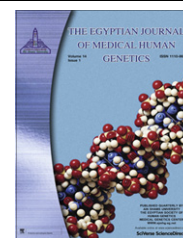




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CORRESPONDENCE

Sequencing *Closterium moniliferum*: Future prospects in nuclear waste disposal

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Abstract Genome sequencing can play a vital role in health and several other domains such as in nuclear outflow related environmental issues. The power of information derived out of sequencing has been used in the field of health care, evolutionary studies and for better understanding of the biological framework of life. Through the recent advancements in sequencing studies, now the researchers are aiming to use its power in non conventional areas. Here we have discussed on the importance of sequencing the *Closterium moniliferum* genome which will prove to be a future endeavour in nuclear cleanup and radioactive waste disposal.

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1. Introduction

DNA sequencing technologies have become an epitome of success for the discovery of the wide aspects of several genomic disorders. A remarkable feat has been achieved by the recent advancements in sequencing technologies that has revolutionized the conceptual foundations in a wide range of scientific fields including archaeology, anthropology, genetics, molecular biology, evolutionary genomics and forensic sciences. It all started with the advent of the Sanger Method of sequencing by Frederick Sanger in the 1970's. This led to an array of genome sequencing which enabled the complete genome sequencing of ϕ -x 174 bacteriophage which was then followed by

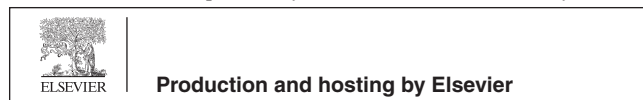
sequencing of several other organisms such as *Heamophilus influenzae*, *Caenorhabditis elegans*, *Saccaromyces cerevisiae*, *Escherichia coli*, *Drosophila melanogaster*, *Arabidopsis thaliana*, etc. This frenzy in sequencing has later enthused towards the most remarkable achievement ever made, through the mission popularly referred to as “*The Human Genome Project*”.

The past decade in genomics is acknowledged for some outstanding developments in the technological advances in sequencing techniques. Some of the highly efficient and time saving sequencing machines such as Illumina HiSeq 2000 and Solexa have replaced the old classical sequencing technologies. As of now, the techniques such as nanopore, fluorophore and DNA nanoball sequencing are considered as high throughput among those so far developed. Everyday growing genome sequence databases have mounted up around 3150 complete genome sequences which include 152 archeal, 2825 bacterial and 173 eukaryotic genomes [1]. The genetic blueprint of life forms has enabled us to gain a deeper understanding of life and helped to unravel the mystery and bust the myths such as “eukaryotes have more number of functional genes” or “Non coding DNA is total junk”.

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The scientific dream of sequencing and decoding “The Human Genome”, which still stands as one among the many endeavours of mankind and as a landmark event in scientific history, has commenced with clamour regarding its usefulness in the field of medicine. Although the scientific community believes that the results obtained and their applications in the field of medicine have been slow, in reality it has inspired some of the “big biology” efforts such as HapMap, ENCODE, Human Epigenome Project, 1000 genome project. It has further embarked upon a new era of genomics bringing about new developments in sequencing technologies, lowering costs and increasing the accuracy of results as well as developing methods and technologies for deciphering information from “omics” data. According to the latest NHGRI’s report, the cost of sequencing technologies are now outstripping the Moore’s law thereby setting the stage for the dawn of a new era [2].

2. Change in the scenario

Genome sequencing has the potential of answering some of the complex questions in various domains of science. Until now the power of information derived out of sequencing has been mostly used in the field of health care, evolutionary studies and for better understanding of the biological framework of life. It is evident from the nature of genomes that have been the choice for sequencing till now, that it mostly included model organisms, and disease related organism or organisms which occupy a promising position in the tree of life. But the obvious question which comes into one’s mind is that if the genome sequencing holds such potential then why it is not utilised in non conventional areas. Some big sequencing centres launched initiatives to address this question. For example, JGI is shifting its focus to use the power of genomics to solve other burning issues like energy crisis, environmental issues, pollution, green house emission capture etc. Some of the projects include sequencing of a biomass degrading fungus *Trichoderma reesei* [3] which secretes a biomass degrading enzyme, sequencing of the rhizosphere microbiomes of maize [4], *Arabidopsis* and a mustard relative known commonly as Drummond’s rockcress, as well as potential biofuel crop *Miscanthus* and wild prairie grasses, to understand the plant genetics involved in determining the microbial communities associated with plant species.

3. What should be sequenced?

The right choice of sequencing a particular genome would facilitate the future researches in environmental, pharmacogenomics, proteomics and in computational genomic studies [5–10]. The power of genomics is no longer limited to areas of health care and biology and can be channelized in any field to save and serve the society. In this context, one of the major concerns of the modern world is the disposal of nuclear waste obtained from nuclear reactors. The disasters like Chernobyl oil spills of 1987 and the most recent Fukushima nuclear disaster have imposed some serious questions over the security issues related to the use of nuclear energy. According to the reports from world nuclear association each year, nuclear power generation facilities worldwide produce about 200,000 m³ of low- and intermediate-level radioactive waste, and about 10,000 m³ of high-level waste and it is estimated

that around 5% of income obtained from nuclear energy is used for waste management but still radioactive waste management is the major concern.

If there was one genome that we could sequence it would be an organism that may have the potential to combat the issue of radioactive wastes. The sequenced data of such an organism would be able to pave the way for the development of a new technique/technology that could dispose radioactive wastes without posing as a biohazard to the environment. “*Closterium moniliferum*” is the organism which immediately strikes our mind. It is a freshwater green alga which belongs to the desmid order. Recent studies have shown that this alga has the property to selectively sequester ⁹⁰Sr from the radioactive waste [11]. The most common problem of the radioactive waste from nuclear reactors and accidental spills is that they contain high amounts of calcium in comparison to strontium making it more difficult to clean up strontium without also disposing the enormous amount of harmless calcium. Strontium 90 is also very dangerous to handle as it is very similar in size and properties to calcium. Hence biologic processes cannot differentiate them effectively and as a result it can be easily incorporated into various body parts and tissues like bone marrow, bones, and blood where the radiation that it emits can cause cancer. This alga has the unique ability to selectively remove strontium and barium from aqueous environment and store them in the form of crystals of barium strontium sulphate in its vacuole. It not only stores strontium but also differentiates it from calcium which is almost similar in its properties with strontium, thus providing a unique mechanism of selective sequestration which can prove to be a boon in radioactive waste management.

At present we are deficit in our knowledge about the mechanism of how this alga differentiates between different elements and selectively stores strontium and barium as sulphates in its vacuole. Ongoing studies suggest that the cell has its own inbuilt filter-like mechanism. Its cell wall is pervious to water containing all kinds of minerals/elements. Once inside the cell, the strontium and barium ions from the water are separated out based on atomic size (mechanism unknown) and are retained within a vacuole, and the remaining water is excreted out. As the concentration of sulphate ions is higher in the vacuoles it forms crystals of barium strontium sulphate rendering it in the form of harmless sulphate crystals.

The information obtained from whole genome sequencing has always been an important tool for knowing the genetic know-how of an organism. There are several examples where genomic data have proven their worth. For example the case of *Jatropha curcas*, a plant commonly known for oil bearing seeds, which is thought to be a potential candidate for the source of biodiesel. With the help of whole genome sequencing of this plant, the genes responsible for increased oil content in the seeds have been identified. It is proposed that enhanced expression of these genes can improve the quality as well as quantity of oil in the seeds, thus improving the overall quality of biodiesel obtained from the plant [12].

Once the genome of this alga is completely sequenced, its genome can be annotated for the genes involved in all major processes leading to mapping of all the biochemical and cellular networks and pathways. The information thus obtained from the “omics data” can then be simulated on the computational environment leading to enhanced understanding of its working machinery. This would help elucidate the molecular

mechanisms behind selective mobilisation of radioactive material by this organism. The findings obtained from the sequencing of this organism can also be utilised in the following ways:

- To enhance the selective sequestration property of the alga and thereby making it efficient by engineering its genetic makeup
- It can be modulated in such a way to adapt and function at extreme environmental conditions
- The knowledge of the mechanism of selective absorption by the alga can be used for designing a new and efficient method of radioactive waste treatment, as most advanced technologies like artificial neural networks are inspired from their biological counterparts.
- This could be a good learning exercise for us to be able to pick up the cue from nature for an adaptable and self-sustaining environment.

4. Conclusion

Genome sequencing can play a vital role in all dimensions even beyond health care and can also solve environmental issues. The technology is evolving rapidly and we are now capable enough to sequence any and every genome that sounds useful in any of the varied aspects of scientific research. The reduction in cost and increase in accuracy has increased our sequencing efficiency several folds leading to an exponential rise in the number of organisms sequenced every year. But the pile of data which are accumulating at this alarming pace has conjured some very obvious questions which need immediate attention by the researchers.

- We are lacking behind in the field of analysing the data obtained from the omics studies. Heavy focus on wide range sequencing has produced huge amounts of data that are yet to be analysed. Proper attention towards the analysis of available sequence data must be given before the lag between sequenced and analysed data reaches magnanimous proportions.
- With the advent of newer techniques and the evolution of existing technologies we must put in effort towards developing efficient algorithms and bioinformatic tools which divert our focus towards training the researchers who are working on sequence based genomic studies.
- The data being generated by the recent technologies are in terms of terra and gigabytes which require proper storage and infrastructural facilities such that the data obtained can be retained for a longer time.
- The number of organisms being sequenced is increasing day by day, although the cost of sequencing is dropping but still the amount spent is huge. So before sequencing a genome the cost vs. worth analysis is very necessary. This will not only lead to reduction in the number of worthless genomes

being sequenced but will also solve the problem of storage and availability up to a certain extent.

- Genome sequencing is no longer limited to a particular domain of science rather it has multidisciplinary applications. So there should be increased collaboration among different domains of science in order to obtain more fruitful results.

We learn by our experiences that nature has been known to adapt to all the adverse effects of mankind. It is time for us to learn to use this property of nature to have a safer and cleaner tomorrow through the concept of 'genomics for environment clean-up' and genome sequencing can prove to be a valuable asset towards this goal.

Conflict of interest

The authors declare that they have no conflict of interest

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