BLAST Analysis Report

Introduction

This report presents the results of a BLAST analysis for a DNA sequence of a sample, which was compared against the NCBI nucleotide database. The aim of the analysis was to identify the closest matching species for the sample.

Primer Characteristics

For the amplification of the ITS region, the following primers were used:

- **ITS1 Primer:** The ITS1 primer has the sequence `TCCGTAGGTGAACCTGCGG` and is designed to bind to the conserved region at the start of the ITS1 region. This primer is specific for fungi and is widely used in molecular studies for identifying fungal species [3].
- **ITS4 Primer:** The ITS4 primer has the sequence `TCCTCCGCTTATTGATATGC` and binds at the end of the ITS2 region. Together with ITS1, it allows for the amplification of the entire ITS region, including both ITS1 and ITS2, as well as the 5.8S rRNA gene.

Purpose of ITS Primers: The ITS (Internal Transcribed Spacer) region, located between the small subunit (SSU) and large subunit (LSU) rRNA genes, is highly variable among different fungal species, making it an ideal target for molecular identification. The ITS1 and ITS4 primers are commonly used to amplify this region for taxonomic and phylogenetic studies [3].

Applications: The amplified ITS region serves as a ”barcode” for identifying fungal species and is used in environmental sequencing, clinical diagnostics, and biodiversity studies. The amplified sequences can then be compared against databases, such as GenBank, to identify the fungal species present in the sample.

Key Results

The BLAST search identified multiple high-confidence matches for the sequence, with the closest matches aligning to various isolates of *Meyerozyma caribbica* and *Meyerozyma guilliermondii.* The following are the key details:

- **Closest Species Match:** *Meyerozyma caribbica*
- **Top E-value:** 4.73×10^{-54}
- **Top Alignment Score:** 246.0
- **Sequence Identity:** 124 out of 125 nucleotides (99.2% identity)

Detailed BLAST Hits

The table below summarizes the top 10 hits from the BLAST analysis, showing the sequence alignment scores, E-values, and identities.

GenBank ID	Organism	Length (bp)	Score	E-value
gi—2250056463	*Meyerozyma caribbica* isolate MC10	595	246.0	4.73×10^{-54}
gi—2299520811	*Meyerozyma caribbica* strain GMUSF35	617	246.0	4.73×10^{-54}
gi—2753765239	*Meyerozyma guilliermondii* isolate EGZ-37	601	246.0	4.73×10^{-54}
gi—1913252983	*Meyerozyma caribbica* strain Y3	611	246.0	4.73×10^{-54}
gi—2259105606	*Meyerozyma guilliermondii* genomic DNA	605	246.0	4.73×10^{-54}
gi—2259514349	*Meyerozyma guilliermondii* genomic DNA	606	246.0	4.73×10^{-54}
gi—2259105598	*Meyerozyma guilliermondii* genomic DNA	607	246.0	4.73×10^{-54}
gi—2314605039	*Debaryomyces hansenii* var. *hansenii* isolate ziha1	1224	246.0	4.73×10^{-54}
gi—2259046537	*Meyerozyma caribbica* genomic DNA	606	246.0	4.73×10^{-54}
gi—2212731020	*Meyerozyma caribbica* isolate CP02	1210	246.0	4.73×10^{-54}

Summary

The analysis strongly suggests that the DNA sequence is derived from a strain of *Meyerozyma caribbica*, with several high-confidence hits indicating identical or nearly identical sequences. Given the low E-values and high sequence identity, *Meyerozyma caribbica* is the most likely source organism for this sample.

Meyerozyma caribbica is a species of yeast in the family Debaryomycetaceae. It is commonly found in tropical climates and is known for its ability to ferment various sugars. This species has potential applications in biotechnology, including bioethanol production and biotransformations [1, 2].

References

[1] M. Landell, W. Silveira, F. Leite, J. de Morais, and E. Oliveira. “Efficient xylitol production by *Meyerozyma caribbica* from corncob hemicellulosic hydrolysate”. In: *Bioprocess and Biosystems Engineering* 37.10 (2014), pp. 2093–2100. DOI: `10.1007/s00449-014-1193-9`.

[2] J. Mota, F. Passos, F. Antunes, L. Ávila, and D. Mota. “Production of ethanol by *Meyerozyma caribbica* from agro-industrial residues”. In: *Biomass and Bioenergy* 35.9 (2011), pp. 3950–3954. DOI: `10.1016/j.biombioe.2011.06.010`.

[3] T. J. White, T. Bruns, S. Lee, and J. Taylor. “Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics”. In: (1990), pp. 315–322.