Challenges and Prospects of Establishing a Genome Sequencing Laboratory in Bangladesh

*Rahman DA

In 2001, first human genome was sequenced, the cost to sequence a single humangenome was approximately US$3 billion and it required years of dedicated and collaborative efforts from laboratories across the globe.[1] Then next-generation sequencing (NGS) technology was invented in 2005 and enter into the sequencing market in 2007, the cost to sequence a full human genome at 30X coverage has dropped substantially from US$1 million in 2008 to US$10,000 in 2011. Now a whole humangenome can be sequenced for less than US$1000.[2]

Next-generation sequencing (NGS) technologies are high throughput genome sequencing method for extracting the genetic information in massive amounts and within reasonable costs. Despite the remarkable increase in speed and decrease in costs, establishing a genome sequencing facility with NGS technology remains challenging, to the developing world country like Bangladesh, in part because the estimated cost of establishing a facility ranges between $100 K to $700 K U.S. dollars.[3] In addition, infrastructure and computational facilities are required. Furthermore, the limited funding for the operational costs of such facility (cost of reagents and instrument maintenance) is one of the main factors that limit genome sequencing facilities in Bangladesh. This is not affordable for most educational, research and clinical laboratories in Bangladesh.

Genome sequencing is an interdisciplinary field that requires knowledge in biology, chemistry and big data analysis also known as bioinformatics. The personnel working in this field require extensive training. Developing countries, however, have limited capacities in education and human development. Insufficient training, therefore, is a formidable obstacle that limits the use of such facilities.[4]

The genomic data manipulation and analysis tools i.e bioinformatics tools are an indispensable component of genomic analysis. Although several tools are distributed under different open source licenses, many advanced tools are commercialized by companies or require complicated and expensive licensing procedures to be used. Such expenses are frequently beyond the abilities of institutions in the developing world.[5] In addition, genomic data download and manipulation require very fast (at least 25 MBps) and stable internet connections that are not always available in Bangladesh. Moreover, the development of genomic lab infrastructure is complicated. It requires strictly controlled temperature, humidity, earth voltage with stable and uninterrupted power supply. Moreover, negative pressured infrastructure required for molecular diagnosis of infectious diseases.

The discipline of bioinformatics has developed rapidly since the complete sequencing of the first genomes in the 1990s. There are many challenges faced in bioinformatics education that are commonly encountered throughout the world. Lack of trained bioinformaticians, lack of bioinformatics infrastructure, and lack of internet speed are the main obstacles in this field. The lack of access to genome sequencing and particularly bioinformatics facilities in Bangladesh makes outsourcing the only available option to utilize these technologies, at least for the initial period. However, outsourcing companies provide

low-quality services in many developing countries. Typically, the companies do expensive and time-consuming process that may take up to several months for bioinformatics analysis. Furthermore, the entire outsourcing process can fail at any stage, which wastes more time and cost.[6]

Now we are in the era of precision medicine whereas cancer management and patient outcome is dramatically improved. Cancer treatment is fine-tuned according to a patient's genome. This concept is known as personalized medicine also commonly referred as precision medicine. Now we can identify therapeutically actionable genetic lesions in some cancers by cancer NGS. One classic example is lung cancer, in which we can detect individual mutations and manage the patient in a personalized approach by means of using "targeted therapy." Moreover, the recent cancer classification is mostly based on their molecular signature which aids "targeted therapy."

Targeted therapy is a type of cancer treatment that uses drugs or other substances to precisely identify and attack certain types of cancer cells. A targeted therapy can be used by itself or in combination with other treatments, such as traditional or standard chemotherapy, surgery, or radiation therapy. Although expensive these targeted therapies are specific for cancer, having less side effects and overall excellent therapeutic outcomes than chemotherapy or radiotherapy.

Development of a targeted biomolecule or biomarkers for a specific cancer requires translational research (TR) and extensive clinical trials. TR describes a continuum of research in which basic science discoveries are utilized to prevent or treat human disease. That research aimed at improving utilization of proven therapies in clinical practice and community settings.[7] To determine if a biomarker can offer prognostic-predictive or predictive clinical utility, a prospective or retrospective exploratory analyses of clinical study data could be performed. This could be followed by a validation step in a well-designed randomized controlled clinical trials.[8] Without an accredited genome sequencing laboratory development of the targeted therapy is almost impossible.

Several challenges confronting researchers and scientists in developing countries like Bangladesh have delayed their ability to participate in the genomic revolution. While, many developing countries including India, South Africa, Mexico, and Brazil were able to make significant improvement in utilizing genomic technologies through the availability of sufficient funds, establishing institutions for genomics, and the training of personnel. However, the situation of Bangladesh is remaining unaltered.

References

1. Evans JP. The Human Genome Project at 10 years: A teachable moment. Genetics in Medicine. 2010 Aug; 12(8):477.
2. Kruglyak KM, Lin E, Ong FS. Next-generation sequencing in precision oncology: challenges and opportunities. Expert review of molecular diagnostics. 2014 Jul 1; 14(6):635-7.
3. El-Metwally S, Ouda OM, Helmy M. Next generation sequencing technologies and challenges in sequence assembly. Springer Science & Business; 2014 Apr 19; pp47
4. United Nations, 2014. Human Development Report 2014.pp192-196
5. El-Metwally S, Hamza T, Zakaria M, Helmy M. Next-generation sequence assembly: four stages of data processing and computational challenges. PLoS computational biology. 2013 Dec 12;9(12):e1003345.

6. Awad M, Ouda O, El-Refy A, El-Feky FA, Mosa KA, Helmy M. FN-identify: novel restriction enzymes-based method for bacterial identification in absence of genome sequencing. Advances in Bioinformatics. 2015; Pp2
7. Homer-Vanniasinkam S, Tsui J. The continuing challenges of translational research: clinician-scientists' perspective. Cardiology Research and Practice. 2012 Aug 9;pp1-2
8. Wang SJ. Biomarker as a classifier in pharmacogenomics clinical trials: a tribute to 30th anniversary of PSI. Pharmaceutical Statistics: The Journal of Applied Statistics in the Pharmaceutical Industry. 2007 Oct; 6(4):283-96.

**Dr. DM Arifur Rahman, Associate Professor (Histopathology), TMSS Medical College, Bogura.*
arifurrahmandm@gmail.com