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Human Genome - Underlying Scientific Mysteries

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Introduction

A gene refers to the functional unit of heredity. Genes are made up of DNA (deoxyribonucleic acid). In humans, the size of genes varies from a few hundred DNA bases to more than 2 million bases. The genes in human beings (Homo sapiens) are referred as human genome. It is made up of 23 chromosome pairs with a total of about 3 billion DNA base pairs. The gene sequences to make a protein occupy only about 1.1% of the chromosomes. The rest is well known as junk DNA; that is useful in genetic fingerprinting.

Many scientists now believe that the junk DNA has a role in evolution. The human genome is more than 95% worthless, but 5% of the 3.2 billion nucleotides make the whole human genome [1,2]. A critical implication of the human genome is that as long as we move up in the complexity of the organisms, it surely doesn't correspond to the increase in genes, but is proportional to the number of controls and regulations on these genes. The scientists have used software and programs to go through billions of DNA letters and then locate these gene sequences. These programs advanced with time, but there is still a lot of scopes as a lot is going on in the protein manufacturing including splicing, transposable elements, assembling and post-translational reframing. As a contrast, a recent finding shows that a Japanese fish that is also known as "Fugu" has no junk DNA at all. This discovery helps us to understand more deeply the cause and consequence of development from coding and non-coding sequences [1].

Another contribution is in explaining the variations in humans by the human genome by the common changes in the nucleotides of genetic code called the single nucleotide polymorphisms (SNPs). However, differences between any two individuals in the same population could be greater than that between two different groups. As published lately in a magazine, nobody knows the identities of the people who donated their DNA to the project, but Dr. Venter knowingly selected DNA from five individuals, one African-American, one Asian-American, one Hispanic-American and two others and found no way of telling which was which [2-4].

It has been predicted by the genome scientists that by 2020, the information will be sufficient enough to diagnose most of the diseases before the symptoms appear. Till now 1,778 genes identified with illness and only 483 prospective candidate genes targets for therapy are known in the human body. The upcoming research will speedily increase the number of genes [2,5]. Some other questions need to be answered before the large scale application of the data, including epigenetic status of the genes, vulnerability to variations and evolution. The more information regarding these could also open up a new era of personalized medicine and therapeutics. Personalized medicine has a control over individualizing medicine both in terms of treatment and diagnosis [6]. But we should also be prepared for the more challenging ethical questions which will arise with the advancements in this knowledge bank [7].

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