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16S rRNA SEQUENCE-BASED PHYLOGENY OF A NOVEL PROPIONIBACTERIUM FOR ENHANCED FERMENTATION OF HIGH MOISTURE CORN

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A propionibacterium named DH42 was previously isolated from fermented, high moisture corn and evaluated as a starter culture to enhance bunk stability of high moisture corn. To determine phylogenetic relationships between DH42 and other representatives of the phylum *Actinobacteria*, a 1529-bp fragment of its 16S rRNA was PCR-amplified and sequenced. Out of 1,900 BLAST hits on the query sequence, the most probable similarity of the DH42 sequence to 16S rRNA sequences of *Propionibacterium microaerophilus*, *Eubacterium combesii*, and *P. acidipropionici* was found. Subsequently, the multiple alignment of 16S rRNA sequences of DH42 with 25 *Propionibacterineae* species, 23 other *Actinobacteria* species and *Escherichia coli* (as a non-related organism) was performed using the Clustal V method, Neighbor-Joining technique being employed to reconstruct phylogeny for the putative alignment. The propionibacterium DH42 formed a cluster of the closely related species including *E. combesii*, *P. acidipropionici* and *P. microaerophilus*. Judging from the metabolic profile, DH42 closely matched *P. acidipropionici* that confirms its 16S rRNA sequence-based affinity to this species. These comparative studies based on 16S rRNA sequences may shed light on the phylogenetic relationships between organisms inside the suborder *Propionibacterineae* and make its classification more precise.

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