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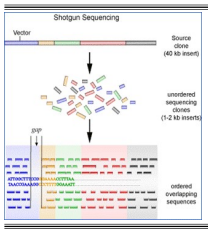

Overture of WGS and NGS

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Whole genome sequencing (WGS): Whole genome sequencing (also known as WGS, full genome sequencing, complete genome sequencing or entire genome sequencing) is ostensibly the process of determining the complete DNA sequence of an organism's genome at a single time. This entails sequencing all of an organism's chromosomal DNA as well as DNA contained in the mitochondria and for plants, in the chloroplast. In practice, genome sequences that are nearly complete are also called whole genome sequences. Inprinciple, full genome sequencing can provide the raw nucleotide sequence of an individual organism's DNA. However, further analysis must be performed to provide the biological or medical meaning of this sequence, such as how this knowledge can be used to help prevent disease. Methods for analysing sequencing data are being developed and refined. Because sequencing generates a lot of data (for example, there are approximately six billion base pairs in each human diploid genome), its output is stored electronically and requires a large amount of computing power and storage capacity. While analysis of WGS data can be slow, it is possible to speed up this step by using dedicated hardware. Rapidly dropping sequencing budgets and the capability to produce large volumes of data with today's sequencers make whole-genome sequencing a powerful tool for genomics research. Whole-genome sequencing has largely been used as a research tool but was being introduced to clinics in 2014. In the future of personalized medicine, whole-genome sequence data may be an important tool to guide beneficial interference.

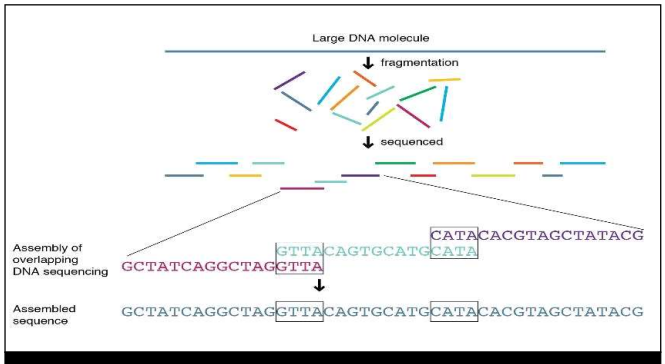

Fig. 1: Illustration of DNA sequencing

What is sanger sequencing? Sanger sequencing, also known as the "chain termination method," was developed by the English biochemist Frederick Sanger and his colleagues in 1977. This method is considered for defining the sequence of nucleotide base in a piece of DNA (commonlyless than 1,000bp in length). Sanger sequence with 99.99 per cent base accuracy is considered the "gold standard" for validating DNA sequences, including those already sequenced through next-generation sequencing (NGS). Sanger sequencing was used in the Human Genome Project to determine the sequences of relatively small fragments of human DNA (900 bp or less). These remains were used to assemble larger DNA fragments and ultimately, whole chromosomes.

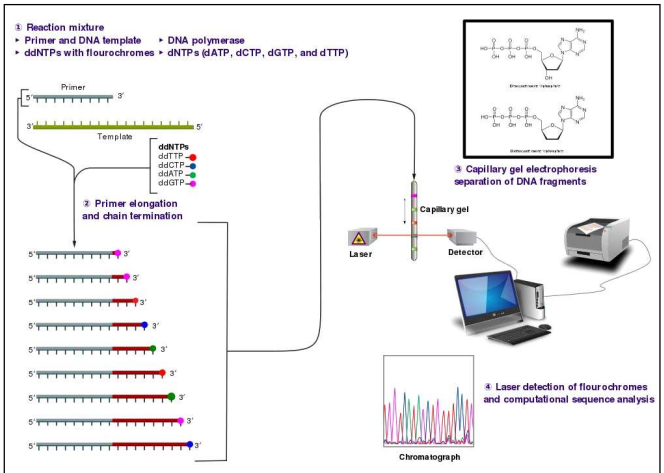

Fig. 2: Sanger sequencing method of WGS

Next-generation sequencing: Next-generation sequencing (NGS) refers to the deep, high-throughput, in-parallel DNA sequencing technologies developed a few decades after the Sanger DNA sequencing method first emerged in 1977 and then dominated for three decades. The NGS technologies are different from the Sanger method in that they provide massively parallel analysis,

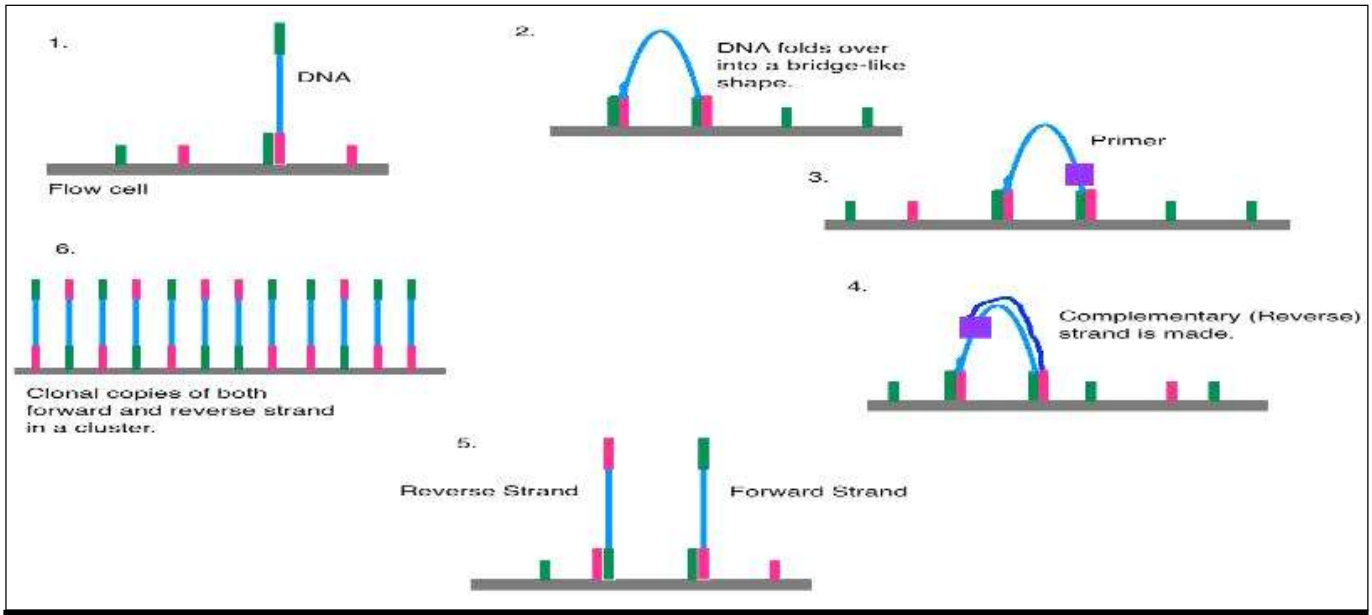

Fig. 3: NGS sequencing method of WGS

extremely high-throughput from multiple samples at a much-reduced cost. Millions to billions of DNA nucleotides can be sequenced in parallel, yielding substantially more throughput and minimizing the need for the fragment-cloning methods that were used with Sanger sequencing. The second-generation sequencing methods are characterized by the need to prepare amplified sequencing libraries before undertaking to the sequence of the amplified DNA clones, whereas third-generation single molecular sequencing can be done without the need for creating the time-consuming and costly amplification libraries. Next-Generation Sequencing (NGS) is a powerful platform that has enabled the sequencing of thousands to millions of DNA molecules simultaneously. This powerful tool is revolutionizing fields such as personalized medicine, genetic diseases and clinical diagnostics by offering a high throughput option with the capability to sequence multiple individuals at the same time.

Use of next-generation sequencing (NGS) in agriculture filed:

– The advent of next-generation sequencing (NGS) technologies holds the potential to dramatically impact the crop improvement process. NGS enables whole-genome sequencing (WGS) and re-sequencing, transcriptome sequencing, metagenomics, as well as high-throughput genotyping, which can be applied for genome selection (GS).

– Genome sequencing has the power to revolutionize food security and sustainable agriculture including food safety, animal, plant and public health, reducing the risks from disease outbreaks and improving agriculture through the effective plant and animal breeding.

– Next-generation sequencing (NGS) provides a powerful tool for the discovery of domestication genes in crop plants and their wild relatives. The accelerated domestication of new plant species as crops may be facilitated by this knowledge. The re-sequencing of domesticated genotypes can identify regions of low diversity associated with domestication.

Use of NGS in medicines plants:

– Recent advances in next-generation sequencing (NGS) technologies have accelerated research on medicinal plants with reduced cost and efforts. NGS technologies not only provide an opportunity for high throughput whole-genome sequencing, but they also facilitate direct RNA sequencing.

– We utilized sanger and next-generation sequencing (NGS) for taxonomic authentication of fifteen herbal supplements representing three different producers from five medicinal plants: Echinacea purpurea, Valeriana officinalis, Ginkgo biloba, Hypericum perforatum and Trigonella foenum-graecum. The experimental design included three modifications of DNA extraction, two lysate dilutions, Internal amplification control and multiple negative controls to exclude background contamination. Ginkgo supplements were also analyzed using HPLC-MS for the presence of active medicinal components.

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