

GENOME DISCOVERIES

by
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Introduction

This program analyses the microbial genome *Acetobacter ascendens*. This microbe is formed by *Acetobacter oryzafermentans*, isolated from Korean traditional vinegar, and reclassification of the type strains of *Acetobacter pasteurianus* subsp. *ascendens* (Henneberg 1898) and *Acetobacter pasteurianus* subsp. *paradoxus* (Frateur 1950).

Methods

A fully sequenced microbial genome, *Acetobacter ascendens* (strain LMG 1590 in FASTA-format) was downloaded from the National Center of Biotechnology Information (NCBI) (<ftp://ftp.ncbi.nlm.nih.gov/genomes/Bacteria/>), on February 14, 2019. A Python program analyzes the string and computes the various characteristics of the string e.g. proportion of nucleotides, probability of nucleotide combinations.

Results

Acetobacter ascendens has a higher GC percentage as compared to AT percentage.(see Table 1)

Nucleotide	Raw Count	Proportion	Percentage (%)
A	700581	0.23	23
C	798410	0.27	27
G	796382	0.27	27
T	703904	0.23	23

(Table 1. Shows the proportion and percentage of the A,C,T,G nucleotides in the entire genome.)

Discussion

The percentage of GC (54%) is higher than the percentage of AT (46%). Additionally, the probability of finding an 'ACGTACGT' 8mer in the sequence is $1.5 \cdot 10^{-5}$.

References

Acetobacter oryzafermentans sp. nov., isolated from Korean traditional vinegar and reclassification of the type strains of *Acetobacter pasteurianus* subsp. *ascendens* (Henneberg 1898) and *Acetobacter pasteurianus* subsp. *paradoxus* (Frateur 1950) as *Acetobacter ascendens* sp. nov., comb. nov. (2018, April 05). Retrieved from <https://www.sciencedirect.com/science/article/pii/S0723202018301279>

