Global environment concerns and solid waste management complications have generated much curiosity in the development of biodegradable plastics that hold the desirable physical and chemical properties of the conventional synthetic plastics. Polyhydroxyalkanoates are biodegradable polyesters which are synthesized by many bacteria. They are accumulated intracellularly as carbon and energy reserves under certain conditions. The major contributor to PHA production cost is carbon substrate, therefore it is desirable to design and use products that are reusable, recyclable or compostable. In pursuit of new bioactive entities, investigations are being expanded to marine habitats including marine sediments and organisms. In the present study, the soil sample was collected from unexploited coastal area Sethubavachatram, located in east coast of Thanjavur District at four different seasons viz, post monsoon, summer, premonsoon and monsoon were analysed. Determination of 25 diverse bacterial species in marine soil by culture method showed the predominance of 13 bacterial genera such as *Melissococcus* sp., *Marinococcus albus* sp., *Salinococcus* sp., *Rohella* sp., *Oscillospira* sp., *Saccharococcus* sp., *Sulfidobacillus* sp., *Brucella* sp., *Plannococcus* sp., *Edwardsiella* sp., *Brochothrix* sp., *Veillonella* sp., and *Syntrophococcus* sp. Seasonal variations of soil physico-chemical parameters includes pH, electrical conductivity (dsm⁻¹), organic carbon (%), organic matter (%), available carbon(%), nitrogen (%), phosphorous (%), available micro nutrients (ppm), calcium, Zinc, copper, iron, sodium and manganese were investigated. There was a significant impact of pH, organic carbon (%), organic matter (%) and available macro nutrients (%) on bacterial diversity; seasonally was revealed by correlation at positive significance (P<0.01) level. Then the efficacy of PHA accumulating bacterial isolates were primarily screened by Sudan blank staining and confirmed by acridine orange fluorescence staining based on intensity. KSN1 *Brochothrix* sp., KSN2 *Edwardsiella* sp., KSN5 *Bacillus* sp. KSN6*Oscillospira* sp. and KSN7 *Saccharococcus* sp. were screened as PHA positive.
KSN1 Brochothrix sp., KSN2 Edwardsiella sp., KSN5 Bacillus sp., KSN6 Oscillospira sp. and KSN7 Saccharococcus sp. accumulated PHA yields of 65.41% (CDW 11.84±0.01 g/L), 68.12% (CDW 11.58±0.11 g/L), 71.47 % (CDW 15.31±0.01 g/L), 59.87% (CDW 10.86± 0.22 g/L), 61.48 % (CDW 11.22± 0.02 g/L) respectively. Among the five, three isolates such as KSN1 Brochothrix sp., KSN2 Edwardsiella sp. and KSN5 Bacillus sp. accumulated more PHA that necessitate to study for further. Followed by quantification of PHA, KSN1 Brochothrix sp., KSN2 Edwardsiella sp., KSN5 Bacillus sp. were chosen as resourceful PHA producers. In our proposed study, KSN1 Brochothrix sp. and KSN2 Edwardsiella sp. were evidenced for the first time can accumulate more PHA. To enhance the efficiency of bacterial isolates to accumulate more PHA, UV mutagenesis was performed. Optimization of different parameters such as pH, temperature, and incubation period are evaluated. Some agro industrial wastes, molasses, paddy chaff, coconut oilcake, coir pith and vermicompost are used as a cheap carbon sources. Among which, molasses was chosen as the best carbon source as KSN5 Bacillus sp. yielded 95% of PHA with 20.54±0.14 g/L CDW in presence of molasses. Some nitrogen sources, yeast extract, malt extract, casein, ammonium nitrate and ammonium sulphate were used to make further assessment. Among the nitrogen sources, ammonium sulphate served as the best supplement for 73.81% (CDW 12.18±0.01 g/L) PHA accumulation by KSN5 Bacillus sp. The PHA obtained from these isolates was validated by TLC, GC-MS and TGA. Then molecular confirmation of nominated bacterial species was determined by 16S rRNA gene sequencing. (NCBI Gen Bank accession number: KC346293, KC346294, KM370132 respectively). That was further endured for phylogenetic analysis, secondary structure and restriction sites prediction.

Key words: PHA (Polyhydroxyalkoanates), UV mutagenesis, TLC, GCMS, TGA.