MEDDOCS Open Access Publisher

ISSN: 2578-8760

Journal of Nanomedicine

Open Access | Review Article

New Challenges in Infectious Disease Research: Innovations in the Research Paradigm

***Corresponding Author(s):** Shalala Zeynalova

Ministry of Agriculture of the Azerbaijan Republic, 3-rd Biosafety level, Central Reference Laboratory, Baku, Azerbaijani.

E-mail: zeynalovaeddm@gmail.com

Received: Jan 01, 2022

Accepted: Feb 14, 2022

Published Online: Feb 18, 2022

Journal: Journal of Nanomedicine

Publisher: MedDocs Publishers LLC

Online edition: http://meddocsonline.org/

Keywords: Bioinformatics; Lipidomic; Sequence; NGS.

Abstract

Recent developments in our understanding of communicable diseases have been marked by remarkable progress. The COVID 19 pandemic has increased the importance of research and study of biological hazards. According to the FAO reports, 75% of emerging diseases are zoonoses. The main reasons for the spread of infectious diseases are globalization, climate change and the intensification of agriculture. H1N1, H5N1, Acute Respiratory Syndrome (SARS), dengue fever, bacterial infections, recurrent Salmonella epidemics in the food industry are a constant threat to society.

New research strategies and tactics need to be applied to minimize threats. Timely detection of unidentified or unforeseen pathogens is a key factor in disease control. A wide range of diagnostics, new equipment is available to identify pathogens based on phenotypic or genetic characteristics. The scientific approaches of the past, including work with individual genes and proteins specific to molecular biology, are not sufficient to solve these problems. The article describes biotechnologies and new challenges, reducing biological hazards, creating vaccines, and researching genes.

Introduction

New research strategies and tactics need to be applied to minimize threats. Timely detection of undetected or unforeseen pathogens is a key factor in disease control. A wide range of diagnostics, equipment to identify pathogens based on phenotypic or genetic characteristics are available [1]. The scientific approaches of the past, including work on individual genes and proteins specific to molecular biology, are not sufficient to solve these problems [2-5].

The first decade of the twenty-first century saw significant innovations in technology and computational methods. The Systems Virology Center (http://www.systemsvirology at the University of Washington.org) has comprehensively analyzed the progression or modification of acute respiratory viral infection by molecular and cellular event modeling, pathogen-host interactions, and cellular response networks. This study focuses on the highly pathogenic H5N1 avian influenza virus and Coronavirus Associated with Acute Respiratory Syndrome (SARS-CoV). For each virus, the level of pathogenicity of the host organism against H5N1 and the created attenuated virus is analyzed and modeled [6]. These new tools provide an almost comprehensive view of complex biological systems and can provide a deeper understanding of pathogen-host interactions, respectively [4,7,8].

There are systems needed to successfully implement a biological system approach: technologies, computational methods and genome data, and so on. Next Generation Sequencing (NGS) - technologies such as next generation sequences have

Cite this article: Zeynalova SK. New Challenges in Infectious Disease Research: Innovations in the Research Paradigm. J Nanomed. 2022; 5(1): 1051.

emerged. Conditions were created for long RNA and mRNA that encompassed microRNAs and did not encode or encode common transcriptomes. This suggests that RNAs that do not encode a previously unappreciated RNA class for a long time may play an important role in the body's immune response to viral infection [9].

Determination of nucleotide sequence-DNA sequencing

Sequence - method for determining the ordering of nucleic acids. This is the determination of the exact sequence of nucleotides present in a particular DNA and RNA molecule. NGS can be used to analyze DNA and RNA samples and is an important tool in functional genomics. In the last decade, the use of nucleic acid has become important for research and clinical laboratories around the world. The first major project - the Human Genome Project, worth $ 3 billion and 13 years of operation, was completed in 2003. The Human Genome Project was implemented with the first generation and is known as the Sanger sequence. Sanger sequence (chain termination method), developed in 1975. The method developed by Edward Sanger was considered the gold standard. Once the first human genome sequence is complete, the demand for cheaper and faster sorting methods is greatly increased. This requirement has led to the development of second generation sequencing methods or New Generation Sequencing (NGS). Based on the Sanger sequence, it uses DNA-dependent polymerase to create additional velocity in a single-stranded DNA template [10-12]. In each reaction, a single primer complementary to the template initiates DNA synthesis from its 3′ end. DNA monomers, such as deoxynucleotides or nucleotides, form phospho-diether bonds between the 3′ hydroxyl and 5′ tri-phosphate groups of the growing end of the primer, one after the other, depending on the pattern. Each reaction represents four di-deoxynucleotide mixtures (A, G, T, and C), one for each DNA base [13,14].

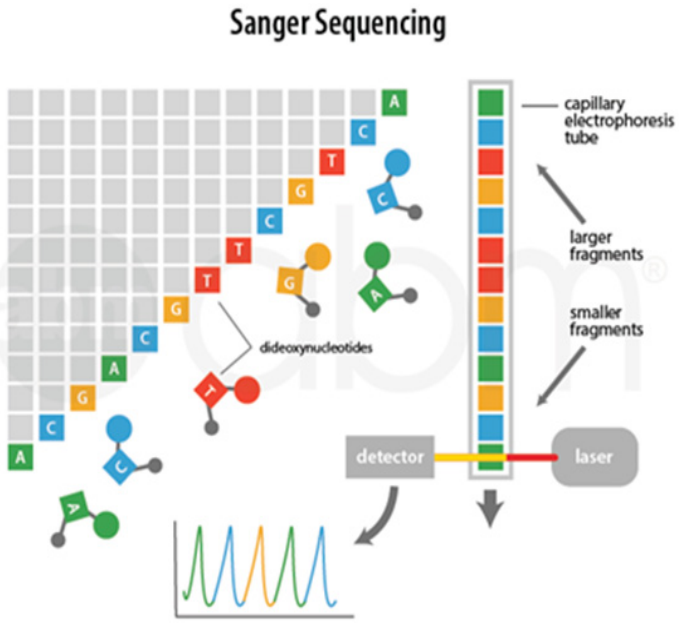

Figure 1: Principles of Sanger sequencing. (http://old.abmgood.com/marketing/knowledge_base/next_generation_sequencing_Introduction).

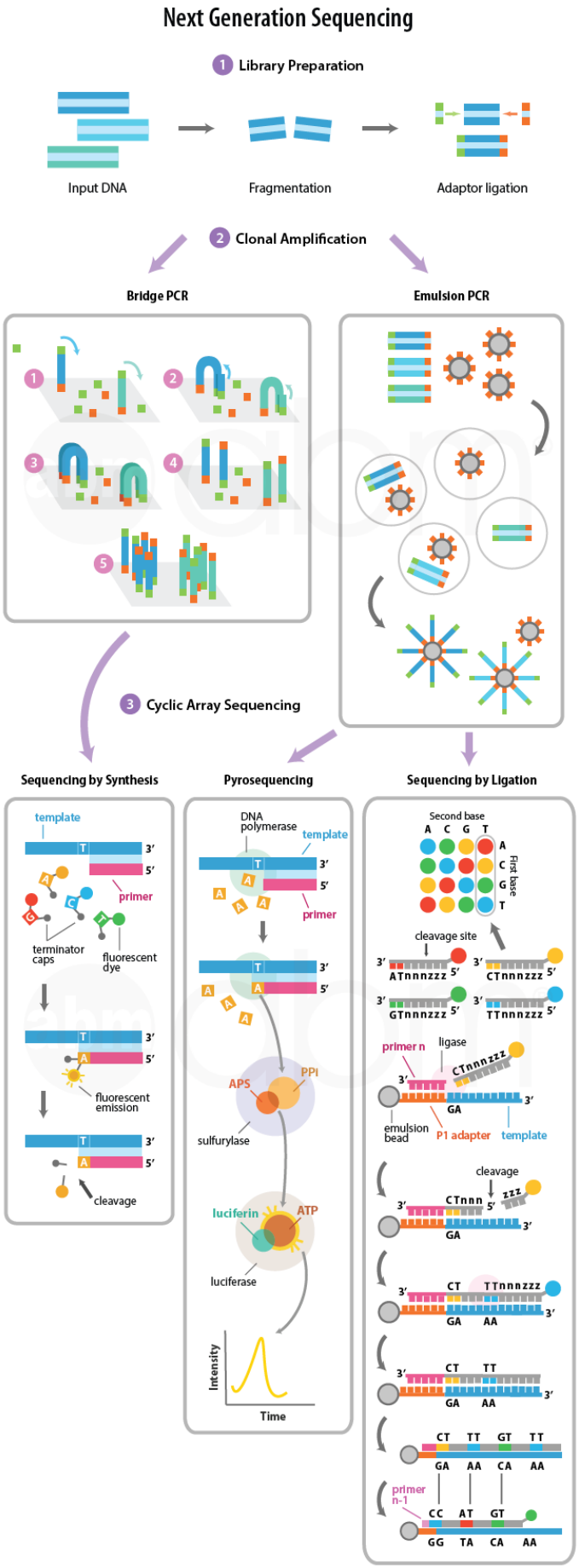

Figure 2: Description of similarities and differences between different New Generation Sorting platforms. https://www.ebi.ac.uk/training-beta/online/courses/functional-genomics-ii-common-technologies-and-data-analysis-methods/next-generation-sequencing

NGS platforms make massive parallel sequences, and during this time, millions of DNA fragments are arranged in a single sample unison. Mass parallel sequencing technology simplifies high-order sequencing as a whole and allows genome sequencing in less than a day. Several NGS platforms have been developed over the past decade: low-cost, high-performance sequences. Two of the most widely used platforms are used today in research and clinical laboratories: Life Technologies Ion Torrent Genome Machine (PGM) and Illumina MiSeq. While each NGS platform is unique in how sequencing is implemented, Ion Torrent PGM and Illumina MiSeq have a similar basic methodology that includes template development, sequencing, imaging, and data analysis. The creation of these and other NGS platforms has made sequencing more accessible to the laboratory, rapidly increasing the volume of research and clinical diagnostics performed with nucleic acid sequencing [10,11,15,].

The importance of NGS technology

NGS can be used to analyze DNA and RNA samples and is a popular tool in functional genomics. Unlike microarray methods, NGS has several advantages, including approach-based approaches:

- No prior knowledge of the genome or genomic features is required
- Offers a single nucleotide solution that allows the detection of related genes (or traits), alternatively combined transcripts, allelic gene variants, and single nucleotide polymorphisms.
- Higher dynamic range of the signal
- Requires less DNA / RNA as input (nanograms of materials sufficient) higher repeatability [https://old.abmgood.com/marketing].

The concept of bioinformatics

The main goal is to create a current and future perspective on the opportunities and challenges associated with the application of mass parallel sequencing technologies in veterinary medicine, especially to focus on applications that have the potential to affect disease control and management. The development of high-transmittance molecular technologies and related bioinformatics has dramatically changed the ability of scientists to produce, manage, and analyze large amounts of genomic, transcriptomic, and proteomic data. A clear example of this step change is represented by the amount of DNA sequence data that can be generated using Next-Generation Sequencing (NGS) platforms. Data are obtained, emailed and stored using computational methods [16,17].

Proteomic technologies and metabolomics, glycomics, lipidomics and phosphoproteomics began to develop rapidly. For example, identify commonalities and differences in the body's response to different respiratory viruses; to characterize regulatory and metabolic networks that adapt the pathogen to intracellular persistence.

The identification of these pathogens - metagenomic studies, such as the detection of microbiomes, whole genomes and viral variants - is carried out through various applications [18,19]. For all applications, it is important to compare genomic sequence data with known ones. Comparative genomic analyzes are used at the molecular level to facilitate taxonomic classification, functional interpretation, and study genomes and evolutionary processes [20].

Omika technologies

Omic technologies based on mass spectrometry - i.e. proteomics, metabolomy and lipidomy - provide the study of organisms at the molecular level. At the same time, advances are being made in a comprehensive, functional understanding of the biological consequences associated with cellular heterogeneity in medicine, cancer research, and various research fields, such as microbiome science. Similarly, recent developments in protein and peptide separation efficiency and highly accurate mass spectrometry have helped to increase the identification and quantity of proteins in a particular sample. These advances in biotechnology have been increasingly applied to the study of infectious diseases in animals and have begun to revolutionize the study of biological and evolutionary processes at the molecular level [20,21].

Studies have demonstrated the value of NGS technologies for molecular characterization, from the metagenomic characterization of unknown pathogens or microbial communities to molecular epidemiology and the evolution of viral quasicycles. Moreover, high-transmittance technologies now allow a detailed study of host-pathogen interactions at the level of genomes (genomics), transcriptomes (transcriptomes) or proteomes (proteomics). Integrative OMICS and system biology offer solutions that allow the detection of single-nucleotide-linked genes (or traits), alternatively combined transcripts, allelic gene variants, and polymorphisms.

Proteomics is the study of biological processes by analyzing the state or expression of protein in cells or tissues [22]. Proteins are ubiquitous life blocks and are composed of peptides, a chain of amino acids formed by translating mRNA. Contains 20 amino acids abbreviated by a single letter. Peptides can be described as a string of letters corresponding to amino acids. Although protein sequences are determined by DNA sequences, post-translation protein modifications (e.g., acetates, phosphates, lipids, etc.) are not easily predicted. These modifications rapidly diversify and regulate / complicate protein function and cellular protein content, and are characteristic of most cellular processes and diseases. Therefore, the purpose of MS-proteomics is to provide information on the impossibility of determining the DNA sequence - individual protein concentrations and post-translational modifications https://omics.pnl.gov/metabolomics-and-lipidomics.

Lipidomics is the systematic analysis of lipids (fat molecules) and their interactions. A science is still in its infancy; however, a science that promises to revolutionize biochemistry. Lipids are divided into eight categories that share common physical and chemical properties, and there are currently approximately 38,000 documented lipids.

Metabolomics is the study of metabolomics, which are small molecular products of cellular regulatory pathways that can provide an image of cell physiology. Metabolites are much smaller than proteins and smaller than most lipids. The small size precludes direct overlap of some techniques used in proteomics or lipidomic, but can generally be analyzed in similar ways. Lipids can be classified as subtypes of metabolites; however, mass spectrometers consider lipids to be different from metabolites because they must be treated analytically separately [11].

Summary

Growing global populations, rapid migration, immunotherapy/deficiencies, resistance to pathogen-directed therapists, and global climate change are leading to the emergence of new pathogens and increased threats from known pathogens. Thus, there is a great deal of attention in the study of many bacterial and viral infectious diseases, such as Staphylococcus aureus, Mycobacterium tuberculosis, Influenza, Dengue, SARS-CoV, and their effects on humans [14,28]. Proteomics, chemistry, proteomics, metabolism and lipidomic characterize the expansion of our ideas about pathogens, the formation of our goals for new drugs and the response of the owner to the pathogen.

Acknowledgments

The author would like to acknowledge to the Steven Van Borm, Sciensano, Belgium Senior Scientist, Virology Department.

References

1. Buchan BW, Ledeboer NA. Emerging technologies for the clinical microbiology laboratory.Clin. Microbiol. Rev. 2014; 27: 783-822.
2. Ashraf U, Ye J, Ruan X, Wan S, Zhu B, et al. Usutu virus: an emerging flavivirus in Europe. Viruses. 2015; 7: 219-238.
3. Jones BA, Grace D, Kock R, Alonso S, Rushton J, et al. Zoonosis emergence linked to agricultural intensification and environmental change. Proc.Natl Acad. Sci. USA. 2013; 110: 8399-8404.
4. Wilson ME. Travel and the emergence of infectious diseases. Emerg. Infect. Dis. 1995; 1: 39-46.
5. Tatem AJ, Rogers DJ, Hay SI. Global transport networks and infectious disease spread. Adv. Parasitol. 2006; 62: 293-343.
6. Cotten M, Watson SJ, Kellam P, Al-Rabeeah AA, Makhdoom HQ, et al. Transmission and evolution of the Middle East respiratory syndrome coronavirus in Saudi Arabia: a descriptive genomic study. Lancet. 2013; 382: 1993-2002.
7. Phan TG, Kapusinszky B, Wang C, Rose RK, Lipton H, et al. The fecal viral flora of wild rodents. PLoS Pathog. 2011; 7: 1-9.
8. Phan TG, Vo NP, Boros A, Pankovics P, Reuter G, et al. The viruses of wild pigeon droppings. PLoS ONE. 2013; 8: 1-12.
9. Woolhouse ME, Gowtage-Sequeria S. Host range, emerging and reemerging pathogens. Emerg. Infect. Dis. 2015; 11: 1842-1847.
10. Sanger F. Nucleotide sequence of bacteriophage phi X174 DNA. Air, GM and Barrell, BG. Nature. 1977; 265: 687-695.
11. Sanger F, Nicklen S, Coulson AR. DNA Sequencing with chain-terminating inhibitors. s.l. Proc Natl Acad Sci USA. 1977; 74: 5463-5467.
12. Schbath S, Martin V, Zytnicki M, Fayolle J, Loux V, et al. Mapping reads on a genomic sequence: an algorithmic overview and a practical comparative analysis. J. Comput. Biol. 2012; 19: 796-813.
13. Liao YC, Lin HH, Sabharwal A, Haase EM, Scannapieco FA. MyPro: a seamless pipeline for automated prokaryotic genome assembly and annotation. J. Microbiol. Meth. 2015; 113: 72-74.
14. Simpson JT, Pop M. The theory and practice of genome sequence assembly. Annu. Rev. Genomics Hum. Genet. 2015; 16: 153-172.
15. Sachse K, Moebius P. Molecular typing tools: from pattern recognition to genome-based algorithms. Meth. Molec. Biol. 2015; 1247: 287-310.
16. Hatem A, Bozdag D, Toland AE, Catalyurek UV. Benchmarking short sequence mapping tools. BMC Bioinformatics. 2013; 14: 184.
17. Rosseel T, Lambrecht B, Vandenbussche F, Berg T, Van Borm S. Identification and complete genome sequencing of paramyxoviruses in mallard ducks (Anas platyrhynchos) using random access amplification and next generation sequencing technologies. Virol. J. 2011; 8: 463.
18. Verbist BM, Thys K, Reumers J, Wetzels Y, Van der Borght K, et al. VirVarSeq: a low-frequency virus variant detection pipeline for Illumina sequencing using adaptive base-calling accuracy filtering. Bioinformatics. 2015; 31: 94-101.
19. Wan Y, Renner DW, Albert I, Szpara ML. VirAmp: a galaxy-based viral genome assembly pipeline. GigaScience. 2015; 4: 19.
20. Ratnere I, Dubchak I. Obtaining comparative genomic data with the VISTA family of computational tools. Curr. Protoc. Bioinformatics. 2009; 10: 1061-1067.
21. Benjamin HM, Laura SO, Julian RM, Julie AK, McDonald A. The implementation of omics technologies in cancer microbiome research. Ecancermedicalscience. 2018; 12: 864.
22. Scott W, RobinsonaAvid M, AfzalbDavid P. Leaderc Handbook of Pharmacogenomics and Stratified Medicine, Chapter 13 - Bioinformatics: Concepts, Methods, and Data. Academic Press. 2014: 259-287.