

Abstract

Co-digestion of water hyacinth (WH) (*E. crassipes*) with ruminal slaughterhouse waste (RSW) has the potential for improving biogas production by complementing process parameters. This study evaluated microbial communities in co-digestion of WH with RSW at 32°C by isolation, phenotype analysis, DNA extraction and PCR amplification of the 16S rRNA genes. Digestion of WH and RSW separately exhibited lag times of 5 to 20 days that were associated with pH drop to acidic zone. The pH drop was attributed to rapid production of volatile fatty acids by acidogenesis process without corresponding consumption by methanogenesis. Co-digestion at 30% RSW maintained alkaline pH and increased biogas yield for WH from 47 to 95% of the 42.1 L CH₄/kg observed for RSW suggesting synergy in the co-digestion. Morphologies of colonies isolated from the reactors were dominated by short and long rods bacilli with some cocci, and streptococcus mainly in WH samples. About 77% of the isolates were Gram positive, suggesting dominance of Firmicutes phyla that includes *Bacillus* genus. Molecular analysis observed a shift in microbial community during the acidic lag phase from *Bacillus* genus to acetogenic bacteria *Lysinibacillus* and *Solibacillus* genera that consume volatile acids increasing pH. Recovery of alkaline conditions resulted in emergence of diverse species of *Bacillus* sp. associated with fermentation and syntrophic processes that included *Bacillus aerophilus*, *Bacillus pumilus*, *Bacillus cereus*, *Bacillus thuringiensis*, *Bacillus licheniformis*, *Bacillus glycinifermentans*, and *Bacillus aquimaris*. Co-digestion of WH with RSW collated processes parameters and constrained drop in pH to alkaline levels conducive for growth of *Bacillus* sp.