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Commentary

Genomics And Proteomics In Evolutionary Medicine And Comparison With Human Species

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This article is based on the keynote address given at the third biennial Asan Medical Center-Harvard Medical International Symposium “Genetics and Proteomics: Impact on Medicine and Health” on July 3–4, 2001 in Seoul, Korea. The author summarised exciting advances in genomics and introduced the related and emerging field of proteomics in his address. Genomic and proteomics are dramatically accelerating the pace of biological research by employing industrialised high-throughput approaches. They have sparked a scientific revolution whose consequences will range from elucidating the structure of our chromosomes to providing powerful new tools for disease research, and from understanding human evolutionary history to novel applications in future medicine.The author’s overview highlighted the two fields’ recent history and laid the groundwork for the rest of the symposium presentations. In the spring of 2001, the announcement of the completion of the draught sequencing of the human genome marked a watershed moment in biology. The information provided by the Human Genome Project (HGP), as well as the powerful technologies developed in the process of completing it, have already changed the way biomedical research is conducted dramatically. In the spring of 2001, the announcement of the completion of the draught sequencing of the human genome marked a watershed moment in biology.The human genome contains over 3 billion letters. Typical sequencing read lengths were in the 200–300 base range when the project was conceived. With a simple calculation of the number of required reads and the amount of computing power required to handle the data (not to mention special technical problems such as repeated sequences), it is not surprising that many argued that taking on this project would be an inappropriate use of research funds and possibly a total folly. Nonetheless, the draught version of the human sequence has been completed far ahead of the many decades expected. This project involved more than 20 major sequencing centres and hundreds of scientists.The High-Throughput Sequencing Project (HGP) was not always a high-throughput sequencing project. That aspect of its operations did not begin until late in the 1990s, following an earlier phase in which genetic maps and technologies were developed that were critical to the high-throughput sequencing that took place at the end. This could be a valuable lesson for us as we enter the “Proteomic Era.” Much time will be spent in the beginning developing new methods, new computational tools, and mapping out the projects that must be completed. Furthermore, the HGP has demonstrated that the technologies are at least as powerful as the data collected. New tools, such as DNA microarrays and transcriptional profiling, serial gene expression analysis, and haplotype mapping, are being developed.Although the HGP will have an impact on all aspects of biology, some areas will be directly influenced, as indicated. Not surprisingly, advances in our understanding of genome structure and function, as well as human evolution, are the two disciplines that have been most directly impacted by the genome project. The manuscripts describing the draught sequencing went into great detail in these areas. Furthermore, the number of papers published about human evolution and genome structure has increased at an unprecedented rate in recent years. The sequence is a rich information store that will be mined for years, becoming even more fruitful as additional vertebrate genomes, such as those of the mouse, rat, and dog, are completed.Finally, the level of sequence similarity among human species was perhaps the most dramatic evolutionary conclusion from the genome. At the nucleotide level, humans are 99.9 percent identical. That is an astonishing level of identity in an organism. In fact, the majority of our genetic differences, as measured primarily by SNPs, are shared by all ethnicities and races. The majority of these differences can be traced back to when humans lived in Africa. In fact, humans are far more similar to one another than most other species on the planet. The majority of today's human population appears to have descended from a very small group of common ancestors who spread rapidly when the population left the African continent.

Acknowledgment

None

Conflict of Interest

None