Microbial Biodiversity and Their Functions Involved in the Efficient Degradation of COD in Potato Waste Water

Professor Yang Qian

Professor, Supervisor, Biotechnology, School of Life Science and Engineering

Agorinya Sarah

Biotechnology, School of Life Science and Engineering

Abstract:

Food processing industries produce a lot of waste water during processing, resulting in the accumulation of high organic matter content in the form of COD, which is highly unsuitable to the environment and receiving water bodies when disposed off without treatment. This has called for the use of more ecofriendly methods in waste water treatment, of which microorganisms play a key role in biological waste water treatment. This study aimed at isolating microorganisms from sludge samples that were used in treating potato processing waste water and further using the isolates, in a fermentation process to ascertain their COD removal abilities. Potato processing waste water was prepared in the laboratory using potatoes that had been crushed with water in a blender to obtain the juice. The microorganisms were isolated using culture technique under anaerobic and aerobic conditions and were preliminarily identified through biochemical characterization and by PCR, using 16Sribosomal RNA sequencing. The microorganisms identified were made up both bacterial and fungal species including *B. licheniformis, B. subtilis, B. haynesii, B. sonorensis, B. velezensis*, *Streptomyces echinatus, Pseudomonas fragi, Pseudomonas parafulva, Paenibacillus cookie strain, Cryptococcus sp, Saccharomyces sp , Candida sp, Aspergillus sp and Rhodotorula sp*. Bacterial species were the dominant species making up 69% of isolates while fungal species made up 31%. 49% of the isolates belonged to the phylum Firmicutes which comprised all of the Bacillus species, making it the most dominant species. The second dominant phylum was Ascomycota which contained 18% of the isolates including *Candida* and *Saccharomyces* species. Phylum Proteobacteria (15%) was the third dominant phylum and was made up of two species; *Pseudomonas parafulva* and *Pseudomonas fragi.* Other phyla included Actinobacteria, Basidiomycetes and Basidiomycota respectively.

Single microbial species which were used in the fermentation process achieved COD removal efficiency of between 79.30% - 92.56% after 72 hours. Saccharomyces, Candida and B. licheniformis achieved 92.56%, 91.54% and 91.33% COD removal respectively. The highest recorded COD removal efficiency during the fermentation process was however achieved using three different microbial consortia made of only bacterial species, only fungal species and a mixed consortium of both fungal and bacterial species. The highest COD removal of 95.97% was achieved by the mixed consortium. This was followed by a 91.56% removal by the fungal consortium and an 88.95% removal by the bacterial consortium.

It can therefore be concluded from this study that the most effective way of COD removal is through a combination of different microorganism.

Keywords:

Microorganism, Bacterial, Fungal, Anaerobic, COD.