

Editorial

ENCODE and ChIP-chip in the genome era

Comparative genomic sequence analysis is a powerful approach to the identification of both new genes and potential regulatory sites [1, 2] but it is not sufficient: experimental analysis is ultimately necessary to substantiate and elaborate biological function. This is why the National Human Genome Research Institute (www.genome.gov) will be spending \$36 million over the next 3 years on a program designated ENCODE—the ENCyclopedia Of DNA Elements [3]. The ENCODE Request for Applications (RFA), published in February 2003, included two categories of projects. RFA HG-03-003 solicited applications to identify functional elements (including but not limited to transcription units) in a preselected 1% of the human genome as a pilot project to determine the value and feasibility of annotating these elements in the remaining 99% of the genome. RFA HG-03-004 was aimed at the development of new and improved technologies for the efficient, comprehensive, and high-throughput identification and verification of functional elements, particularly those other than protein-encoding sequences.

In October 2003 NHGRI announced the first grants to be awarded under this program, with \$10.5 million going to five projects applying existing technologies to identify and map transcription, regulation, and DNA replication sites and with \$2.6 million distributed among six projects aimed at developing new and improved methods [3]. One common methodological theme that recurs throughout many of these projects is chromatin immunoprecipitation (ChIP), followed by the identification of immunoprecipitated genomic fragments through the use of “whole genome” microarrays (or “DNA chips”). Given the emerging importance of this so-called ChIP-chip approach to experimental, functional annotation of genomes in terms of DNA–protein interactions, we are pleased to publish a comprehensive review of this technology and its genomic applications in the current issue [4]. In the words of one anonymous reviewer, “This field is poised to undergo the same type of revolution that gene expression technologies did in the late 1990s.” Comprehensive information on DNA–protein interactions, combined with gene expression and proteomics data and SNP association and genotypic data in segregating populations, has the potential to revolutionize our understanding of complex systems.

The article by Buck and Lieb is just the first of a number of important and interesting reviews on the functional interpretation of the human and other genomes that will appear in the pages of *Genomics* in the coming months (a sneak preview of these was included in the December 2003 issue [5]).

References

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Mark S. Boguski
Editor-in-Chief