genes, the evolution of pleiotropy, the accumulation of modifier mutations, and so on. The authors themselves brand the chapter "conceptual meanderings." But it is one thing to meander, another to synthesize. This lack of coherence lends the book a diffuse, unrigorous quality and is, in the end, its most serious problem. Now and then the clash of ideas gets so bad that the text slips into unintelligibility, as when we are told, "The innate complexity of genetic systems necessarily leads to emergent properties arising from epigenetic processes that integrate the output components of myriad local genetic programs into a functional global phenotype." Such talk seems an unlikely first step to clearer understanding.

Phenotypic Evolution is representative of a popular trend—some pet theory (take your pick: plasticity, development, complexity theory, or chaos) gets elevated to its rightful place as "the" way to think about evolution. But this longing to dress up biology in unusual new perspectives has, so far, yielded more book deals than results. Although new ways of thinking will surely be required in the attempt to unravel the genetical evolution of the phenotype, considerable care and taste are needed in their selection. Schlichting and Pigliucci's confused admixture is not the perspective we have been waiting for.

SCIENCE'S COMPASS

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SCIENCE'S COMPASS

The Difficulty in

Separating Sisters Terry L. Orr-Weaver

ne of the defining events during cell division (mitosis) is the separation of sister chromatids that are attached to each other and to the mitotic spindle, a process called cohesion release. But we are only now beginning to understand how the powerful cohesive forces that hold the sister chromatids together are overcome. In the budding yeast, Saccharomyces cerevisiae, the chief player seems to be the Esp1 protein—a so-called separin-which is also found in human cells, raising the possibility that the mechanism of cohesion release is highly conserved (1). On page 418 of this issue, Zou et al. add another piece to the puzzle with

their report that an oncogene, PTTG (pituitary tumor-transforming gene), acts as a regulator of Esp1. This suggests that defective regulation of cohesion may contribute to cancer by promoting chromosome instability (2). Like a classic murder mystery plot, the prime suspect for "doing in" sister-chromatid cohesion, the anaphase-promoting complex (APC), now turns out to be a mere accomplice, with the less colorful Esp1 character actually responsible for the deed.

Physical association of the sister chromatids is crucial for their stable attachment to microtubules from opposite spindle poles and for their proper segregation at the transition from metaphase to anaphase. Cohesin, a conserved multiprotein complex, is essential for the tight association of the sister chromatids, which is established as the DNA is replicated during S phase (3). The cohesin complex is localized along the length of the sister chromatids and, as shown by a report in last week's *Science*, is also bound to the centromere (the constricted area of the chromosome to which spindle microtubules bind) (4). In budding yeast, two cohesin subunits, Scc1p (also called Mcd1p) and Scc3p, dissociate from the chromatids at the onset of anaphase, coinciding with release of cohesion.

Ubiquitin-mediated proteolysis is necessary to activate the transition from metaphase to anaphase. The APC tags mitotic cyclins with a ubiquitin marker, targeting them for degradation; the cells are then able to exit mitosis. The APC also has other substrates that must be degraded to ensure sister-chromatid separation (5). The initial theory that the APC directly releases cohesion § by degrading cohesin was disproved by the finding that cohesin subunits persisted into telophase, the final step of cell division (6, 7). Rather, it turned out that APC triggers the degradation of a group of proteins called securins that inhibit sister-chromatid separation. Securins include Pds1p in S. cerevisiae and a different protein, encoded by the *cut2*

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