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Metagenomic Study for the Diversity Analysis of Extremophiles from Hot Water Springs of India

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Abstract

In extreme environment conditions the flourishing microbial community have a specific mechanism for heat tolerance as they are able to grow in those extreme conditions. Due to global climate change heat stress has becomes one of the major problems in agriculture leading to decrease in crop growth, productivity and yield. To gain insight in the tolerance mechanism in microbes, the genes involved in the heat tolerance mechanism in extremophiles can serve as a valuable resource.

Hot water springs harbour a large diversity of microorganisms. There is not sufficient information on bioprospecting of thermo-tolerant genes from hot water springs. In India there are many thermal hot water springs which are not been studied yet. The present investigation was designed to study the diversity of extremophiles from hot water springs and screen them for the presence of genes related to thermo tolerance.

Water samples were collected from three different hot water springs, that are, Bakreshwar, West Bengal; Tattapani, Himachal Pradesh and Talvriksha, Rajasthan. Temperature of the water was 72° C, 63° C and 43° C respectively. Metagenomic DNA was isolated and purified from the water samples. Identification of microbes inhabiting the spring water was carried out using 16S rRNA gene sequences. 16S rRNA gene specific primers were used to amplify 16s rDNA and was cloned in pGEMT vector. *In-silico* analysis showed the presence of both Archaea and Bacteria in the spring water. PCR based screening for the presence of genes related to thermo-tolerance is underway. These genes can be used to transform crops plants and make them heat tolerant.