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Editorial

A WEALTH OF EXPLORATION FOCUSED ON THE HUMAN GENOME PROJECT

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EDITORIAL

Human Genome Project (HGP), with its extensive list of protein-coding genes, spurred a new era of elucidating the role of the non-coding component of the genome and paved the way for therapeutic advances. Crucially, as researchers mapped the interactions between cellular interactions, the findings track the creation of a system-level view of biology alongside the traditional single-gene perspective.

For contrast, there is no universe without an HGP. It is also difficult to tell if these patterns would have existed anyway. In many of these advances, other factors, from increased computational power to advanced sequencing methods, have played a role.

It is nevertheless clear that the catalogue of the HGP catalysed the current genetic revolution. The general understanding is that the HGP marked the beginning of the intense search for genes that are protein-coding. The 2001 draft HGP paper actually marked the end of a decades-long chase.

The HGP also established a way, including that of SNPs, to catalog human genetic variation. The cost of profiling common variations across thousands of people was minimized by other major efforts; these included the International HapMap Project (the third and final phase of which was completed in 2010) and the 1000 Genomes Project.

For the modern age of genomics it ushered in, HGP is more noteworthy than for the protein catalogue itself. As the theory of complex systems shows, to understand any system, an accurate survey of components is important, but not sufficient. Complexity results from the multiplicity of the relationships between elements.

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