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Emergence of Sequencing Technology: A Revolution in Genomic Research

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Perspective Article

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In any organism, to conduct studies genome-wide, genomic information is important. The knowledge of genome information helps scientists to find new genes, functional elements, expression profiles [1] and genetic changes [2] among different tissues of an organism. Hence, sequencing has gained demand which led to many different methods of sequencing. Sequencing refers to determining the exact order of nucleotides from short segments such as genes [3,4] or regulatory elements to entire genome [5-9]. In 1973, very first time, Maxam and Gilbert introduced laboratory intensive sequencing method based on chemical modification of DNA. Due to involvement of hazardous chemicals in Maxam and Gilbert method, high efficient first generation sequencing called Sanger sequencing or chain termination method has gained popularity and it was the first standard method of sequencing developed in 1975. It uses dye labeled nucleotides and capillary electrophoresis in contrast to radioactive labeled nucleotides in Maxam and Gilbert method. Using this technology, after thirteen years of effort, human genome project was completed in 2003. To reduce the time and cost involved in Sanger method, there was an investigation for new methods called second generation or Next generation sequencing (NGS) technologies [10] involving less cost and reduced time. Next generation sequencing (NGS) technology came into market around ten years ago. The development of Next generation sequencing (NGS) technology in the last decade has had tremendous impact on the way the scientific research and clinical investigations are being carried out [11,12]. These improvements in NGS technology has led to reduction of time and cost per base and increase in length of read i.e., Sequencing is done in parallel and massive scale. Several NGS methods have been in use among which the three most commonly used are such as Illumina (Sequencing-by-synthesis) [13], Roche 454 (Pyrosequencing), and SOLiD (Sequencing-by-ligation). The other popularly used NGS technique next to these three methods is ion torrent technique [14].

The applications of NGS span numerous research areas pertinent to biology [15-17]. Comparative studies at genome level which were impossible before are imaginable now and can be conducted in small span of time [18]. It helps to sequence whole genome in less time on a large scale at low cost. The NGS technology has been applied to variety of research areas

which include whole exome studies [19,20], personalized medicine [21], mutational studies [22,23], studying genetic disorders [24], annotating new sequences [25,26], Identification of genes and regulatory elements involved in pathological processes [27-30], forensic research, agricultural genomics [31], environmental genomics [32] and diagnosis of diseases at molecular level [33-35]. Detail analysis of transcriptome is now possible with NGS. The RNA studies [36-38] have been possible not only on mRNA but also on tRNA and rRNA. The research is currently into developing third generation sequencing methods [39-43] which reduce the costs involved and time consumed.

With the discovery of large amount of genetic information, the need for computational methods [44-48] to manage [49], retrieve, process, and analyze sequence data [50-52] and ensure correct interpretation [53] are in high demand.

REFERENCES

1. Minaeva E and Ermilova E. Sequencing and Expression Analysis of the Gene Encoding PII Signal Protein in Chlorella Variabilis NC64A. J Plant Biochem Physiol. 2015;3:142.
2. Chang KCN et al. Validation of Next Generation Sequencing Cancer Panels for Clinical Somatic Mutation Profiling- Identification of Source of Variations and Artifacts using FFPE Tissues. Next Generat Sequenc & Applic. 2014;1:109.
3. Emma L Edghill et al. Sequencing of Candidate Genes Selected by Beta Cell Experts in Monogenic Diabetes of Unknown Aetiology. Journal of the Pancreas. 2010;11:14-17.
4. Martins IM et al. Isolation and Sequencing of Actin1, Actin2 and Tubulin1 Genes Involved in Cytoskeleton Formation in Phytophthora cinnamomi. J Plant Pathol Microb. 2013;4:194.
5. Mabey T and Honsawek S. Genome Wide Association Studies and Next Generation Sequencing Technologies in Osteoarthritis. Next Generat Sequenc & Applic. 2014;1:108.
6. Blum HE and Oexle K. Clinical Interpretation and Implications of Whole Genome Sequencing. Next Generat Sequenc & Applic. 2014;1:105.
7. Gryganskyi AP and Muszewska A. Whole Genome Sequencing and the Zygomycota. Fungal Genom Biol. 2014;4:e116.
8. Blum K et al. Genome Wide Sequencing Compared to Candidate Gene Association Studies for Predisposition to Substance Abuse a Subset of Reward Deficiency Syndrome (RDS): Are we throwing the Baby Out with the Bathwater?. Epidemiol. 2014;4:158.
9. Hens K. Whole Genome Sequencing of Childrenâ€™s DNA for Research: Points to Consider. J Clinic Res Bioeth. 2011;2:106e.
10. Fox EJ et al. Accuracy of Next Generation Sequencing Platforms. Next Generat Sequenc & Applic. 2014. 1:106.
11. Santucci-Pereira J, Barton M, Russo J. Use of Next Generation Sequencing in the Identification of Long Non-Coding RNAs as Potential Players in Breast Cancer Prevention. Transcriptomics. 2014;2:104.
12. Ebomoyi EW. Establishing Genome Sequencing Centers, the Thematic Units in the Developing Nations and the Potential Medical, Public Health and Economic Implications. J Drug Metab Toxicol. 2011;2:108.
13. Li D et al. Transcriptome Analysis of Tessellated and Green Leaves in Paphiopedilum Orchids Using Illumina Paired- End Sequencing and Discovery Simple Sequence Repeat Markers. J Plant Biochem Physiol. 2014;2:136.
14. Veras AAO et al. Efficiency of *Corynebacterium pseudotuberculosis* 31 Genome Assembly with the Hi-Q Enzyme on an Ion Torrent PGM Sequencing Platform. J Proteomics Bioinform. 2014;7:374-378.

15. Dirisala VR. Illuminating the Role of Next-Generation Sequencing Approaches in Transgenesis. Clon Transgen. 2013;2:e104.
16. Sheehan D. Next-Generation Genome Sequencing Makes Non-Model Organisms Increasingly Accessible for Proteomic Studies: Some Implications for Ecotoxicology. J Proteomics Bioinform. 2013;6:e21.
17. Weier HUG. Rags to Riches: Re-viewing the Tumor-specific Expression of Long Non-coding DNA and Satellite DNA Repeats in Humans in the Era of Next Generation Sequencing. J Data Mining Genomics Proteomics. 2012;3:e101.
18. Chang KCN et al. Validation of Next Generation Sequencing Cancer Panels for Clinical Somatic Mutation Profiling- Identification of Source of Variations and Artifacts using FFPE Tissues. Next Generat Sequenc & Applic. 2014;1:109.
19. Lin H et al. A New Homozygous ABCB4 Mutation Identified in Two Chinese Siblings Based on Exome Sequencing. J Genet Syndr Gene Ther. 2014;5:243.
20. LaRusch J et al. Whole exome sequencing identifies multiple, complex etiologies in an idiopathic hereditary pancreatitis kindred. JOP. 2012;13:258-262.
21. Blum K et al. Genome Wide Sequencing Compared to Candidate Gene Association Studies for Predisposition to Substance Abuse a Subset of Reward Deficiency Syndrome (RDS): Are we throwing the Baby Out with the Bathwater? Epidemiol. 2014;4:158.
22. Ye F et al. Detection of Mitochondrial Mutations in Cancer by Next Generation Sequencing. Next Generat Sequenc & Applic. 2014;1:102.
23. Santos RCV et al. Current Trends in Sporotrichosis. Fungal Genom Biol. 2012; 2:e105.
24. Russo CD et al. Comparative Study of a CGH and Next Generation Sequencing (NGS) for Chromosomal Microdeletion and Microduplication Screening. J Clin Case Rep. 2014;4:455.
25. Zhao S. Clinical Applications of Next Generation Sequencing. J Health Med Informat. 2014;5:e129.
26. Sharma S and Madan M. Detection of Mutations in rpob Gene of Clinically Isolated M. tuberculosis by DNA Sequencing. J Mycobac Dis. 2014;4:156.
27. Ye F et al. Detection of Mitochondrial Mutations in Cancer by Next Generation Sequencing. Next Generat Sequenc & Applic. 2014;1:102.
28. Li J et al. The Contribution of Next Generation Sequencing Technologies to Epigenome Research of Stem Cell and Tumorigenesis. Human Genet Embryol. 2011;S2:001.
29. Niba ET et al. Targeted Next-generation Sequencing Reveals a Homozygous Nonsense Mutation in CAPN3 that Causes Limb-girdle Muscular Dystrophy Type 2A First in Vietnam. J Mol Biomark Diagn. 2014;5:194.
30. Al-Haggar MMS et al. Bioinformatics in High Throughput Sequencing: Application in Evolving Genetic Diseases. J Data Mining Genomics Proteomics. 2013;4:131.
31. Sablok G et al. Next Generation Sequencing for Better Understanding Alternative Splicing: Way Ahead for Model and Non-Model Plants. Transcriptomics. 2013;1:e103.
32. Bihari Z. Current Trends in Bioremediation and Biodegradation: Next-Generation Sequencing. J Bioremed Biodeg. 2013;4:e138.
33. Mishra H and Kumar V. Pharmacovigilance: Current Scenario in a Tertiary Care Teaching Medical College in North India. J Pharmacovigilance. 2013;1:109.

34. Li J et al. The Development of Cancer Genome Research and its Clinical Opportunity brought by Next Generation Sequencing. J Health Med Informat. 2012;S1.
35. Russo CD et al. Comparative Study of a CGH and Next Generation Sequencing (NGS) for Chromosomal Microdeletion and Microduplication Screening. J Clin Case Rep. 2014;4:455.
36. Shyr D and Li CI. Sample Size Calculation of RNA-sequencing Experiment-A Simulation-Based Approach of TCGA Data. J Biomet Biostat. 2014;5:198.
37. Sablok G et al. Next Generation Sequencing for Better Understanding Alternative Splicing: Way Ahead for Model and Non-Model Plants. Transcriptomics. 2013;1:e103.
38. Roy A et al. A Case Study on Discovery of Novel Citrus Leprosis Virus Cytoplasmic Type 2 Utilizing Small RNA Libraries by Next Generation Sequencing and Bioinformatic Analyses. J Data Mining Genomics Proteomics. 2013;4:129.
39. Blighe K et al. Next Generation Sequencing in the National Health Service England: A Pipeline that Completely Agrees with Sanger. J Cancer Sci Ther. 2014; 6:406-410.
40. Krstic PS. Challenges in Third-Generation DNA Sequencing. J Nanomed Nanotechol. 2012;3:e116.
41. Lu C and Yu P. Biological and Solid-State Nanopores for DNA Sequencing. Biochem Pharmacol (Los Angel). 2012;1:e109.
42. Srinivasan S and Batra J. Four Generations of Sequencing- Is it Ready for the Clinic Yet?. Next Generat Sequenc & Applic. 2014;1:107.
43. Claudia V et al. Targeting Cancer Related Genes by Multiplex PCR Followed by High Throughput Parallel Sequencing. Int J Genomic Med. 2014;2:115.
44. Ananth Prabhu G and Ganesh Aithal. Parallelization of Biological Gene Sequencing Technique with Optimized Smith Waterman Algorithm. 2014.
45. Francesco F et al. SAM-Profiler: A Graphical Tool for Qualitative Profiling of Next Generation Sequencing Alignment Data. J Comput Sci Syst Biol. 2013;6:188-193.
46. Roy A et al. A Case Study on Discovery of Novel Citrus Leprosis Virus Cytoplasmic Type 2 Utilizing Small RNA Libraries by Next Generation Sequencing and Bioinformatic Analyses. J Data Mining Genomics Proteomics. 2013;4:129.
47. Samir Kumar Bandyopadhyay. Data Hiding Using DNA sequence Compression. Journal of Global Research in Computer Science. 2011.
48. Al-Haggar MMS et al. Bioinformatics in High Throughput Sequencing: Application in Evolving Genetic Diseases. J Data Mining Genomics Proteomics. 2013;4:131.
49. Miller NA et al. Management of High-Throughput DNA Sequencing Projects: Alpheus. J Comput Sci Syst Biol. 2008;1:132-148.
50. Lipsky EB et al. Node-Oriented Workflow (NOW): A Command Template Workflow Management Tool for High Throughput Data Analysis Pipelines. J Data Mining Genomics Proteomics. 2014;5:159.
51. Davis C et al. mblast: Keeping up with the Sequencing Explosion for (Meta) Genome Analysis. J Data Mining Genomics Proteomics. 2013;4:135.
52. Datta S et al. Statistical Analyses of Next Generation Sequence Data: A Partial Overview. J Proteomics Bioinform. 2010;3:183-190.

53. Bhensdadia DV et al. Isolation, Molecular Characterization and Insight into the Genome Sequence of E. Coli Bacteriophage ADB-2 from Poultry Fecal Sample. Next Generat Sequenc & Applic. 2014;1:101.