

Editorial

Life Sciences is a multi-disciplinary subject, requires a systematic approach to query the survivability of life and dynamics of struggle. It do not allow swindles of interrogation, it requires a concrete evidence to envisage the underlying forces. Hitherto, our knowledge is very limited to comprehend the natural life and its fullest possibility. In a pinch of soil, a million bacteria, fungi, and viruses are there that articulates the enormous volumes of species richness. Our technology and knowledge can provides the chance to realize only 1% of the diversity itself, but 99 percent of the diversity still unexplored. To harness the gap, it strongly necessitated the invention of various methods to understand the microbial interactions. Since last 40 years, there is high priority in invention of most effective, reliable, fast, accurate methodology, and tools. Conventional methods are replaced with molecular technologies, which could deal with the signature molecules of life i.e DNA, RNA proteins and metabolites. However, capacity-building programmers equipped with conceptualization, understanding, training, handing, and analysis and reporting are the main. A scientific approach made to conduct, segregate, polish, and project the recent advances in the life sciences field in the form of a scientific journal.

The first paper “Current trends in designing of microbial enzymes; protein engineering, directed evolution and metagenomics approaches” by by S Jeevan Chandra and his scholars is a persistent version of the main concepts of molecular evolution. This paper ventures many advances in computational designing of enzymes. In view of the author, present knowledge about enzymes is not sufficient to realize the molecular architecture and evolution of peptides into the most splendid enzymes. “The miniature, subcellular biocatalysts, chemically proteins, but they behave strategically and meticulously”. Further, we must be update the knowledge on how to utilize the recent advances of directed evolution and metagenomics in understanding, discovery and synthesis of the novel artificial peptides, enzymes with added advantage, that can cater the present and future needs of the society. At the same time, academia and industrial sector at various levels should implement the capacity building and training to scientific community of life sciences is obligatory to achieve the sustainable goals of enzyme research for better tomorrow.

Vaddem Kiran Kumar from Central Pollution Control Board, Regional Directorate, Kolkata, conveys the uncultivable diversity conquers in the Ganga and its tributaries ecosystem. Metagenome analysis of various bacteria found in river Ganga and its tributaries - an integrative study. This review provides insights into how river Ganges is polluted. Ganges is the one of the holy and longest river in the world. Ganga is originates at Uttarakhand and travels to West Bengal before voiding into Bay of Bengal. The mighty Gangetic basin a great fertile basins and provides livelihood for millions of people, who dwell in on its outer banks. However, due to waste water contamination, there is high incidence of metal resistant and antibiotic resistant bacteria through water chain would eventually cause human infections which are untreatable. The present review aims at summarizing the various studies for identifying various contaminating bacteria with metagenomic methods. This would help in identifying the pollution hotspots and help in controlling the pollution of the river.

R. Kishore’s paper “A rare case of klinefelter's syndrome with ISO X chromosome’ this article projects the classical as well as the modern FISH-Fluorescent Insitu Hybridization with Cytovision. It explanations the

rarity of Klinefelter syndrome disease and the phenotype of subjects associated with isochromosome Xq. Klinefelter syndrome is important to provide meaningful genetic counseling. However, due to only further evaluation with a larger group of such patients would be able to determine more clearly the prevalence and clinical features and appropriate genetic counseling required.

Shikha Kapil and his scholars from University Institute of Biotechnology, Chandigarh University “Isolation of Bio-surfactant Exhibiting Bacteria from the Northern Regions of India and Their Phylogenetic Relationships” this paper reveals the effective methodologies to elucidate the Phylogenetic Relationships of novel Bio-surfactant producing bacteria.

Lavaynya and Pogu Srinivas in their article “Chemical analysis of renal stones in Telangana population” provides a greater insights into the renal crystals and its chemical composition. The article also throws light on gender wise discrepancies among the population.

Anuradha’s “Isolation of Keratonophilic fungi and related dermatophytes from the soil” explains the associaton of Keratonophilic fungi prevailing in the soil, they also explained the methodology to isolate and investigate. .

Raja Abhilash’s article explains various development and validation of new rp-hplc method for the quantitative estimation of secnidazole in tablet dosage form, A novel, rapid, sensitive, reverse phase High Performance Liquid Chromatography (RP-HPLC) technique was developed for the quantitative estimation of Secnidazole in bulk and tablet dosage form. The developed HPLC. method and validated according to the International Conference on Harmonization (ICH) guidelines with respect to linearity, accuracy, precision, specificity and robustness.

Shilpaveni and her colleagues enlighten the concept of drought resistance, they hythesized the “Role of rhizobacteria in induced drought resistance in crop plants”. Root associated microbes help to stabilize the phytobiont drought. At the same time plants regulate the composition of signature bacterial community. These microbes provide the carbon, nitrogen compounds, and other metabolites required to harness the drought.

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