

Bacterial community structure and biochemical changes associated with composting of lignocellulosic oil palm empty fruit bunch

ABSTRACT

Bacterial community structure and biochemical changes during the composting of lignocellulosic oil palm empty bunch (EFB) and palm oil mill effluent (POME) anaerobic sludge were studied by examining the succession of the bacterial community and its association with changes in lignocellulosic components by denaturing gradient gel electrophoresis (DGGE) and the 16S rRNA gene clone library. During composting, a major reduction in cellulose after 10 days from 50% to 19% and the carbon content from 44% to 27% towards the end of the 40-day composting period were observed. The C/N ratio also decreased. A drastic change in the bacterial community structure and diversity throughout the composting process was clearly observed using PCR-DGGE banding patterns. The bacterial community drastically shifted between the thermophilic and maturing stages. 16s rRNA clones belonging to the genera *Bacillus*, *Exiguobacterium*, *Desemzia*, and *Planococcus* were the dominant groups throughout composting. The species closely related to *Solibacillus silvestris* were found to be major contributors to changes in the lignocellulosic component. Clones identified as *Thermobacillus xylanilyticus*, *Brachybacterium faecium*, *Cellulosimicrobium cellulans*, *Cellulomonas* sp., and *Thermobifida fusca*, which are known to be lignocellulosic-degrading bacteria, were also detected and are believed to support the lignocellulose degradation.

Keyword: Composting; Lignocellulose degradation; Denaturing gradient gel electrophoresis; 16S rRNA gene clone library