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Data Article

Genomics dataset on unclassified published organism (patent US 7547531)

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ABSTRACT

Nucleotide (DNA) sequence analysis provides important clues regarding the characteristics and taxonomic position of an organism. With the intention that, DNA sequence analysis is very crucial to learn about hierarchical *classification of that particular organism. This dataset* (patent US 7547531) is chosen to simplify all the complex raw data buried in undisclosed DNA sequences which help to open doors for new collaborations. In this data, a total of 48 unidentified DNA sequences from patent US 7547531 were selected and their complete sequences were retrieved from NCBI BioSample database. Quick response (QR) code of those DNA sequences was constructed by DNA BarID tool. QR code is useful for the identification and comparison of isolates with other organisms. AT/GC content of the DNA sequences was determined using ENDMEMO GC Content Calculator, which indicates their stability at different temperature. The highest GC content was observed in GP445188 (62.5%) which was followed by GP445198 (61.8%) and GP445189 (59.44%), while lowest was in GP445178 (24.39%). In addition, New England BioLabs (NEB) database was used to identify cleavage code indicating the 5, 3 and blunt end and enzyme code indicating the methylation site of the DNA sequences was also shown. These data will be helpful for the construction of the organisms' hierarchical classification,

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determination of their phylogenetic and taxonomic position and revelation of their molecular characteristics.

Specifications Table

Study area	Biological Sciences
More definite study area	Genomics, Microbiology, Bioinformatics
Data types	Table, figure, graph and QR Code
How data was obtained	Through NCBI BioSample database
Data format	Raw and analyzed
Experimental factors	Dataset obtained through bioinformatics tool
Experimental features	Only disclosed genome sequences were used
Data source location	Department of Biochemistry and Molecular Biology, Jahangirnagar University, Savar, Dhaka-1342, Bangladesh.
Data accessibility	Data available within this article and via the NCBI repository http://www.ncbi.nlm.nih.gov/nuccore/?term=patent+US+7547531

Value of the data

- Data regarding AT and GC percentage of the DNA sequences would give idea about their stability at different temperatures.
- The QR code would be useful for the identification, qualitative, quantitative analysis of the isolates and for their comparison with other organisms.
- These data give information about exact position of restriction sites to create blunt and sticky ends and also give an idea about the sites where cleavage is being affected by methylation.

1. Data

This paper contains data on quick response (QR) codes, guanine and cytosine (GC) content, analyzed DNA sequences and microorganisms having similar regions of 48 nucleotide sequences of unclassified disclosed microorganism from patent US 7547531. All the sequences of unidentified microorganisms disclosed from the patent US 7547531 were downloaded in FASTA format via NCBI nuccore database. These retrieved nucleotide sequences were utilized to generate QR codes, calculate GC content along with GC plot, determine number of cleavage code (blunt end cut, 5′ and 3′ sticky ends extension) and identify number of enzyme code (cleavage affected by CpG and other methylation).

2. Experimental design, materials and methods

At the beginning, a total of 48 nucleotide sequences (GP445164, GP445165, GP445166, GP445167, GP445168, GP445169, GP445170, GP445171, GP445172, GP445173, GP445174, GP445175, GP445176,