GENOMICS 1, 1–2 (1987)

EDITORIAL

A New Discipline, A New Name, A New Journal

In recent times there has been a rallying call for complete mapping/sequencing of the human genome. Technical advances in mapping beginning 20 years ago and in sequencing 10–15 years ago have made this feasible or at least conceivable. The two operations—mapping and sequencing—have the same objective, namely, analysis of the structure and organization of the human genome. Mapping determines the general location of genes on chromosomes and their positions relative to each other. The nucleotide sequence is the ultimate map. The two operations must go hand in hand. For example, the mapping of segments of DNA, e.g., overlapping cosmid clones, is seen as a desirable initial step for efficient sequencing of the human genome. Blind sequencing is not likely to be as efficient, and certainly not as interesting, as sequencing the expressed parts of the genome, whose chromosomal location is known. Mapping all expressed genes, cloned through their messenger RNAs, regardless of whether their function is known, sequencing these genes together with their introns, and sequencing out from these is seen by many as "the way to go." The ultimate map, the sequence, is seen as a rosetta stone from which the complexities of gene expression in development can be translated and the genetic mechanisms of disease interpreted.

For the newly developing discipline of mapping/sequencing (including analysis of the information) we have adopted the term GENOMICS. We are indebted to T. H. Roderick of the Jackson Laboratory, Bar Harbor, Maine, for suggesting the term. The new discipline is born from a marriage of molecular and cell biology with classical genetics and is fostered by computational science. Genomics involves workers competent in constructing and interpreting various types of genomic maps and interested in learning their biologic significance. Genetic mapping and nucleic acid sequencing should be viewed as parts of the same analytic process—a process intertwined with our efforts to understand development and disease.

In his essay entitled "What is Semantics?", Anatol Rapoport wrote:

> There are two suffixes in our language (and similar ones in other European languages) which suggest organized knowlege. One is the venerable, academic "ology," that reminds one of university curricula and scholarship. The other is the energetic and somewhat mysterious "ics," which has a connotative flavor of magic. Where "ology" suggests academic isolation (ichthyology, philology) "ics" suggests a method of attack on life's problems. It contains a faint throwback to the ancient dreams of the philosopher's stone and of "keys" to the riddles of the universe. Ancient words ending in "ics" are mathematics and metaphysics. Of more recent origin are economics, statistics, semantics, and cybernetics.

One might add *genetics,* and now, *genomics.*

While we are on words: *Genome* is an irregular hybrid of *gene* and *chromosome.* Both parents are Greek. In their *Glossary of Genetics and Cytogenetics,* Rieger, Michaelis, and Green (1976), stated that the hybrid term was first used in 1920 by Winkler, who also introduced the term *conversion* into genetics.

The necessity for communication, coordination, and education in this emerging field dictates the founding of a new journal dedicated to genomics in all of its ramifications. *Genomics* will not only report new data concerning genome maps and improved methods for mapping and sequencing—those will certainly be very important components of the journal—but also will publish analyses of the information, methods for those analyses, methods for storage, retrieval, searching, pattern recognition, comparisons, etc., as well as interpretation of structural findings in light of their biologic significance and biomedical applications.

Genomics will be a common meeting ground for molecular biologists and biochemists, human and somatic cell geneticists, cytogeneticists, population and evolutionary biologists, genetic epidemiologists, clinical geneticists, theoretical biologists, and computational scientists, all interested in the biology and genetics of the human and other complex genomes.

Topic areas for this interdisciplinary forum include:

- Chromosomal assignments of genes and DNA fragments by Mendelian and physical mapping approaches, including the description of new techniques
- Reports of nucleic acid sequences of cloned genes or other interesting portions of a genome
- Descripton of chromosomal and spatial distributions of gene families and genes that share nucleic acid or amino acid sequence domains

- Comparative analyses of genomes to yield structural, functional, or evolutionary insights
- Patterns of organization within the genome that provide insights into gene regulation and development
- Methods for large-scale genomic cloning, restriction mapping, and DNA sequencing
- Computational methods and descriptions of algorithms for the manipulation of DNA and protein sequence data
- Novel means for representing and correlating DNA sequence, restriction endonuclease cleavage, and chromosomal gene mapping data—toward understanding the hierarchy of chromosome structure
- Analysis of genetic linkage data in pursuit of information on inherited disorders
- Development of experimental, computational, and database management techniques of broad applicability for obtaining or using data on human genome organization, as well as the illustration of innovative parallel studies on genomes from lower organisms.

A NEW JOURNAL: THE HUXLEY PRINCIPLE

When we told him about our plans for a new journal devoted to gene mapping and nucleotide sequencing, Sir Andrew Huxley made a cogent comment: "Usually when people start a new journal they say 'The purpose of this journal is to publish the very best work in this field.' That is not the reason one needs a new journal. The 'best work in this field' can be published, and will be published, anywhere. One needs a new journal, in a rapidly advancing field, as a place where a considerable portion of the sound work going on in the field can be published, where the workers in the field can easily keep abreast of recent advances in methods, results, and interpretations." This is especially the case when the field is being pursued by workers with a variety of backgrounds and approaches.

The editors see *Genomics* as serving a triple function in communication, coordination, and education. The main body of material published will be original basic research communications, the unsolicited submissions of scientists. Solicited reviews and commentaries, including book reviews, will be regular features. On a regular basis, a section entitled "Genomics Update" will reference new or confirmatory gene assignment information reported elsewhere, as well as various accessions to the mapping and sequencing databases.

Coordination of efforts in this interdisciplinary field will be encouraged by a close interaction between *Genomics* and several databases, particularly the Human Gene Map Library in New Haven, under the sponsorship of the Howard Hughes Medical Institute, the Catalog of Mendelian Inheritance in Man at Johns Hopkins, and the DNA sequence databases coordinated by GenBank and the European Molecular Biology Laboratory (EMBL). In connection with the NIGMS Human Genetics Mutant Cell Repository at Camden, short reports of unusual families from which cells and DNA have been deposited will be published or referenced. DNA probes available from the American Type Culture Collection (ATCC) will be listed periodically. Pains also have been taken to coordinate efforts with the resources of CEPH (Centre d'Étude du Polymorphisme Humain) in Paris.

We hope that *Genomics* will facilitate communication among those involved in creation of physical (overlapping clone) maps, those who are concerned with the functional or genetic linkage (e.g., RFLP) maps, and yet others who focus on fine-level restriction mapping and nucleotide sequencing. We feel the "ics" of *Genomics* serves well to connote the interaction with electronic means of information handling (informatics) and that the journal can help lead the way in merging the strengths of publishing and database technologies.

Finally, the potential role of *Genomics* in our education is, we trust, obvious. With this first issue, we welcome you to our readership and encourage you to participate in the growth of this new discipline and new forum.

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