

2nd World Congress on

Beneficial Microbes: Food, Pharma, Aqua & Beverages Industry

September 22-24, 2016 Phoenix, USA

Thermus nepalensis sp nov., a thermophilic bacteria from a geothermal area

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From a local hot spring, myagdi, in mid western geothermal area of Nepal, Two aerobic, Gram-negative, non-motile, non-sporulating, yellow-pigmented thermophilic bacteria, strains TH-1 and TH-2, were isolated. They exhibited circular, convex, non-transparent and yellow pigment colonies. The isolates grew at 55–75°C (optimally at 72°C) and at pH 6.5–8.5 (optimally at pH 7.5–8.0) and were sensitive to salt concentration, 1.5% NaCl was found to be lethal. Both culture dependent and culture independent strategies were implemented for the identification of the isolates. Phylogenetic analysis of 16S rRNA gene sequences and analysis of FAME as well as levels of DNA–DNA relatedness together indicated that the new isolates represented a novel species of the genus *Thermus* with closest affinity to *Thermus aquaticus*, *Thermus igniterrae*, *Thermus thermophilus* and *Thermus arciformis*. The genomic DNA G+C contents of strains TH-1 and TH-2 were 62.3 mol% and 64 mol% Compared with their closest relatives, strains TH-1 and TH-2 were able to assimilate a wider range of carbohydrates, amino acids and organic acids as sole carbon sources for growth. The isolates were found to be very effective in production of various Extracellular enzymes like amylase, pectinase, protease, caseinase, gelatinase and lipase. The new isolates have very high potential for industrial upgrade for production of thermostable enzymes. They had higher combined levels of C15:0 iso, C15:0 anteiso, C16:0 and C17:0 compared with their closest relatives. Based on the results of physiological and biochemical tests, polyphasic taxonomic characterization and phylogenetic analyses, the isolates strains could not be classified as representing any species of the genus *Thermus* with a validly published name. Thus the two strains TH-1 and TH-2 are considered to represent a novel species of the genus *Thermus*, for which the name *Thermus nepalensis* sp. nov. is proposed.

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Production of biogas from the co-digestion of plantain peels, yam peels and cow dung

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The biogas production potential of the co-digestion of plantain (*Musa paradisiaca*) peels, yam (*Discorea rotundata*) peels and cow (*Bos primigenius*) dung was investigated. Two waste combinations of plantain peels with cow dung (A), yam peels with cow dung (B) and three waste combination of plantain peels, yam peels with cow dung (C) were used for biogas comparison. The waste was charged into a glass type digester of 1000 ml capacity and a rubber type digester of 5 L within a retention period of 4 weeks. Biogas production was determined using water displacement method. Changes in methane concentration of the biogas, the bacteria associated with biogas production and the pH of the slurry before and after the biogas production was determined. Bacteriological analyses showed the presence of *Pseudomonas* sp., *Klebsiella* sp., *Bacillus* sp., *E. coli*, *Clostridium* sp., *Streptococcus* sp., *Micrococcus* sp. and *Bacillus* sp., *E. coli*, *Clostridium* sp. from the fresh and spent slurry respectively. The highest volume of biogas (680 ml) was obtained from the co-digestion (C1) followed by (428 ml) from the yam peels treatment option (B3) while the least (0 ml) was from the plantain peels treatment option (A1). The purification system using lime water and iron filings was able to remove about 74% of the CO₂ and 82% of the H₂S respectively from the biogas generated.

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