

The Human Genome Project and DNA Sequencing

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DESCRIPTION

Human and other organisms has been identified by Blue eyes, brown hair and all are determined by the human genome. Hereditary characteristics are determined by biological components called genes. The molecular biology of DNA, the massive molecule from which genes are formed, has greatly increased our understanding of these genes in recent years. It is now possible to obtain the ultimate description of genes and DNA and recently developed techniques that allow us to map locate the genes in any organism's DNA and then sequence order each of the DNA units known as nucleotides that comprise the genes as more of our genes are identified and their DNA sequenced, we will have a more valuable resource an essential database that will aid research in biochemistry, physiology, cell biology, and medicine. This database will have a significant impact on health care, disease prevention, and our understanding of cells and organisms. The idea of organizing a large project to map and sequence the DNA in genes and the intragenic regions that connect the entire human DNA complement or genome which has gained traction around the world. Several countries have expressed interest in starting such a project sequencing of the genome the nucleotide sequence of the genome is the highest-resolution physical map. It provides the information that makes up an individual's genetic complement. A total of approximately 3 billions of nucleotides must be ordered for a human simple printing such a DNA sequence would require nearly a million years ago. A special effort must be made to obtain this critical resource promptly, but because of the high cost and slow rate of DNA sequencing with current technology, sequencing of the entire genome should not be initiated at this time. Instead, the committee believes that two types of efforts should be encouraged to improve DNA efficiency. To begin, projects should be carried out to sequence approximately one million continuous nucleotides which are 5 to 10 times as large

as the largest continuous regions that have been sequenced to date. Such projects will allow for the implementation and testing of existing technology improvements as they occur, as well as provide a practical impetus for technological developments. They will also reveal where the most serious data analysis issues are likely to arise in future projects which repetitive sequences or cloning make the assembly of a unique, contiguous sequence more difficult and new genes be correctly identified

Only gain insight into these issues by attempting relatively large-scale nucleotide sequencing. Second, advancements in existing sequencing technology as well as the development of completely new technologies should be vigorously encouraged. This would include the use of automation and robotics at all stages of the sequencing process. Consider attempting to achieve 5- to 10-fold incremental improvements in the scale and speed of DNA sequencing.

CONCLUSION

To reap the greatest benefits from a human genome sequence, a large database of DNA sequences from mice the genome is the same size as the human's and simpler organisms with much smaller genomes, such as bacteria, yeast, *Drosophila melanogaster* and *Caenorhabditis elegans*, will be required a nematode worm. This would allow important human gene counterparts to be easily identified in organisms where their functional roles are generally easier to study. Furthermore, many genes will initially be discovered to be important in these other organisms, leading to corollary human studies. Comparative sequence analysis using an organism such as the mouse is a powerful technique for distinguishing between important and thus conserved during evolution and unimportant elements of a nucleotide sequence. To be successful, this project must not be limited to the human genome rather it must include extensive sequence analysis of selected other species' genomes.

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