Published in final edited form as:

Science. 2008 October 3; 322(5898): 43–44. doi:10.1126/science.322.5898.43b.

Epigenomics: A Roadmap, But to Where?

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Recently, The Director Of The National Institutes of Health (NIH) allocated $190 million for an “Epigenomics” Roadmap initiative (1). As investigators in this area, we endorse the idea that chromatin biology is an appropriate, if not essential, area for the NIH to support, not only for its fundamental biological significance but also its relevance to human disease. Nonetheless, we believe that this initiative, at least in its current form, will not yield significant benefits. If the use of the term “epigenome” is intended to equate the value of this Roadmap initiative with the Human Genome Project, it fails on several grounds.

First, it does not consider our current understanding of the roles of sequence-specific DNA recognition events and transcriptional networks in controlling epigenetic changes. A multifaceted effort that elucidates transcriptional circuits that tell us where and when signal-responsive, sequence-specific regulators function would be more useful for understanding cell type programming. Second, merely cataloging modification patterns offers comparatively little new or useful information. We already know that most genes are associated with one of a few patterns of chromatin modifications and that the patterns themselves do not tell us how that gene is regulated or how its expression state is inherited. Most histone modifications are highly dynamic and change rapidly in response to changes in signals that turn genes on or off.

This initiative will divert substantial resources, enough to fund 200 multiyear individual grants. There is a notion favored by some that individual scientists need to be corralled to work together under a more rigid, directed framework to solve important problems. We

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disagree. Real innovation comes from the bottom up, and good science policy requires promoting the free market of ideas rather than central planning (2).

References and Notes

1. NIH Roadmap for Medical Research. (http://nihroadmap.nih.gov/epigenomics/).
2. Links to a full version of this letter and petition for readers to sign can be found at http://madhanilab.ucsf.edu/epigenomics/.