

Ash microbiology: a molecular study

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ABSTRACT

South African fly ash is a fossil fuel by-product and is managed either wet (dams) or dry (dumps). In the case of dry handling, ash is conditioned with approximately 10% waste water to minimise dust during transport. Dust suppression on the dump is maintained by irrigation with reverse-osmosis-brine from a mine-water-based cooling water treatment. The brine is sodium chloride based having high sulphates (>10700mg/l), a pH of 6 – 7 and an electrical conductivity of 25 000 – 30 000µs/cm. Due to the nature of its production and its final properties (>1700°C, pH > 11), ash is considered to be sterile. However, the addition of a nutrient rich waste water, for conditioning and dust suppression irrigation, creates an ideal environment within the dump for microbial extremophiles. Various ash samples were collected from the dump at different points, indicating different ages, and at different depths throughout the dump. DNA was extracted from these samples and was amplified by polymerase chain reaction, to obtain amplicons of partial 16S and ITS genes for analysis of both pro- and eukaryotes, respectively. PCR amplicons were separated on a denaturing gradient gel electrophoresis gel that distinguishes between microbial species on the basis of genetic sequence. Resulting amplicon bands were excised, reamplified and sequenced in order to tentatively identify microbial species. Various genera of bacteria and fungi were distinguished within ash samples, and the possible contribution of their metabolism to ash composition is now being studied.

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