Kinesin’s parts pull together

Kinesin creates a new domain to generate its power, according to Wonmuk Hwang (Texas A&M University, College Station, TX), Matthew Lang (Massachusetts Institute of Technology, Cambridge, MA), and Martin Karplus (Harvard University, Cambridge, MA).

Kinesin’s structure includes a cargo-binding domain, a long stalk, and a pair of motor heads, which move along microtubules mostly hand over hand. Each motor head is connected to the stalk by a short neck linker. The neck linker has been suggested to help kinesin motility by making a large, ATP-driven conformational change that docks it to the motor head and results in a forward-stepping motion. But an unbound neck linker is flexible and interacts only weakly with the motor head; thus, it alone cannot generate the required force. The authors now discover an additional mechanical element not previously implicated in kinesin motility—the cover strand, which dangles nearby.

When ATP binds to the motor head, the cover strand and the neck linker form a new β-sheet domain, which the authors named the cover neck bundle. The bundle pushes the neck linker into its binding pocket, where it then latches on, powering the free motor head forward. Force analysis indicated that forces generated by the cover neck bundle agreed with experimental measurements.

“The force is generated by the formation of this domain rather than by switching between well-defined conformations,” Hwang says. “It was not possible to obtain these results from structural studies only, since it’s a dynamic structure.”

Reach out and gRab something

When families cooperate, their effects can be far reaching, according to Suzanne Pfeffer (Stanford University, Stanford, CA) and colleagues, whose study of Rab6 and Arl1 shows that these members of different GTPase families work together to anchor a vesicle-tethering protein onto the Golgi.

The tethering protein, GCC185, is thought to bind to transport vesicles destined for the Golgi. GCC185 contains a GRIP domain, which is known to bind to a possible anchor at the Golgi called Arl1. But previous work showed that Arl1 only bound weakly, if at all, to GCC185.

Since Rab6 is another tether-linking Golgi protein, the authors looked in detail at its possible interactions with GCC185. They found a pair of Rab6-binding sites just distal to those for Arl1 on GCC185. When Rab6 bound the tether first, Arl1 bound much more strongly. “Nobody expected that two different classes of GTPases would work cooperatively to localize this protein,” Pfeffer says. The structure of the complex suggests how they may cooperate. Rab6 has a long tail that enables it to reach up to ~100 Å away from the membrane to grab onto distant GCC185. Once Rab6 latches onto the tether, Arl1 binds it closer in to secure it in place. “It may be a molecular handoff,” says Pfeffer. Once the protein passes into the “GRIP” of Arl1, Rab6 is free to reach out and grab some more.

Self-assembly of the cell wall

For plant cell walls, opposites attract, according to Maura Cannon (University of Massachusetts, Amherst, MA), Marcia Kieliszewski (Ohio University, Athens, OH), and colleagues. Their results suggest that a positively charged protein network forms the frame to which negatively charged carbohydrates attach to make the mature wall.

Previously, the authors characterized a mutation that prevents normal development of the new cell wall that separates cells at the end of plant mitosis. In the current work, they identified the mutated gene as AtEXT3, one of 20 cell wall extensins in Arabidopsis.

As a new cell wall forms at the end of mitosis, AtEXT3-carrying Golgi vesicles fuse along the plane between daughter cells. Using atomic force microscopy in vitro, the authors showed that AtEXT3 formed a meshwork by cross-linking its multiple, repeating tyrosine residues. The authors propose that the highly periodic primary structure of AtEXT3 helps align copies of itself for cross-linking within the plane between daughter cells.

The protein’s many lysines give it a strong positive charge—perfect for attracting cell wall sugars such as pectin. “Since pectins are strongly negatively charged,” Cannon says, “we propose that the network of the cell wall forms by extensin laying down a framework on which pectins can assemble.” The pectins and extensins bond through an acid–base reaction, and pectins themselves can also form linkages with each other.

"For plant cell walls, opposites attract," says Maura Cannon (University of Massachusetts, Amherst, MA), who with her colleagues used atomic force microscopy to show that extensin AtEXT3 forms a network that attracts oppositely charged carbohydrates to make the mature wall. They identified the mutated gene as AtEXT3, one of 20 cell wall extensins in Arabidopsis. As a new cell wall forms at the end of mitosis, AtEXT3-carrying Golgi vesicles fuse along the plane between daughter cells. Using atomic force microscopy in vitro, the authors showed that AtEXT3 formed a meshwork by cross-linking its multiple, repeating tyrosine residues. The authors propose that the highly periodic primary structure of AtEXT3 helps align copies of itself for cross-linking within the plane between daughter cells. The protein’s many lysines give it a strong positive charge—perfect for attracting cell wall sugars such as pectin. “Since pectins are strongly negatively charged,” Cannon says, “we propose that the network of the cell wall forms by extensin laying down a framework on which pectins can assemble.” The pectins and extensins bond through an acid–base reaction, and pectins themselves can also form linkages with each other.

Reference:
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