PL-III. THE HUMAN GENOME PROJECTS: SCOPE, METHODOLOGY AND DIFFICULTIES

Introduction to mapping and sequencing. Definition of genetic maps and physical maps

George COHEN

Institut Pasteur, Paris, France

Scope of the genome projects. Development of diagnostic tools, isolation of genes associated with disease, development of human therapeutics, prospects for human gene therapy, identification of protein coding sequences, approaches to understanding gene function and regulation, applications in molecular evolution and in population biology.

Methodology. Instrument development for automation (robots), restriction fragment length polymorphism markers, restriction enzyme maps with rare cutters, random oligonucleotide screening, chromosome separation, identification of functional sequences by cDNA libraries, new cloning methods, establishment of contigs (sequence tagged sites), establishment of databases, human pedigree analysis, advanced human genetics on specific diseases and reverse genetics.

All the above except perhaps instrument development, requires extensive collaboration between groups working on specific genes, gene clusters, or specific chromosomes.

Efforts made in the different parts of the world

United States (Department of Energy, National Institutes of Health, National Science Foundation)

Japan (MESC, STA, MITI, Ministry of Agriculture <genome of rice> Human Frontier Science Program)

European Community

United Kingdom (genome of a nematode, *Caenorhabditis elegans*)

France: detailed description of the activities of CEPH (Centre d'Etudes du Polymorphisme humain)

Italy, Germany, Denmark

Others

Description of HUGO. The rest of the lecture has been devoted to the presentation of alternative strategies, such as cDNA mapping, and to the presentation of the arguments of those opposed to the Human Genome Project and to the answers to their objections.