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Note Added in Proof

A recent paper by Duursma and Agami (2005) (*Mol. Cell Biol.* 25, 6937–6947) also reports a link between Cdc6 degradation and cdk2 activity.

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The Kinky Propulsion of *Spiroplasma*

Bacteria have evolved many different means of generating movement. In this issue of *Cell*, Shaevitz et al. (2005) describe the swimming movement of a helical bacterium called *Spiroplasma*. They discover that *Spiroplasma* propels itself by generating two temporally distinct kinks that travel the length of the bacterium. These results point to the existence of a contractile apparatus that drives cell movement.

Bacteria are the smallest forms of life, and yet, they have evolved remarkably diverse mechanisms to generate motion. There are two primary categories of prokaryotic motility: swimming and gliding (Berg, 2003). Generally speaking, if a bacterium lives out its life on a wet surface, it glides; if it lives in a fluid, it swims. And some bacteria can do both, depending on where they find themselves.

However, one should not be deceived by these simple categories. There are, in fact, many different modes of prokaryotic movement. For example, during gliding some bacteria extend a pilus that adheres to substrates; the bacterium then retracts this long grappling hook to pull itself forward (Kaiser, 2003). In contrast, other bacteria secrete a slime that mysteriously pushes them along (Kaiser, 2003). Meanwhile, *Mycoplasma mobile* walks along surfaces using an ATP-driven mo-

tor. Remarkably, this movement occurs even in *M. mobile* “ghosts” that have had their membranes rendered permeable by detergents (Jenoyama and Miyata, 2005).

Mechanisms of bacterial swimming are also diverse. The most studied mechanism has been the stochastic, run-and-tumble swimming of bacteria like *Escherichia coli*, *Salmonella enterica* serovar Typhimurium, and *Bacillus subtilis* (Berg, 2003). This behavior has become so familiar that when bacterial swimming is mentioned, most of us immediately think of directed random walks and rotary motor reversals. However, it is now clear that bacteria bearing a single flagellum, such as *Rhodobacter sphaeroides*, do not run-and-tumble in the simple sense and, instead, modulate the rotational speed of their flagellum to change direction (Armitage and Schmitt, 1997).

Some swimming bacteria lack flagella. Although this group has received less attention until recently, their movements are no less strange and surprising. In this issue of *Cell*, Shaevitz and colleagues (2005) describe a new form of bacterial movement in one such organism, the helical bacterium *Spiroplasma*, which propagates pairs of kinks down its body axis to push its way forward.

Spiroplasma, like *Mycoplasma mobile*, has no cell wall. Only a single membrane bilayer separates the inside of the cell from the outside. *Spiroplasma* has protofilament ribbons that span the length of the cell to maintain its helical form. It was originally suggested that a single ribbon composed of seven protofilaments made of a single protein (Trachtenberg, 2004) was responsible for maintaining the shape of the cell. However, more recent experiments using cryo-electron tomography reveal not one but three ribbons. Of these three ribbons, two are made of the previously reported protein, and the other may be composed of a homolog of the bacterial protein MreB, rendering it similar to the shape determining cables found in *E. coli*, *B. subtilis*, and *Caulobacter crescentus* (Moller-Jensen and Lowe, 2005).

But how does a bacterium with such a simple morphology swim? *Spiroplasma*'s shape immediately brings to mind other swimming helical bacteria, such as the spirochetes (Charon and Goldstein, 2002). However, unlike *Spiroplasma*, spirochetes possess flagella. The spirochetes internalize their flagella in the periplasmic space between the cell wall and the outer cell membrane rather than sticking them out into the external fluid, as do many flagellated bacteria. The rotation of these flagella deforms the cell body causing it to roll. This corkscrew motion propels many species of spirochete through fluids, a method that is very effective for movement through gel-like media such as methylcellulose. Indeed, spirochetes swim faster in gel-like media than in water. Interestingly, this is also true of *Spiroplasma*. However, for *Spiroplasma*, this increase in speed is not dependent on the gel-like nature of the medium; it only depends on the viscosity. In higher-viscosity media, including non-gel-like solutions of Ficoll, *Spiroplasma* swim faster than in low-viscosity media (Gilad et al., 2003). This finding indicates that the mechanism of motility in *Spiroplasma*, although sharing po-

tential similarities with that of spirochetes, is likely to differ from the known swimming mechanisms of other helical organisms.

Could a rotary mechanism such as that seen in spirochetes be at play during *Spiroplasma* movement? Initial evidence suggested that deformation of the cytoskeletal ribbon produces traveling kinks in the cell body of *Spiroplasma* that induce movement (Trachtenberg, 2004). In their new work, Shaevitz et al. (2005) show that kinking in *Spiroplasma* is actually composed of two temporally distinct types of cell deformation. The first deformation flips the handedness of the cell helix (a right-handed helix becomes left-handed) at one end of the cell body. The deformation grows in the direction of the opposite end of the cell. After an average of 0.26 s, the initiating end of the cell, in a second deformation, flips back to its original handedness and creates a packet of opposite handedness that travels the length of the cell to the distal end. Propagation of these double kinks produces motility in the direction of the cell body helix axis and also rotation of the cell body around the helix axis.

This type of movement behavior in *Spiroplasma* can best be explained by the presence of an internal contractile apparatus (Kurner et al., 2005; Trachtenberg, 2004; Wolgemuth et al., 2003). A mathematical model describes how periodic changes in helix pitch can produce propulsive force (Wolgemuth et al., 2003). This mathematical model predicts that deformations driven by contractions would lead to swimming velocities that increase with increasing fluid viscosity, if kink velocity is independent of the viscosity. Confirming this prediction, Shaevitz et al. (2005) show that the kink velocity is indeed independent of viscosity. It should be mentioned that no contractile apparatus has yet been definitively shown for any bacterial motility apparatus (although the bacterial tubulin-like protein, FtsZ, does form a contractile ring during cell division [Bi and Lutkenhaus, 1991]). Also, no genes encoding eukaryotic contractile proteins have been detected in the *Spiroplasma* genome.

Although *Spiroplasma* movement mediated by an internal contractile apparatus is the favored explanation, another possibility that cannot be ruled out is the presence of a rotating internal filament. A rotation model would require that the helical ribbons be polymorphic like bacterial flagella, which change handedness upon reversal of the flagellar motor. Torque placed on the ribbons could flip the handedness of the cell shape thereby causing kinks.

Many questions remain to be answered. For instance, observations of *Spiroplasma* do not suggest that this bacterium has polarity: one end of the cell appears no different than the other. Yet, the results presented by Shaevitz et al. (2005) suggest that the same end of the cell always initiates the kinks. This result may have bearing on the motility of many other bacterial species. For example, it remains unclear how spirochetes can simultaneously regulate their flagellar motors at both ends of the cell during chemotaxis. Polarity of the cell may provide an easy answer. However, the most intriguing questions relate to how the kinks are generated.

The answers to these questions will likely come from the establishment of a system that allows kinks to be studied *in vitro*. We excitedly await this development.

Charles W. Wolgemuth¹ and Nyles W. Charon²

¹University of Connecticut Health Center
Department of Cell Biology
Farmington, Connecticut 06030

²Robert C. Byrd Health Sciences Center
West Virginia University
Department of Microbiology, Immunology,
and Cell Biology
Morgantown, West Virginia 26506

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