ABSTRACT

Traditional microbiological techniques do not represent the scope of the entire microbial diversity in nature. However, metagenomics paves the way for culture independent assessment and exploitation of microbial communities present in complex ecosystems. The metagenome of the microbes is also a major resource for prospecting biocatalysts of industrial importance. Cellulase, a major industrial enzyme sought after in this work, for which both culture dependent and independent (metagenomic) methods were used. Following the preliminary morphological and biochemical characterization of microbes, (bacterial) genomic DNA was isolated from the cellulase positive bacterial isolates. As an initial step towards metagenomic library construction, DNA was isolated from different soil and cow dung samples. A modified method of DNA isolation and purification was applied in view of the problem of humic acid co purification with that of sample DNA. The procedure could yield quality DNA with less humic acid content. Isolated DNA samples were successfully digested with *Eco*R1 and *Hind* III restriction endonucleases and electrophoresed in 0.8% agarose gel for their subsequent use in gene library construction.