

Metagenomics - Redefining the Concept of Genome

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Science is endless. Discovery is incremental. Evolution is uninterrupted. A fraction of human population in the name of scientists, have explored a lot, which is enabling the remaining human population a comfortable and present scientific survival. However, their endeavors left the foundations for today's scientists, for the future scientific excellence. Observations led to questions, answered by theories and subsequent hypotheses. One excellent example of this is Charles Darwin's theory of evolution, which must be an opportunistic survey of biodiversity. It is a fact that the evolution still is a mere theory to the public. Therefore surveys for new data need to be taken to the next level.

Metagenomics is the one which is most important comprehensive contemporary survey technique revolutionized microbiology by paving the path for a cultivation-independent assessment and exploitation of microbial communities (Fungi, Bacteria and Viruses) present in complex ecosystems with the direct access to their genomes. Moreover, lab experiments are artificial and always needs to contextualize the results with environmental observation. Metagenomics is a most unrestricted and comprehensive approach for the survey of microbial biodiversity "...if I could start my life over, I would work in microbial ecology" Edward O. Wilson a contemporary scientist's statement proves the power of this approach.

Over the past three decades the scientists theorized and hypothesized that the global microbial community as a network is providing the vast range of services to the macro organisms in the

ecosystems. But it is again a challenge to produce the critical mass of potential data to enable the testing of the hypothesis without the aid of Metagenomics. Like Darwin, several large scale observational studies have aided the development of Microbial diversity. Global Ocean Survey (GOS), a marine metagenomic transect survey of the world's oceans, Earth Microbiome Project (EMP) which used the largest collection of samples have without a doubt, been the most authoritative microbial ecology surveys ever. Besides microbes, metagenomics is the only effective tool to analyze comprehensive populations of viruses that exist at 10 times the abundance of microbes in all ecosystems, so their characterization as drivers of gene exchange is equally necessary.

What actually important at this juncture of global interest on microbes is the balance between "what is possible to hypothesize and test, and what is known" which has been unexplored so far satisfying the truth "everything is everywhere, but the environment selects".

Therefore private organizations, funding authorities, supporting agencies globally should take the initiative of encouraging the discovery studies, identification and exploration of novel microbes in virtually all ecosystems at this time when the scientific community is realizing the truth which we know very little about the microbial world and their exploitation is piddling.

So, possibly the surveys like GOS, TARA and the EMP may harvest a following theory of evolution and some young scientists be the scions of Darwin as Evolution is uninterrupted.

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