Data in Brief

The complete mitochondrial genome of the acid-tolerant fungus *Penicillium* ShG4C

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Abstract

Complete mitochondrial genome of the acid-tolerant fungus *Penicillium* ShG4C, isolated from oxidized sediments of an abandoned polymetallic mine site, has been sequenced using high-throughput sequencing approach. The mitochondrial genome represents a circular DNA molecule with size of 26,725 bp. It encodes a usual set of mitochondrial genes, including 15 protein coding genes, large and small ribosomal RNAs and 27 tRNA genes. All genes are located on H-strand DNA and transcribed in one direction. Taxonomic analysis based on concatenated sequences of mitochondrial proteins confirmed taxonomic position of this fungus within the genus *Penicillium*. The sequence of the complete mitochondrial genome of *Penicillium* ShG4C was deposited in DBJ/EMBL/GenBank under accession number KX931017.

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1. Direct link to deposited data

https://www.ncbi.nlm.nih.gov/nuccore/KX931017.

2. Introduction

Fungi of the genus *Penicillium* of Trichocomaceae family of Pezizomycotina order (filamentous fungi) of Ascomycetes are widely distributed in nature. Generally they are saprophytes and use dead organic material for feed. Eukaryotic organisms could inhabit extreme environments, for example, fungi of the genus *Penicillium* sp. were found in acidic Rio Tinto in Spain and Iron Mountains in California [9,10], hot soil of Yellowstone Part in USA [12]. A few Ascomycetes fungi were found in Zanjan province (Iran) as potential species for cadmium removal from soils [11]. Evolutionary adaptation of fungi to metal-contaminated soils is a well-documented phenomenon, particularly because it is one of the most striking examples of microevolution driven by edaphic factors [8]. They have considerable potential in the solution of bioremediation tasks [2]. These fungi can absorb different metals from soil and water [3], they are easily isolated, grow quickly and adjust to environmental conditions, so they have a major potential for bioremediation [2]. In this paper we present the results of sequencing and analysis of the mitochondrial genome of acid tolerant strain of fungus *Penicillium* ShG4C. The obtained data will be useful for further research in the field of taxonomy and evolution of filamentous fungi.

3. Experimental design, materials and methods

3.1. Features of the mitochondrial genome of *Penicillium* ShG4C

In 2013 the fungal strain ShG4C belonging to the genus *Penicillium* was isolated from wastes of the ore mining deposit “Sherlovaya Gora” located in Transbaikal region, Eastern Siberia, Russia. Chemical analysis of water at the sampling site showed low pH value (1.9) and high
concentrations of iron (320 mM), arsenic (39 mM), zinc (41 mM), aluminum (100 mM), and copper (31 mM). Strain ShG4C is able to grow in presence of high concentration of arsenic and metals. Due to these properties, strain ShG4C is a potential object for development of new bioremediation approaches.

Genomic DNA was extracted from mycelium by modified protocol described in works of [1]. Whole genomic DNA was sequenced using Illumina HiSeq2500 platform (10 millions of 100-bp long reads). The sequencing reads were de novo assembled into contigs using the Spades v. 3.7.1 [4]. A single circular contig with an average 1158 X coverage representing the mitochondrial genome was identified based on sequence similarity to the mitochondrial genome sequence of *Penicillium polonicum* (KUS30219). Identification of protein-coding genes, ribosomal and tRNA genes was carried out using Mitos server [5] and tRNAscan-SE [6]. The obtained automatic annotation was checked and corrected manually using BLAST search against the NCBI sequence database (http://www.ncbi.nlm.nih.gov/genbank/).

The complete mitochondrial genome of *Penicillium* ShG4C was a circular 26,725 bp long DNA. Its size is comparable to mtDNA of other closely related fungi of genus *Penicillium*, e.g. mtDNA of *Penicillium polonicum* – 28,192 bp (NC_030172), and *Penicillium roqueforti* – 29,908 bp (KR952335). The standard set of genes, including 15 protein-coding genes, 27 tRNA genes and 2 genes of ribosomal RNA is encoded by the mitochondrial genome of *Penicillium* ShG4C (Table 1). All identified genes are encoded on H-strand of mtDNA. All protein-encoding genes have the same start codon ATG, except for COX1 gene with TTG start codon. NAD6 gene has stop codon TAG and the other encoding genes have the same start codon ATG, except for COX1 gene.

| Gene     | Start | Stop  | Length, bp |
|----------|-------|-------|------------|
| rrnL     | 113   | 4705  | 4593†      |
| RPSb     | 2861  | 4072  | 1212       |
| tmN-UGU  | 4753  | 4823  | 71         |
| tmE-UUC  | 4861  | 4934  | 74         |
| tmW-UAC  | 4936  | 5008  | 73         |
| tmM-CAU  | 5010  | 5080  | 71         |
| tmM-CAU  | 5081  | 5153  | 73         |
| trnL-CAA  | 5158  | 5239  | 82         |
| trnA-UGC  | 5245  | 5316  | 72         |
| trnF-GAA  | 5564  | 5636  | 73         |
| trnL-UGU  | 5649  | 5731  | 83         |
| trnQ-UUG  | 5744  | 5816  | 73         |
| trnM-CAU  | 5820  | 5891  | 72         |
| trnC-GCA  | 5915  | 5985  | 71         |
| trnH-UUG  | 6118  | 6188  | 71         |
| COX1     | 6376  | 8088  | 1713       |
| ATP9     | 8452  | 8676  | 225        |
| tmN-GUJ  | 8731  | 8801  | 71         |
| NAD5     | 8990  | 9397  | 408        |
| COX2     | 9537  | 10298 | 762        |
| trnR-ACG  | 10404 | 10474 | 71         |
| NAD4L    | 10744 | 11013 | 270        |
| NAD5     | 11013 | 12992 | 1980       |
| NAD2     | 13047 | 14735 | 1689       |
| COB      | 16400 | 17557 | 1158       |
| trnY-GUA  | 17648 | 17713 | 66         |
| NAD1     | 17897 | 18952 | 1056       |
| NAD4     | 19213 | 20679 | 1467       |
| trnR-UUC  | 20749 | 20819 | 71         |
| trnG-GUJ  | 20851 | 20921 | 71         |
| ATP8     | 21045 | 21191 | 147        |
| ATP6     | 21356 | 22129 | 774        |
| rns      | 22660 | 24049 | 1390       |
| trnY-GUA  | 24177 | 24261 | 85         |
| NAD6     | 24349 | 25002 | 654        |
| COX3     | 25052 | 25861 | 810        |
| trnK-UUU  | 25900 | 25971 | 72         |
| trnG-ACC  | 26014 | 26084 | 71         |
| trnG-UCC  | 26105 | 26175 | 71         |
| trnD-GUC  | 26188 | 26260 | 73         |
| trnS-GCT  | 26314 | 26394 | 81         |
| trnW-UCA  | 26395 | 26466 | 72         |
| tmL-CAU  | 26483 | 26554 | 72         |
| tmS-UCG  | 26559 | 26644 | 86         |

* a Contains intron (2517–4200).

* b Gene encoding ribosomal protein, located within rnl intron.

![Fig. 1. Phylogenetic analysis of representatives of the genera Aspergillus and Penicillium.](image-url)
[3] D.S. Hibbett, J.W. Taylor, Fungal systematics: is a new age of enlightenment at hand? Nat. Rev. Microbiol. 11 (2) (2013) 129–133.

[4] A. Bankevich, S. Nurk, D. Antipov, A.A. Gurevich, M. Dvorkin, A.S. Kulikov, V.M. Lesin, S.I. Nikolenko, S. Pham, A.D. Pyshkin, A.V. Pyshkin, N. Vyahhi, G. Tesler, M.A. Alekseyev, P.A. Pevzner, SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J. Comput. Biol. 19 (5) (2012) 455–477.

[5] M. Bernt, A. Donath, F. Jühling, F. Externbrink, C. Florentz, G. Fritzsch, J. Pütz, M. Middendorf, P.F. Stadler, MITOS: improved de novo metazoan mitochondrial genome annotation Mol. Phylogenet. Evol. 69 (2013) 313–319.

[6] T.M. Lowe, S.R. Eddy, tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. 25 (1997) 955–964.

[7] K. Tamura, G. Stecher, D. Peterson, A. Filipski, S. Kumar, MEGA6: molecular evolutionary genetics analysis version 6.0. Mol. Biol. Evol. 30 (2013) 2725–2729.

[8] J.V. Colpaert, P. Vandenkoornhuyse, K. Adriaensen, J. Vangronsveld, Genetic variation and heavy metal tolerance in the ectomycorrhizal basidiomycete Suillus luteus. New Phytol. 147 (2000) 367–379.

[9] Z. Amaral, F. Gómez, E. Zettler, B.G. Keenan, R. Amils, M.L. Sogin, Microbiology: eukaryotic diversity in Spain’s River of Fire. Nature 417 (6885) (2002) 137.

[10] B.J. Baker, M.A. Lutz, S.C. Dawson, P.L. Bond, J.F. Banfield, Metabolically active eukaryotic communities in extremely acidic mine drainage. Appl. Environ. Microbiol. 70 (10) (2004) 6264–6271.

[11] M. Mohammadian Fazli, N. Soleimani, M. Mehrasbi, S. Darabian, J. Mohammadi, A. Ramazani, Highly cadmium tolerant fungi: their tolerance and removal potential. 2015. J. Environ. Health Sci. Eng. 13 19, http://dx.doi.org/10.1186/s40201-015-0176-0.

[12] R.S. Redman, A. Litvintseva, K.B. Sheehan, J.M. Henson, R.J. Rodriguez, Fungi from geothermal soils in Yellowstone National Park. Appl. Environ. Microbiol. 65 (12) (1999) 5193–5197.