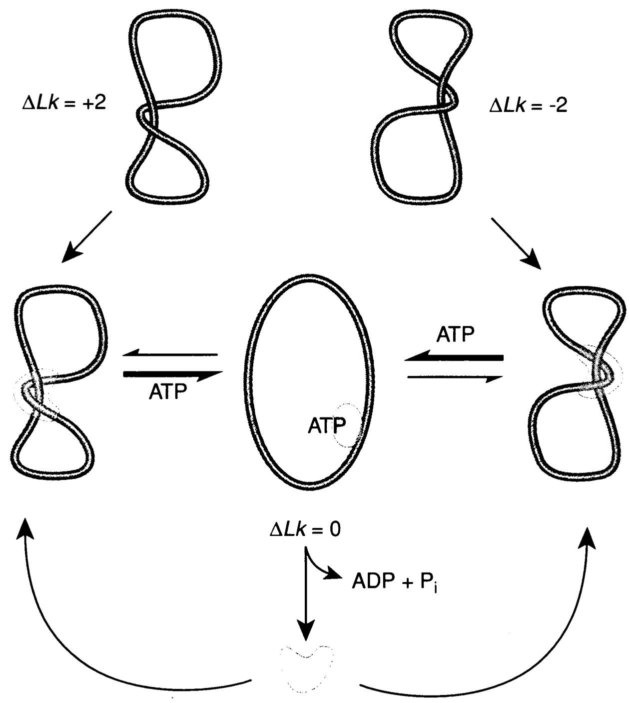

Proposed mechanism for Topo II–induced change in topoisomer distribution. ATP-directed unkinking associated with strand transfer reduces the relative concentration of topoisomers with either right- or left-handed superhelical turns relative to the concentration of a topoisomer having no supercoils. P$_i$ inorganic phosphate.

which it initially bound, a strand passage reaction either decatenates [see figure 4A in (*1*)] or unknots [figure 4B in (*1*)] the molecules as the situation demands. This idea addresses the kinetics of locating topological links. But how can we address the thermodynamic question of how ATP hydrolysis is coupled to give direction to the reaction?

The model can be modified to give direction to the sliding process by ATP hydrolysis, in effect committing the sliding clamps to converge. Catenated or knotted molecules would then be efficiently trapped so that they could be unlinked. If each clamp inadvertently associated with a different, unlinked molecule, trapping would never occur. Decatenation and unknotting would be selective, and the hydrolysis of ATP would have a defined function. Even with this amendment, the model appears to have an (acknowledged) difficulty [see figure 4C in (*1*)] in accounting for the increased homogeneity in linking number upon reaction with unknotted circular molecules, because in this case there is no trapped segment of DNA.

The action of topo II/IV on supercoiled DNA [figure 4C in (*1*)] provides a test that may discriminate between the two models. A topoisomer family interacting with topoisomerase I loses its equilibrium character as soon as the enzyme is inactivated. When the structures of molecules having fewer or more helical turns in the backbone are time averaged, negative or positive superhelical turns will be present. The nonzero writhe component of these superhelical turns can be detected by its effect on the electrophoretic mobilities of the topoisomers. A single kink in a DNA molecule cannot constrain writhe, whereas a pair of kinks can (see the figure). Although an enzyme molecule that binds to an isolated kink cannot by itself discriminate between a positive and a negative superhelical turn, it will reduce the total number of superhelical turns if in the course of strand passage, it unbends the kink that is initially detected. The proposed kinkase activity of our anti-kitten, therefore, provides a simple explanation for a reduced topoisomer dispersion in a family after this enzyme has operated.

To the best of my knowledge this is the first time it has been suggested that an enzyme can use a rare and transient conformational state in its substrate to direct an outcome. A quantitative treatment of each model will be difficult but necessary before the system can be fully understood. There are subtleties here that will entertain us for some time to come.

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Viruses A to Z
http://www.tulane.edu/~dmsander/garryfavweb.html

Virology information is replicating rapidly on the Web, and this site—ambitiously entitled "All the Virology on the WWW"—is one of the better-designed and more comprehensive sources. Hosted by R. F. Garry's laboratory at Tulane University, ATVOTW contains many links to virology labs around the world, online tutorials, and virology dictionaries. Not to be missed is the Big Picture Book of Viruses, which tabulates a large number of DNA- and RNA-containing viruses along with related images and links.

Small, smaller, smallest
http://www.pbrc.hawaii.edu/~kunkel/

D. Kunkel's Microscopy Web site at the University of Hawaii is a striking collection of photomicrographs of microbes, insects, and crystals of many kinds. In addition to the aesthetically compelling pictures, there is much of scientific interest, including discussions of different kinds of microscopy and links to microscopy sites. The site's "Zoom In" feature allows the user to enlarge selected portions of several organisms.

Edited by David Voss

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