Avicenna Journal of Clinical Microbiology and Infection
doi:10.15171/ajcmi.2019.01 2019 February;6(1):1 http://ajcmi.umsha.ac.ir

Letter to Editor

Role of Novel Sequencing Approaches in General Health Development

Ramin Mazaheri Nezhad Fard[1]

Department of Pathobiology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
Email: r-mazaherinf@sina.tums.ac.ir

Received: 1 February 2019, Accepted: 17 February 2019, ePublished: 28 February 2019

Dear Editor,

In April 2003, the Human Genome Project (HGP) was completed after 13 years of continuous genome analysis using Sanger sequencing (1). More than 20 institutions, companies, and laboratories were involved in HGP. Although this is commonly acknowledged as a historical improvement in human genetic studies, there are still hundreds of genomic gaps left which must be resolved. Furthermore, the project costed nearly $3 billion (roughly $5 billion considering inflation)! Nowadays, however, such enterprise can be finished only in one day, at a cost a little more than a grant per sample, thanks to next generation sequencing (NGS) platforms. NGS (e.g. Roche, Illumina, SOLiD) and the further novel technology of next-next generation sequencing (e.g. Pac-Bio SMRT) have obviously fueled genetic studies, especially molecular cancer studies, at dramatically lower costs (2). This significantly contributes to the human health improvement and facilitates finding some new treatment modalities for the old diseases (e.g. cancers). The sequencing platforms and related computational biology analyses have even created a novel terminology called dry labs. Dry labs are laboratories where computational/applied mathematical analyses are carried out using computer-generated models to simulate biological processes in silico. Today, projects such as 1000 Genomes Project and 100 000 Genomes Project are programmed to help us better understand human genome and various deficiencies originating from it. Moreover, several other projects such as Human Connectome Project, Human Cytome Project, Human Microbiome Project, Human Proteome Project, and Human Variome Project are carried out to address various factors involving human health/disease balance.

One of the main genetic study areas that can mostly be benefited from is microbiome. Although the vital role of microbiota in eukaryotes has been known for a long time, recent metagenomic studies have amazingly revealed that this role is not limited to what we previously assumed. Generally, human body is the host of approximately 100 trillion microbial cells (3). This number is nearly 10 times greater than the number of human somatic cells and even stars within the Milky Way Galaxy! More than 10 000 microbial species have already been identified in human body. Since nearly 95% of the human microbiota reside in gastrointestinal tract, it is suggested that more than 90% of all diseases are somehow associated to the oral microbiota population. Examples include a wide variety of diseases from simple constipation, obesity, and irritable bowel syndrome to metabolic and mental disorders, autoimmune deficiencies, and cancers. However, this is not limited to those in gastrointestinal tract, as other microbiota such as those in respiratory tract or urogenital system are linked to local or general diseases. Thus, metagenomic studies conducted on the basis of novel sequencing approaches on microflora of human body seem to be a master key for the currently closed medical doors.

Ethical Approval
Not applicable.

Conflict of Interest Disclosures
None.

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