

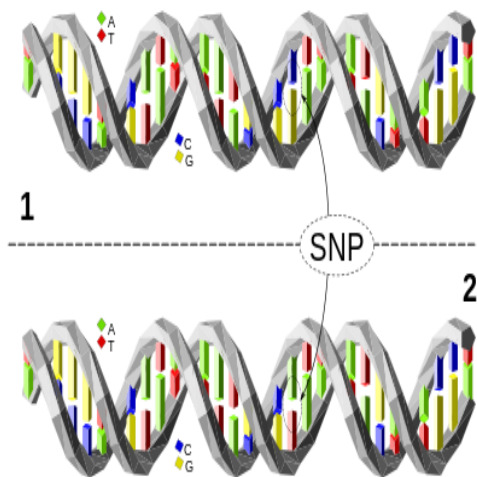
SNPs: the great importance of small differences

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Single nucleotide polymorphisms (SNPs) have been the center of considerable research since the completion of the Human Genome Project in 2001.

Most genomes in human beings are alike. As a result, a somewhat small number of genetic differences has produced the many variations within the human species in characteristics such as skin color, weight and height.

Genes themselves control only part of these characteristics. The intricate relationship between genes and the environment, and between multiple genes, increases the difficulty of understanding and quantifying the human phenotypic variation. Genome analysis and sequencing reveals that only one out of thousands of nucleotides differ in the genomes of two individuals.



This discovery caused scientists to look beyond even the most complex of human traits and search for the nucleotide sequences within the genome that held answers about individual human variation. Identifying single base changes (single nucleotide polymorphisms, aka SNPs -pronounced “snips”) was regarded as the ideal solution.

An SNP originates from a single base mutation in the genetic sequence, such as a mutation from the base adenine (A) to thymine (T), at a particular position on the genome. However, not every point mutation is called an SNP. They must be found in a minimum of one-percent of the general population. SNPs are a normal occurrence in a human beings' DNA. On average, SNPs occur once in every 300 nucleotides, or about 10 million times within the human genome.

Single nucleotide polymorphisms can be found within both coding and non-coding sequences of genes, or in the genes' promoter activity region. SNPs in a coding sequence may not alter the protein's amino acid sequence in the genetic code due to

multiple codons for the same amino acid. SNPs not found in protein coding regions may still affect gene splicing, transcription factor binding, or the sequence of non-coding RNA.

Ultimately, the identification of the many variations in genes and proper analysis of their effects may bring about a deeper understanding of their power over gene function and an individual's health.

The differences found in the DNA sequences of human beings can affect how diseases develop and the response to pathogens, chemicals, drugs, and other factors. These variations are most often found in the DNA between genes. They can function as biological markers to help scientists reveal the genes associated with disease. When SNPs are found in a gene, or in a regulatory region near a gene, they may have a more direct role in disease since they affect the gene's function. SNPs are poised to significantly advance the understanding and treatment of human disease. Researchers have unearthed SNPs that may play a role in predicting individual responses to certain drugs, susceptibility to toxins and other environmental factors, and the likelihood of developing a particular disease.

SNPs are potential biomarkers for drug response

Pharmacogenomics is a discipline whose goal is to discover the genetic factors that contribute to varying drug response, efficiency and toxicity. As mentioned before, SNPs occur in a variety of sites. This example reveals the importance of SNPs in pharmacogenomics:

Consider a drug and its metabolizing enzymes. An SNP exists in the gene coding for these enzymes which, if it takes on the mutant allele, leads to a nonsense mutation. During translation of the gene the nonsense mutation causes a premature truncation and results in a non-functional enzyme. This enzyme cannot play a part in the metabolism of the drug since the drug's metabolism pathway is disrupted. This enzyme may be critical in the cycle of the drug and lead to a lack of response. It is also possible that the enzyme does not play a major role in its metabolism, which causes a minor drop in the efficiency of the drug.

Recently, markers based on single nucleotide polymorphisms (SNPs) have become the focus of plant molecular genetics due to their abundance in the genomes and responsiveness to advanced detection formats and platforms. Many thousands of SNPs at many different loci in a given plant genome can now be identified reliably.