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Draft Genome Sequence of *Neurospora crassa* Strain FGSC 73

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We report the elucidation of the complete genome of the *Neurospora crassa* (Shear and Dodge) strain FGSC 73, a *mat-a*, *trp-3* mutant strain. The genome sequence around the idiotypic mating type locus represents the only publicly available sequence for a *mat-a* strain. 40.42 Megabases are assembled into 358 scaffolds carrying 11,978 gene models.

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Neurospora crassa is a well-established model organism and was the first filamentous fungus to have a publicly available genome sequence (1). It is best known as the organism utilized by Beadle and Tatum to establish the "one gene, one enzyme" hypothesis (2), and it has been utilized recently for studies of cell biology, gene regulation, genome defense, population genetics, and genomics (3). The earliest published report of a gene mutation leading to the loss of an essential enzymatic activity in *N. crassa* was for the synthesis of pyridoxine in *Neurospora* (then called *Sitophila*) (2). Mutation surveys were carried out, leading to the first description of tryptophan requiring mutants in 1944 (4) and over 50 "tryptophanless" strains reported in 1950 (5). The Fungal Genetics Stock Center is the repository for 20,178 *N. crassa* genetic mutant strains, of which 6,630 are classical mutants. FGSC 73 has the C83 (td1) allele of *trp-3* in a mixed genetic background and is one of 80 strains carrying 40 unique *trp-3* alleles. The C83 allele was the first trp-3 allele described (6) and was generated by UV irradiation. The high-resolution genetic map and broad collection of classical mutants makes *N. crassa* an ideal organism for next-generation sequencing approaches aimed at linking phenotype with genotype (7–9).

We have performed whole-genome shotgun sequencing to 144.8× coverage of FGSC 73 using the Illumina sequencing platform. The genome sequence was assembled using AllPathsLG version R42328. The size of the assembled genome is 40.42 Mb and comprises 757 contigs and 358 scaffolds (316 are at least 2 kbp in length). Using the JGI annotation pipeline (10), 11,978 gene models were generated. This is in contrast to 10,357 gene models currently associated with the most recent annotation of *N. crassa* version 12 generated at the Broad Institute. The FGSC 73 genome contained 20,779 single-nucleotide polymorphisms (SNPs) and 2,485 insertion/deletions (indels). The amount of SNPs and indels are consistent with previously published resequencing studies (7, 8), and with this strain having been developed before the research community adopted a shared genetic lineage.

As part of a targeted sequencing project, the *trp-3* locus of this *mat-a* strain has been sequenced previously (11) and the identification of the mutation at the trp-3 locus as a deletion of one adenosine at position 1021 causing a truncation of the predicted protein at residue 379 is recapitulated in the present study.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession number JTEW00000000. The version described in this paper is the first version, JTEW00000000.1.

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REFERENCES

1. **Galagan JE, Calvo SE, Borkovich KA, Selker EU, Read ND, Jaffe D, FitzHugh W, Ma LJ, Smirnov S, Purcell S, Rehman B, Elkins T, Engels R, Wang S, Nielsen CB, Butler J, Endrizzi M, Qui D, Ianakiev P, Bell-Pedersen D, Nelson MA, Werner-Washburne M, Selitrennikoff CP, Kinsey JA, Braun EL, Zelter A, Schulte U, Kothe GO, Jedd G, Mewes W, Staben C, Marcotte E, Greenberg D, Roy A, Foley K, Naylor J, Stange-Thomann N, Barrett R, Gnerre S, Kamal M, Kamvysselis M, Mauceli E, Bielke C, Rudd S, Frishman D, Krystofova S, Rasmussen C, Metzenberg RL, Perkins DD, Kroken S, Cogoni C, Macino G, Catcheside D, Li W, Pratt RJ, Osmani SA, DeSouza CP, Glass L, Orbach MJ, Berglund JA, Voelker R, Yarden O, Plamann M, Seiler S, Dunlap J, Radford A, Aramayo R, Natvig DO, Alex LA, Mannhaupt G, Ebbole DJ, Freitag M, Paulsen I, Sachs MS, Lander ES, Nusbaum C, Birren B.** 2003. The genome sequence of the filamentous fungus *Neurospora crassa*. Nature **422:**859–868. http://dx.doi.org/10.1038/nature01554.
2. **Beadle GW, Tatum EL.** 1941. Genetic control of biochemical reactions in *Neurospora*. Proc Natl Acad Sci USA **27:**499–506. http://dx.doi.org/10.1073/pnas.27.11.499.
3. **Wiest AE, Baker SE, McCluskey K.** 2012. *Neurospora* gene and genome analysis: past through future, p 273–291. *In* Kasbekar DP, McCluskey K (ed), Neurospora: genomics and molecular biology. Caister Academic Press, Norfolk, United Kingdom.

4. **Tatum EL, Bonner D.** 1944. Indole and serine in the biosynthesis and breakdown of tryptophane. Proc Natl Acad Sci U S A **30:**30–37. http://dx.doi.org/10.1073/pnas.30.2.30.
5. **Tatum EL.** 1950. Effects of radiation on fungi. J Cell Physiol Suppl **35:**119–131. http://dx.doi.org/10.1002/jcp.1030350409.
6. **Yanofsky C.** 1952. The effects of Gene change on tryptophan desmolase formation. Proc Natl Acad Sci USA **38:**215–226. http://dx.doi.org/10.1073/pnas.38.3.215.
7. **Pomraning KR, Smith KM, Freitag M.** 2011. Bulk segregant analysis followed by high-throughput sequencing reveals the *Neurospora* cell cycle gene, *ndc-1*, to be allelic with the gene for ornithine decarboxylase, *spe-1*. Eukaryot Cell **10:**724–733. http://dx.doi.org/10.1128/EC.00016-11.
8. **McCluskey K, Wiest AE, Grigoriev IV, Lipzen A, Martin J, Schackwitz W, Baker SE.** 2011. Rediscovery by whole genome sequencing: classical mutations and genome polymorphisms in *Neurospora crassa*. G3 (Bethesda) **1:**303–316. http://dx.doi.org/10.1534/g3.111.000307.
9. **Baker SE.** 2009. Selection to sequence: opportunities in fungal genomics. Environ Microbiol **11:**2955–2958. http://dx.doi.org/10.1111/j.1462-2920.2009.02112.x.
10. **Grigoriev IV, Martinez DA, Salamov AA.** 2006. Fungal genomic annotation, p 123–142. In Aurora DK, Berka RM, Singh GB (ed), Applied mycology and biotechnology (bioinformatics), vol **6.** Elsevier, Amsterdam.
11. **Wiest A, Barchers D, Eaton M, Henderson R, Schnittker R, McCluskey K.** 2013. Molecular analysis of intragenic recombination at the tryptophan synthetase locus in *Neurospora crassa*. J Genet **92:**523–528. http://dx.doi.org/10.1007/s12041-013-0305-4.