Molecular Analysis and Evaluation of Metabolic Capacity of Waste Pesticide Microorganisms Resistant

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Decontamination Biological methods is an improved substitute for costly physico-chemical remediation methods. Nevertheless, only a fraction of total microbial has been harnessed for this purpose. The search for microorganisms capable to reverse soil infertility is critical to production process. The objective of this research was isolate and characterize biochemical and molecular the microorganisms which have possible capacity of different substrats use. Four microorganisms were isolated (A10, B12, C13 and D14). The metabolic capacity of microorganisms was evaluated using 31 differents substrates like carbon source (0,1%) supplemented in mineral medium. Organism A-10 presented higher ability to metabolize glycogen, tween 40 and 80, alpha-cycle dextrin, i-erythritol, gamma-hydroxybutyric acid, D-glucosaminic acid, D-galacturonic acid, malic acid, 4-hydroxybenzoic acid. All microorganisms, except C13 presented similar metabolic capacity to metabolize D-cellobiose. Organism D14 showed higher capacity to use Asparagine, B-12 pyruvic acid methyl ester, and the organism C13 used glucose 1-phosphate and alpha-ketobutyric acid. None of microorganisms were able to use 2-hydroxybenzoic acid and Itaconic acid like sole carbon source. Biochemical analysis of isolated microorganisms showed no similiaridade with database Bactray. The 16S rDNA was amplified using primers Y1 and Y23 resulting in 1266 bp for strain A10, 477 for B12, 323 for C13 and 313 for D14. The correlation of sequence analyzed using GenBank showed 90% of similarity with Klebsiella sp. (R4KTKFVY012), 94% with Enterobacter ludwii (R4M6UTTM012), 98% with Bacillus mojavensis (R4MM2JV601N) and 98% with Trabulsia guamensis (R4MTJ8XG01N) respectively.

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