Characterisation and numerical analysis of the microbial community in raw baker's yeast factory effluent

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Abstract

Microbial counts on 3 different batches from the balancing tank sediment, as well as from the concentrated and general effluents from a baker's yeast factory were determined on 3 media under aerobic, facultative and anaerobic conditions. The microbial enumeration data varied considerably (4.2×10^3 to 2.1×10^8 cfu/ml), with the aerobic counts on the "richer" media generally being higher. A total of 326 microbial strains were isolated, of which 28 isolates were yeast strains. The prevalent strains isolated under aerobic conditions were identified as *Pseudomonas paucimobilis, Acinetobacter Iwoffii* and *Bacillus licheniformis.* The majority of strains isolated under facultative anaerobic conditions were identified as *Acinetobacter Iwoffii, Pseudomonas paucimobilis* and *Citrobacterfreundii.* The prevalent anaerobic bacterial community consisted mainly of *Lactobacillus acidophilus, Clostridium beijerinckii* and *Eubacterium limosum.* The overall similarity of the isolates, based on 74 phenotypic characters, was determined using the Sokal and Michener coefficient. The prevalent bacteria clustered prominently within a few large clusters. The wide distribution and variety of bacteria isolated, reflected the complexity of the raw baker's yeast effluent ecosystem. It is, however, clear that baker's yeast effluent cannot be ignored as a source of bacterial contamination with potential health implications.

Introduction

The release and subsequent treatment of waste streams place tremendous responsibilities on modern waste management practices. It is expected that as waste technology becomes more varied and sophisticated, specific microbial treatment systems for particular effluent types will be developed, using naturally occurring or genetically engineered micro-organisms. Strong emphasis must therefore be placed on the biological components as part of the biotechnological approach to solve environmental problems (Verstraete and Top, 1992). Microbial identification and characterisation of the interacting species in natural or man-made environments is thus an indispensable step towards the understanding of microbial communities. Microbial investigations are also a prerequisite for hazard assessment and the prediction of the success of *in situ* cleaning or treating procedures (Kampfer et al., 1991).

Baker's yeast factories produce a high-strength and very complex effluent which is difficult to degrade. Anaerobic digestion has successfully been used to treat these types of effluents (Van der Merwe and Britz, 1993). However, when the results obtained by these researchers are examined, it is clear that only a part of the raw effluent is readily degraded during the digestion process. This is due to the easily metabolised compounds that are removed during the yeast fermentation process, leaving only the recalcitrant compounds for further utilisation by the anaerobic digester community. Efficient anaerobic digestion systems, therefore, require highly selective and very specific microbial populations which, in turn, are dependent on the composition of the substrate feed.

Extended studies on the culturable micro-organisms and their role within an ecosystem are often neglected (Kämpfer et al., 1991). However, research has been done on the characterisation of microbial communities present in anaerobic digesters while treating different substrates (Ney et al., 1990;Fulthorpe et al., 1993). In contrast, little or no data exist on the taxonomic and substrate utilisation profiles of microbes present in raw effluents, as well as on the identification of bacterial species that may be involved in the pre-degradation of these effluents. A thorough knowledge of the microbial community present in the raw substrate may be the key to enhancing the start-up period and the overall efficiency of the anaerobic digestion process.

The aim of this study was to quantify, characterise and identify the members of the microbial community present in raw baker's yeast effluent.

Materials and methods

Baker's yeast effluent

Two types of baker's yeast effluents were used for the microbial studies: a concentrated effluent with an average chemical oxygen demand (COD) value of 76.8 *g/l,* collected during the first separation process; and a general effluent, with an average COD of 32.8 *gll,* obtained from the yeast factory balancing tank (Table 1). The composition of the effluent was determined using standard methods described in Van der Merwe and Britz (1993).

Media

Three media were used for the enumeration and isolation and these included Nutrient-medium (NA, Merck), MRS-medium (MRS, Merck) and Yeast-medium (YA). The YA-medium consisted of 10.0 *g/l* dried baker's yeast which was boiled for 15 min. The pH of the media was adjusted to 6.5 and 16.0 *g/l* agar was added for solid media preparations. Anaerobic counts were done on the same 3 media and colonies were then transferred to peptone yeast glucose (PYG) medium (Gerhardt et al., 1981) for further purification. The anaerobic media were prepared anaerobically using the serum bottle modification (Miller and Wolin, 1974).

Enumeration and isolation

Three different batches from the concentrated and from the general effluent, as well as from the sediment of the balancing tank of the baker's yeast factory, were sampled once a month, over a period of

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