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Role of Next Generation Sequencing (NGS) in Plant Disease Management: A Review

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Abstract:

A high throughput technique used to determine a part of the nucleotide sequence of an organism's genome is called next generation sequencing (NGS). NGS has been Proven revolutionary in genomics. Clinical diagnostics, Plant diseases diagnostic and other aspects of medical are now made possible by sequencing. Techniques of NGS: there are different techniques of NGS which are being used in real life sciences i.e., Illumina sequencing, Pyrosequencing, Roche 454 sequencing and Ion torrent sequencing. All vintage methods like culturing in bacterial, fungal, and viral samples are being suppressed by next generation sequencing. The potential for random metagenomic sequencing of sick samples to find potential pathogens has surfaced with the development of next-generation high-throughput parallel sequencing technology. NGS enables highly efficient, rapid, low-cost DNA or RNA high-throughput sequencing of plant virus and viroids genomes, as well as specific small RNAs generated during infection. Although this technique is not so much familiar in the field of plant diseases. However, its widespread application in agronomic sciences will make it possible to create solutions to future food-related challenges that involve biotic stress.

Keywords: *NGS, Plant, Pathogen, Diagnosis*

Introduction

A high throughput technique used to determine a part of the nucleotide sequence of an organism's genome is called next generation sequencing (NGS). This methodology is also known as second generation sequencing. This Method uses the sequencing technologies of DNA which are good capable of processing numbers of DNA sequences in parallel. Next generation sequencing also called Also massively parallel sequencing. Simply an advanced DNA, RNA sequencing technique to sequence big or large genome sample at accurately, and quickly as compared to sanger technique.

Next-generation sequencing techniques utilizing methylation, RNA, or DNA sequencing left a great impact on life science. As compared to sanger traditional method which is also called first generation sequencing technique, NGS cost lower and time saving techniques with gigabase range of base pairs. The utilization of molecular biology and genetic information by different species to reproduce and live with or without disease, mutations, and diversity within their population networks and changing surroundings is now more or much more studied by NGS than ever before.

The history of DNA sequencing starts from 1965 when Robert Holley was awarded the Nobel Prize as he sequenced first tRNA, in 1986. In his Nobel Prize speech, he said, "without minimizing the pleasure of receiving awards and prizes, I think it is true that the greatest satisfaction for a scientist comes from carrying a major piece of research to a successful conclusion" (Holley, 1968) From that different technologies are being used to sequence whole genome. In 1977, a scientist named Sanger sequenced the first-time whole genome of a virus (Berg, 2014). Human genome was sequenced in 20 years with 3 billion dollars expenditures. Different techniques got evolutional to reach next generation sequencing. In a many of previous reviews (Mardis, 2011, Margulies et al., 2005, Lam et al., 2012) history of next generation was published in detailed.

Techniques of NGS: there are different techniques of NGS which are being used in real life sciences.

Illumina sequencing

Clonal array building and its unique reversible terminator technology are used in Illumina's sequencing approach for efficient and accurate large-scale sequencing. The process identifies DNA bases while also including them in a chain of nucleic acids. The specific fluorescent signal that each base produces as it is integrated into the growing strand establishes the DNA sequence's order (Quail et al., 2008). Sample-specific barcodes must be incorporated into sequencing libraries in order to parallelize target capture and sequencing for numerous samples while maintaining the ability to identify the origin of each sequence. This technique outlines a quick and dependable process for creating barcoded ("indexed") sequencing libraries for the