

Supporting information



Fig. S1. Quantification and purity assessment of genomic DNA extracted from the soil-derived *A. niger* isolate using NanoDrop spectrophotometry.

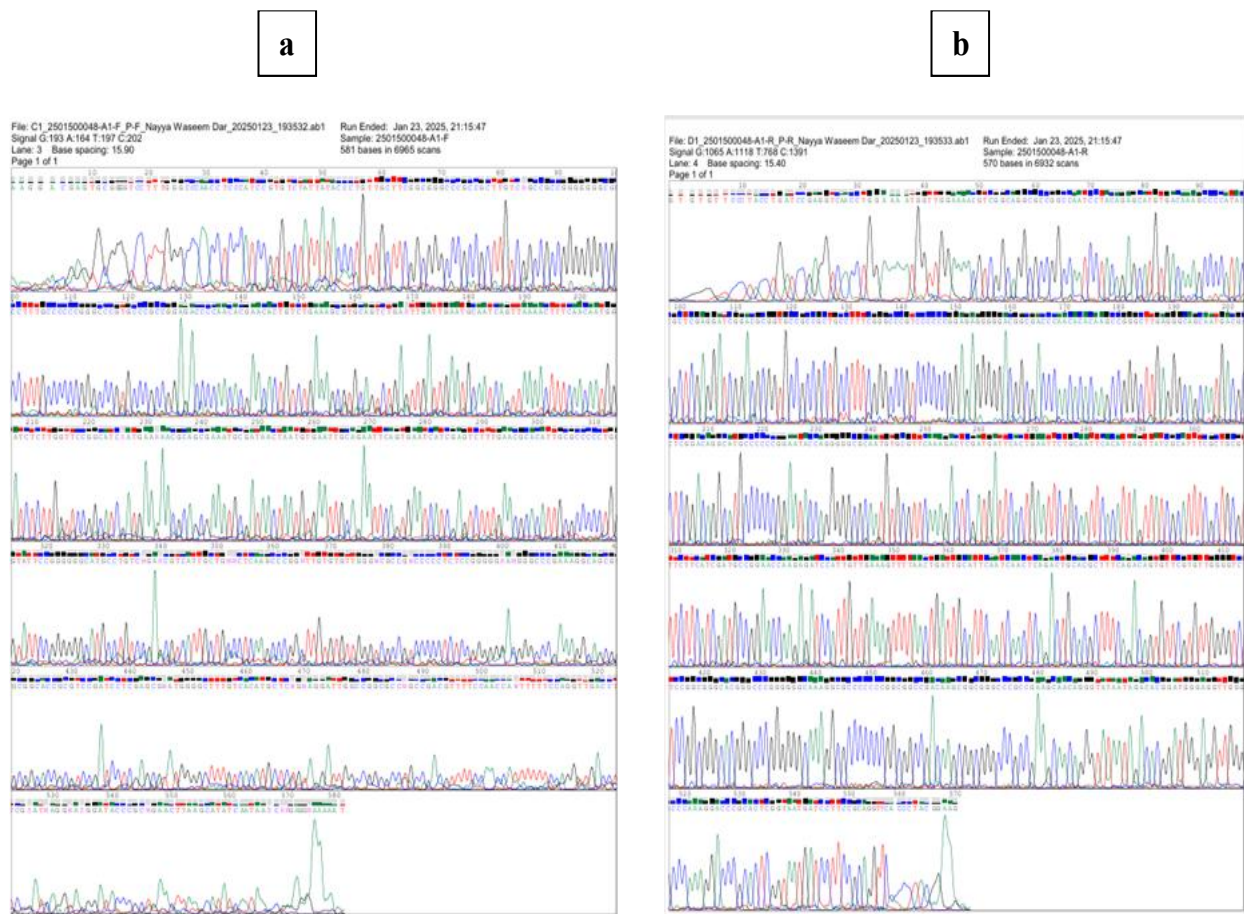


Fig. S2. Quality assessment of bidirectional ITS sequencing reads of the soil-derived *A. niger* isolate: (A) forward sequence chromatogram and (B) reverse sequence chromatogram showing high-confidence base calling regions used for consensus sequence assembly.

OUTPUT FILE [outfile](#)

```
#Sequence    GC content
Aspergillus_niger_ITS_consensus    0.57
```

Fig. S3. GC content distribution analysis of the ITS sequence of the soil-derived *A. niger* isolate using the Geecee program of EMBOSS.

1/19/25, 3:37 PM

tmp_om_dy3_2.7.7.80.10.50.500.1.html

Tandem Repeats Finder Program written by:

Gary Benson
Program in Bioinformatics
Boston University
Version 4.09

Please cite:

G. Benson,
"Tandem repeats finder: a program to analyze DNA sequences"
Nucleic Acid Research(1999)
Vol. 27, No. 2, pp. 573-580.

Sequence: Aspergillus_niger_ITS_consensus
Parameters: 2 7 7 80 10 50 500
Length: 581

Tables: 1

This is table 1 of 1 (0 repeats found)

Click on indices to view alignment

[Table Explanation](#)

Indices	Period Size	Copy Number	Consensus Size	Percent Matches	Percent Indels	Score	A	C	G	T	Entropy (0-2)
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No Repeats Found!

Fig. S4. Identification and schematic representation of tandem repeat finder showing absence of tandem repeat within the ITS region of the soil-derived *A. niger* isolate.

Table S1. BLASTn based sequence similarity analysis of the ITS region of the soil-derived *A. niger* isolate showing homologous reference sequences, alignment statistics, and GenBank accession numbers.

Scientific Name	Max Score	Total Score	Query Cover	E value	Per. ident	Acc. Len	Accession
<i>Aspergillus niger</i>	1053	1941	96%	0	100	570	PV056012.1
<i>Aspergillus niger</i>	1033	1950	96%	0	99.65	580	MZ229697.1
<i>Aspergillus niger</i>	1033	1978	98%	0	99.65	596	MH064151.1
<i>Aspergillus niger</i>	1033	1978	98%	0	99.65	601	PX397517.1
<i>Aspergillus niger</i>	1033	1978	98%	0	99.65	603	OP103930.1
<i>Aspergillus niger</i>	1033	1978	98%	0	99.65	605	MZ229740.1
<i>Aspergillus niger</i>	1033	1978	98%	0	99.65	612	MZ229701.1
<i>Aspergillus sp.</i>	1033	1978	98%	0	99.65	604	MN173117.1
<i>Aspergillus niger</i>	1033	1978	98%	0	99.65	604	OP237079.1
<i>Aspergillus niger</i>	1033	1978	98%	0	99.65	603	MW260101.1
<i>Aspergillus tubingensis</i>	1029	2094	95%	0	99.65	621	MW789023.1
<i>Aspergillus niger</i>	1029	1967	97%	0	99.65	597	MH855928.1
<i>Aspergillus arizonicus</i>	1027	1972	97%	0	99.64	597	OP810889.1

Table S2. Population genetic diversity, differentiation, and gene flow estimates of *A. niger* ITS sequences analyzed using DnaSP.

Population 1 (set1)	
Parameter	Value
Number of sequences	14.00
Segregating sites (S)	31.00
Haplotypes (h)	2.00
Haplotype diversity (Hd)	0.53
Average differences (K)	16.69
Nucleotide diversity (Pi)	0.39
Pi (Jukes-Cantor)	1.67
Population 2 (set2)	
Parameter	Value
Number of sequences	14.00
Segregating sites (S)	41.00
Haplotypes (h)	7.00
Haplotype diversity (Hd)	0.80
Average differences (K)	24.08
Nucleotide diversity (Pi)	0.57
Pi (Jukes-Cantor)	1.68
Total Data Estimates	
Parameter	Value
Number of sequences	28.00
Segregating sites (S)	41.00
Haplotypes (h)	7.00
Haplotype diversity (Hd)	0.67

Average nucleotide differences (Kt)	20.35
Nucleotide diversity (PiT)	0.48

Genetic Differentiation Estimates	
Statistic	Value
Chi-square (Chi2)	6.677 (P = 0.3518, ns)
HBK 1992 Hs	0.670
HBK 1992 Hst	0.006
HBK 1992 Ks	20.390
HBK 1992 Kst	-0.001
HBK 1992 Ks*	2.289
HBK 1992 Kst*	0.001
HBK 1992 Z	188.673
HBK 1992 Z*	5.044
Hudson 2000 Snn	0.539

Gene Flow Estimates	
Parameter	Value
Gst (Nei 1973)	0.006
Nm (Nei 1973)	40.670
DeltaSt (Nei 1982)	0.016
GammaSt (Nei 1982)	0.035
Nm (Nei 1982)	6.820
Nst (Lynch & Crease 1990)	-0.031
Nm (Lynch & Crease 1990)	-8.280
Fst (Hudson et al. 1992)	-0.003
Nm (Hudson et al. 1992)	-74.220

Image description

MFE plain structure drawing

Centroid plain structure drawing

MFE structure drawing encoding base-pair probabilities

Centroid structure drawing encoding base-pair probabilities

MFE structure drawing encoding positional entropy

Centroid structure drawing encoding positional entropy

Download options

[[EPS](#) | [PDF](#) | [IMAGE CONVERTER](#) | [VIEW IN FORNA](#)]

[[EPS](#) | [PDF](#) | [IMAGE CONVERTER](#) | [VIEW IN FORNA](#)]

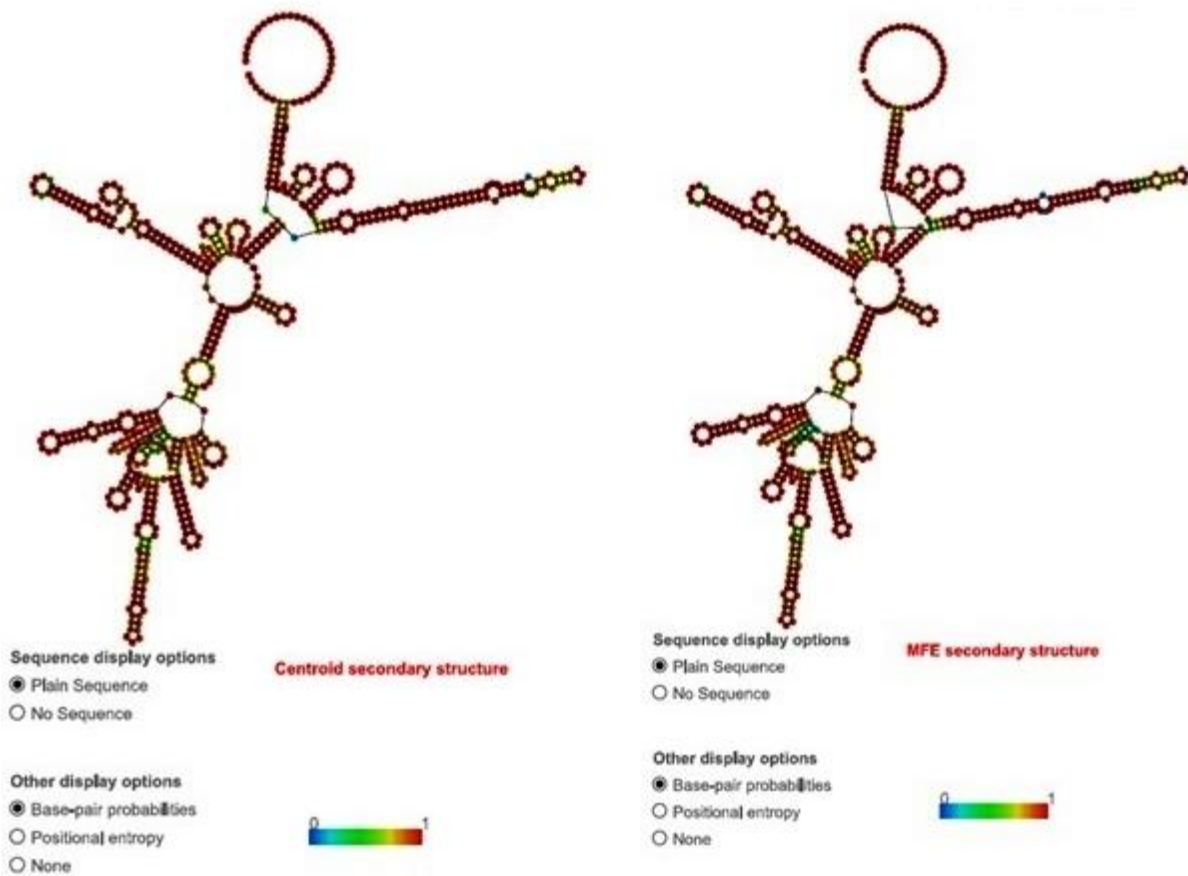
[[EPS](#) | [PDF](#) | [IMAGE CONVERTER](#) | [VIEW IN FORNA](#)]

[[EPS](#) | [PDF](#) | [IMAGE CONVERTER](#) | [VIEW IN FORNA](#)]

[[EPS](#) | [PDF](#) | [IMAGE CONVERTER](#) | [VIEW IN FORNA](#)]

[[EPS](#) | [PDF](#) | [IMAGE CONVERTER](#) | [VIEW IN FORNA](#)]

Here you find a [mountain plot](#) representation of the MFE structure, the thermodynamic ensemble of RNA structures, and the centroid structure. Additionally we present the positional entropy for each position. Download as [[EPS](#) | [PDF](#) | [IMAGE CONVERTER](#)].



A

Results for minimum free energy prediction

The optimal secondary structure in dot-bracket notation with a minimum free energy of **-213.10** kcal/mol is given below.

[☒ color by base-pairing probability] [☐ color by positional entropy] [☐ no coloring]

1 AAGGACGAGUGCGGGGCUUUUGGGCCAACTCCUACUGUGCUUAUUAUACCGUUGCUUGCGGGGCCCGCGUUGUCRGCCTGGGGGGGCGCUUUGCCCCCGGGCCGUGCCGCCGGAGACCCCAACAGCAACUGUCUGAAAGCC
160 CAGUCUGARUUGAUUGAUUGCAUACAGUUAUAAACUUUUAACAAUGGAUCUCUUGGUUUCGGGCAUCSAUGAARAAACGAGCGAAUUGCGAUAAUUAUUGAUUUGAGAAUUGAGAAUUAUCGAAUUAUCGAGUUCUUGAGACGCAUAUUGGCCCCUUGGAUUAU
320 GGGGGGACGCGUUCGCMGARGCUAUUGUUUUGCAACGAGCCGGUUGUUGGAGGACGCCGCCUUCUUGCGGGGGMRAGGCCCGAAGAGCGAGCGCGGACCGGCGUUCGAGCGUUAUGGGGCGUUGUUAUCACUUCMGWAGUAUUG
480 GGGCGCWCWCGGCUUUAUCAAACUUUUGUUCMAGUUCGUCGSAUAGGAGUUGGAGUCCCGGCAUAUUAAGCAUAUUAUUAASCKRGAGGAGRAAAUUA

[illegible]

You can download the minimum free energy (MFE) structure in [[Vienna Format](#)] [[Ct Format](#)]. You can get thermodynamic details on this structure by submitting to our [RNAeval web server](#).

Results for thermodynamic ensemble prediction

The free energy of the thermodynamic ensemble is **-220.17** kcal/mol.

The frequency of the MFE structure in the ensemble is **0.00** %.

The ensemble diversity is **36.42**.

You may look at the **dot plot** containing the base pair probabilities [[EPS](#) | [PDF](#) | [IMAGE CONVERTER](#)].

The centroid secondary structure in dot-bracket notation with a minimum free energy of **-209.60** kcal/mol is given below.

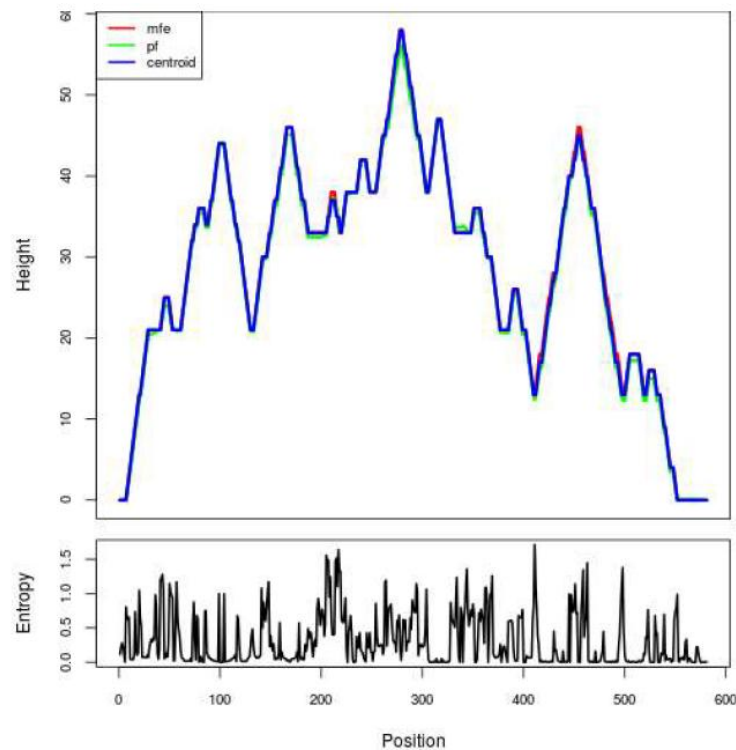
[[color by base-pairing probability](#) | [color by positional entropy](#) | [no coloring](#)][illegible][illegible]

You can download the minimum free energy (MFE) structure in [[Vienna Format](#)] [[Ct Format](#)]. You can get thermodynamic details on this structure by submitting to our [RNAeval web server](#).

Graphical output

You may look at the interactive drawing of the MFE structure below. If you do not see the interactive drawing and you are using Internet Explorer, please install the [Adobe SVG plugin](#). **A note on base-pairing probabilities:** The structure below is colored by base-pairing probabilities. For unpaired regions the color denotes the probability of being unpaired.

C



Results have been computed using RNAfold 2.6.3. An equivalent command line call would have been
 RNAfold -p -d2 --noLP < [Aspergillus_niger_ITS_consensus.fa](#) > [Aspergillus_niger_ITS_consensus.out](#)

RNA parameters are described in

Mathews DH, Disney MD, Childs JL, Schroeder SJ, Zuker M, Turner DH. (2004) Incorporating chemical modification constraints into a dynamic programming algorithm for prediction of RNA secondary structure. *Proc Natl Acad Sci U S A* 101(19):7287-92.

Fig. S5. RNA secondary structure prediction and folding analysis of the ITS sequence of the soil-derived *A. niger* isolate using RNAfold. (A) RNA kinetic folding analysis generated by the Barriers server. (B) Minimum free energy (MFE) secondary structure prediction and base-pairing probability analysis. (C) Reliability assessment of predicted RNA structures based on positional entropy and base-pairing probabilities.