular motility.

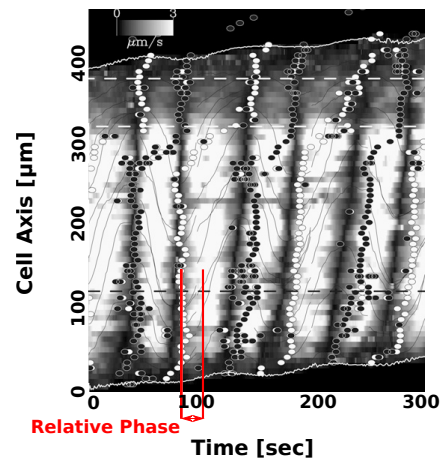


Figure 1: Grayscale indicates measured magnitude of intracellular flow as a function of time and longitudinal body coordinate. White ovals indicate location onset of body contraction. Black ovals indicate onset of body expansion. The phase lag between maximum width (white ovals) and maximum flow is indicated in red. Adapted from [3].

The main goal of this work is to elucidate the mechanisms which allow *Physarum* microplasmodium to migrate by generating the observed peristaltic flows of cytoplasm. Specifically, we are interested in the necessary mechanical asymmetries which render peristaltic *pumping* a viable mechanism for *crawling*. Can the hydrodynamics of cytoplasmic flow alone account for existing observations?

We primarily address this question through a mathematical treatment of a single microplasmodium as a finite length peristaltic chamber filled with viscous “cytoplasm.” The fluid dynamics of the chamber are reduced to a simple Partial Differential Equation (PDE) relating the deformation of the cell boundary and the longitudinal velocity of cytoplasmic flow. The deformation of the cell boundary is prescribed and the resulting fluid flow is solved for. The solution to this PDE is used to estimate the characteristic stresses associated with the flow of cytoplasm within the cell. It is shown that these stresses may be of a biologically relevant scale, but are quite small compared to the stresses associated with cellular motility. Furthermore, a large proportion of these stresses are “canceled out” by the inherent symmetry of the flow pattern. This suggests that hydrodynamical effects alone may not be sufficient to generate the directed motility observed in experiments. Additional mechanical asymmetry (through adhesive interactions and/or rheology of the cytoskeleton) appears necessary.

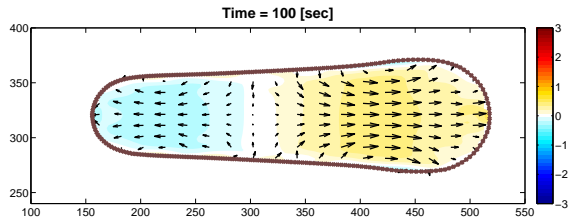


Figure 2: Instantaneous vector field of intracellular fluid velocity computed during simulation. Spatial scale is in $[\mu\text{m}]$ and velocity field is measured in $[\mu\text{m}/\text{s}]$.

We also compare the predictions of our mathematical model to the phase relationship observed between deformation and flow in migrating *Physarum* from [3]. It is seen that purely peristaltic pumping does not accurately capture the observed data, which is hypothesized to contribute to motility. Again, it seems that more mechanical complexity is necessary. With this in mind, we simulate peristaltic-like pumping in a numerical model of *Physarum*. Using the poro-elastic model developed in [2], we drive “pumping” via peristaltic-like contractions of the porous, elastic cytoskeleton. The numerical method is based on an Immersed Boundary (IB) formulation, where the cell membrane and cytoskeleton are represented in a moving, Lagrangian coordinate. Forces from the Lagrangian structures are spread to the intracellular fluid which is represented in a stationary Eulerian coordinate. The resulting deformation of the cell and the flow of cyto-

plasm within the cell interior are computed. Figure 2 shows the instantaneous shape of the numerical cell, as well as the computed intracellular velocity field, during one simulation. To compare our simulations with the results of [3], we measure the average intracellular velocity and the width of the numerical cell as a function of time and longitudinal cell coordinate. The results show that a poro-elastic model of *Physarum* interior accurately captures the phase relationship seen *in vivo* (See Figure 3). Furthermore, it appears that a mechanical heterogeneity in the anterior “head” of the cell is related to the observed behavior.

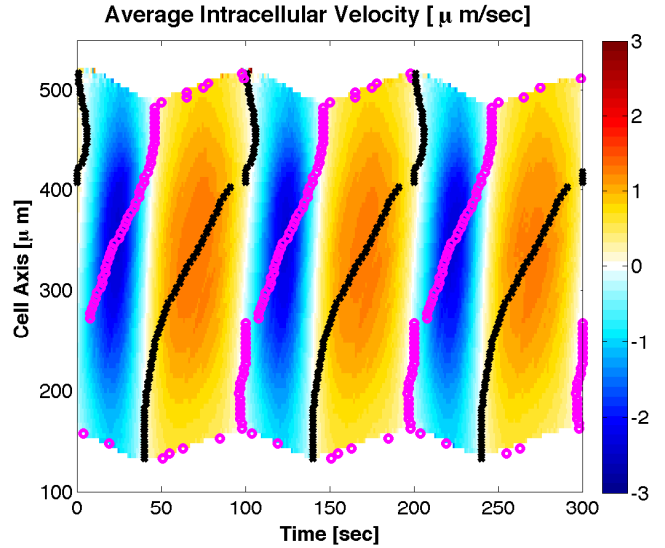


Figure 3: Computed average intracellular flow as a function of time and longitudinal body coordinate. Black exes indicate location onset of body contraction. Magenta circles indicate onset of body expansion.

References

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