EDITORIAL

Genomics of Extremophiles for Sustainable Agriculture and Biotechnological Applications (Part II)

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In the present scenario, increasing pollution and green house effect on climate are serious concerns that lead to extreme environment conditions. Therefore, the major aim of scientist is to resolve environmental issues in an economic and sustainable way. To deal with extreme conditions, extremophiles are safer option for scientist or industries. In industries, most of possesses are completed in extreme environment like temperature, pH, pressure *etc*. However, the majority of enzymes used in industrial process are derived from mesophilic microbes, few are from extremophiles. The mesophilic enzymes are unable to perform at extreme conditions in industrial processes [1]. Thus, the need of extrmophilic enzymes is increasing globally to meet out the industrial requirements. In addition, industrial processes are also performed with chemical compounds or enzymes, which are very cost effective and harmful. In this context, extremophilic microbes can be used directly as a cell or enzymes (extremozymes) to carry out chemical reaction in an eco-friendly manner [2].

Extremophiles are used in food, pharmaceutical, textile, beverages and agricultural industries. Extremophilic microbes possess different types of enzymes and metabolites, which can work on harsh condition and make them perfect for the industrial purposes. These microbes are used at different physical conditions *i.e.* elevated level of extreme temperature, pH, heavy metal contamination, organic solvents *etc* [3]. We can improve the efficiency of extremophiles by using modern technologies such as genetic engineering and protein engineering. The demand of extremophilic products is very large in global market. The fulfilling of this demand requires recombinant technology for large scale production and also purification [3]. However, there is still need to explore multiple extremophilic microbes that can be used for society.

In continuation to first part of this special issue, this part describes different extremophilic microbes and their role in biofuel production, industrial dye degradation and abiotic stress tolerance. Topic is also included on metagenomic analysis of plastic degrading bacteria. In this sense, a review article by Fongaro *et al.* [4] described the importance of muiti-omics tools including (genomics, transcriptomics, proteiomics and metabolomics) in exploitation of extremophile microorganism and their novel metabolites for bioenergitic application. Authors discussed about different types of extremozymes including, thermophilic, psychrophilic, piezophilic, acidophilic and halophilic in details. In another review, Purohit *et al.* [5] documented about metagenomic approach for exploration of microbial population involved in plastic biodegradation. Metagenomic approach helps in harnessing predominant uncultured microbial species and also opens up the scope for mining genes or enzymes (hydrolases, laccase, *etc.*) engaged in polymer or plastic degradation. The comparative metagenomic study allows us to engineer microbial community to speed up the degradation process. Authors have targeted different metagenomic approach based on 16S V2-V6 regions for identifying plastic degrading microbes from different habitat.

In a research article, Ghosh *et al.* [6], studied the diversity of the psychrotolerant actinomycetes sp. nov., in the Bay of Bengal and recovered cold active industrial and pharmaceutical biomolecules. In this study, authors have isolated cold-adapted actinomycetes from 1200 mts below the surface in Bay-of-Bengal. A total number of 37 novel actinomycetes from 17 distinct groups were characterized on the basis of phenotypic and genotypic level. The major dominant group was *Streptomyces*. The optimum growth of isolated strains was observed at 15°C to 20°C and also able to survive at 4°C. All the recovered isolates were able to produce extracellular enzymes including amylase, cellulase, lipase, pectinase, and L-asparaginase and also showed antagonistic activity.

In another study, Mawad *et al.* [7] have applied microbial consortium including *Pseudomoans aeruginosa* and *Aspergillus flavus* for the degradation of Disperse Blue 64 (DB 64) and Acid Yellow 17 (AY 17) dyes. The consortium was able to possess higher ability to degrade dye even at 300mg/L as compared to individual one. This microbial consortium and their derived metabolites were also able to promote *Vicia faba* and *Triticum vulgaris* germination and health of seedlings in *in-vitro* assay.

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Chatterjee *et al.* [8] studied the abiotic stress tolerance mechanism of Cyanobacteria through Alr0765 protein study of *Anabaena* PCC7120. Alr0765 is a novel CBS-CP12 domain protein that has function to provide protection against stress through involving cellular energy mechanism and iron homeostasis. The gene expression of *Alr0765* was found to increase in *Anabaena* PCC7120 treated under heat, arsenic, cadmium, butachlor, salt, mannitol (drought), UV-B, and methyl viologen stresses. Further study with FTIR confirmed the binding of Alr0765 with ATP, ADP, AMP and NADH. The same protein was also able to accumulate iron in *E. coli* cells upon heterologous expression. The ROS content and total cellular H_2O_2 content was reduced when Alr0765 was expressed.

AUTHOR'S CONTRIBUTIONS

All authors AV, JS, HBS, contributed in writing this Editorial article for the research topic "Genomics of extremophiles for sustainable agriculture and biotechnological applications".

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