

## New and Notable

### Engaging the “Clutch” to Move Forward

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It is 20 years since the publication of the geometric clutch (GC) hypothesis as a mechanistic explanation of ciliary and flagellar beating (1). It was an idea that resulted from constructing wooden models of the flagellar axoneme and observing the way they distorted during bending. The key insight was that a structure composed of linear elements that experience curvature while under tension or compression experience transverse forces (t-forces) that can push the linear elements closer together or pry them apart. In the eukaryotic axoneme of cilia and flagella, the linear elements are the nine outer doublets. They are anchored at the base of the cilium by the basal body, and they carry the motor proteins (dyneins) that provide the motive force to bend the cilium or flagellum to make them beat. The t-forces developed during bending can push the doublets closer or separate them. The GC hypothesis proposes that these t-forces are responsible for changing the inter-doublet separation, and engaging and disengaging the motors, thus organizing their action to create the beat. That, in a nutshell, is the conceptual basis of the GC hypothesis.

To test the feasibility of this concept as a mechanism for generating the ciliary/flagellar beat, it was necessary to try out the mechanism in a computed model. The original GC computer models (1–3) are set up rather much like solving a complex physics problem with elementary physics. When

executed on a computer, they produce beating and bend propagation that looks much like real cilia and flagella. In this regard, they served their purpose of supporting the feasibility of the GC mechanism. However, the mathematical treatment was very rudimentary.

The three-element torque balance among active torque from the motors, elastic bending resistance of the structure itself, and drag torque from the surrounding fluid is never fully solved in the original GC models, but is only approximated. Because this torque balance is accepted to be the fundamental physical basis of flagellar movement, the earlier published models by themselves are insufficient to solidly establish the validity of the GC concept. It has remained a possibility that with a more rigorous treatment, the results of the approximated model would not hold up, or the simulations would lose their resemblance to the real thing.

In this issue of the *Biophysical Journal*, Bayly and Wilson (4) independently come to grips with the GC hypothesis and develop it into an elegant continuum model with a sound mathematical basis. They are kind enough to refer to the earlier models as discrete models and numerical simulations with time marching. I like that, as I never really knew what to call them. Bayly and Wilson generate a set of differential equations faithfully incorporating the GC principles. The resulting simulations are remarkably similar to the output of the discrete model. They observe stable beating and wave propagation that simulates the behavior of a *Chlamydomonas* flagellum rather nicely. They manage to go a step further than was possible with the original models, and establish the parameter range for stable beating.

Their work also places the GC mechanism as a type of propagating event described by the Fisher-Kolmogorov equations. This links the GC to an already established group of physical phenomena with a rigorous description and history. Although the results so far

are closely consistent with the discrete or approximated GC model, the older models were not easily suited for direct adoption by the mathematics and biophysics community, as 20 years can attest. The new GC model contributed by Bayly and Wilson is a solid foundation and a more suitable beginning point to build forward. It will provide an analytical tool that will allow for the study of the dynamics, stability, and bifurcations inherent in the GC mechanism. As they state in their presentation, it will allow the GC model to be more directly compared to the alternative theoretical hypotheses. It is also adaptable enough to be incorporated into the hydrodynamic models developed by others in the math and biophysics communities who are experimenting with modeling ciliary and flagellar processes (5,6).

Coupled with the recent work of Brokaw (7,8), it could also be merged with a more sophisticated modeled representation of the dynein motor. Brokaw has recently demonstrated the GC clutch mechanism can regulate the dyneins in a two-doublet interaction. He has replicated the two doublet experimental results of Aoyama and Kamiya (9) using a t-force-based algorithm. He also demonstrates that if the doublets are prevented from total separation, it results in the propagation of bends by a GC-regulated mechanism (8). The complementary results of Mukundan et al. (10), also recently highlighted in the *Biophysical Journal* (11), showed that it may be possible to regulate the dyneins by t-force without complete dissociation of the inter-doublet connections the dynein forms with the adjacent B-subtubule of the next doublet.

The new GC model combined with these more accurate mechanistic models of the dynein power cycle could provide a test platform to probe the axoneme-dynein interaction in a theoretical framework. The new GC model

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may also provide a better platform for expansion to a full nine-element, three-dimensional theoretical model of a flagellum. This would be exciting, inasmuch as very few (if any) biological systems as complex as a flagellum have been rendered tractable to this level of theoretical treatment.

The flagellum is one of nature's most interesting biological nanomachines. It is effective at microscale propulsion and fluid pumping at low Reynold's number. If the beating cycle of the flagellum can be duplicated by the GC mechanism, it may be possible to apply the same GC principle to human engineered devices. There may be uses for an engineered mechanism that can turn nanotubes and molecular motors into pumps and propellers.

## REFERENCES

1. Lindemann, C. B. 1994. A "geometric clutch" hypothesis to explain oscillations of the axoneme of cilia and flagella. *J. Theor. Biol.* 168:175–189.
2. Lindemann, C. B. 1994. A model of flagellar and ciliary functioning which uses the forces transverse to the axoneme as the regulator of dynein activation. *Cell Motil. Cytoskeleton.* 29:141–154.
3. Lindemann, C. B. 2002. Geometric clutch model version 3: the role of the inner and outer arm dyneins in the ciliary beat. *Cell Motil. Cytoskeleton.* 52:242–254.
4. Bayly, P. V., and K. S. Wilson. 2014. Equations of interdoublet separation during flagellar motion reveal mechanisms of wave propagation and instability. *Biophys. J.* 107:1756–1772.
5. Simons, J., S. Olson, ..., L. Fauci. 2014. The dynamics of sperm detachment from epithelium in a coupled fluid-biochemical model of hyperactivated motility. *J. Theor. Biol.* 354:81–94.
6. Smith, D. J., E. A. Gaffney, ..., J. C. Kirkman-Brown. 2009. Bend propagation in the flagella of migrating human sperm, and its modulation by viscosity. *Cell Motil. Cytoskeleton.* 66:220–236.
7. Brokaw, C. J. 2009. Simulation of cyclic dynein-driven sliding, splitting, and reassociation in an outer doublet pair. *Biophys. J.* 97:2939–2947.
8. Brokaw, C. J. 2014. Computer simulation of flagellar movement X: doublet pair splitting and bend propagation modeled using stochastic dynein kinetics. *Cytoskeleton (Hoboken).* 71:273–284.
9. Aoyama, S., and R. Kamiya. 2005. Cyclical interactions between two outer doublet microtubules in split flagellar axonemes. *Biophys. J.* 89:3261–3268.
10. Mukundan, V., P. Sartori, ..., J. Howard. 2014. Motor regulation results in distal forces that bend partially disintegrated *Chlamydomonas* axonemes into circular arcs. *Biophys. J.* 106:2434–2442.
11. Lindemann, C. B. 2014. Dynein regulation: going into circles can set things straight. *Biophys. J.* 106:2285–2287.