

Resource Summary Report

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Neurospora crassa Database

RRID:SCR_001372

Type: Tool

Proper Citation

Neurospora crassa Database (RRID:SCR_001372)

Resource Information

URL: https://fungi.ensembl.org/Neurospora_crassa/Info/Index

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Description: It's strategy involves Whole Genome Shotgun (WGS) sequencing, in which sequence from the entire genome is generated and reassembled. This method is standard for microbial genome sequencing, and has been successfully applied to *Drosophila*. *Neurospora* is an ideal candidate for this approach because of the low repeat content of the genome. *Neurospora crassa* Database has expanded the scope of its database by including a mitochondrial annotation, incorporating information from the *Neurospora* compendium, and assigning NCU numbers to tRNA and rRNAs. They have improved the annotation process to predict untranslated regions and to reduce the number of spurious predictions. As a result, version 3 contains 9,826 genes, 794 fewer than version 2. During the initial phase of a WGS project they sequence both ends of the 4 kb inserts from a plasmid library prepared using randomly sheared and sized-selected DNA. The shotgun reads are assembled by recognizing overlapping regions of sequence and making use of the knowledge of the orientation and distance of the paired reads from each plasmid. Obtaining deep sequence coverage though high levels of sequence redundancy assures that the majority of the genome is represented in the initial assembly and that the consensus sequence is of high quality. Their approach toward the initial assembly was conservative, meaning they would rather fail to join sequence contigs that might overlap each other than risk making false joins between two closely related but non-overlapping genomic regions. Hence, the initial assembly contains many sequence contigs and over time these contigs will increase in size and decrease in number as they are joined together. After shotgun sequencing and assembly there was a second phase of sequencing in which additional sequence was obtained from specific regions that were missing from the original assembly or are recognized to be of low quality in the consensus. The *Neurospora crassa* sequencing project reflects a close collaboration between the Broad Institute and the *Neurospora* research community. Principal investigators include Bruce Birren and Chad Nusbaum from the Broad Institute, Matt Sachs at the Oregon Graduate Institute of Science and Technology, Chuck Staben at the University of Kentucky and Jak Kinsey at the Fungal Genetics Stock Center at the University of Kansas

Medical Center. In addition, we have a larger Advisory Board made up of a number of Neurospora researchers. Sponsors: They have been funded by the National Science Foundation to sequence the N. crassa genome and make the information publicly available.

Abbreviations: NCD

Synonyms: Neurospora crassa Database

Resource Type: data or information resource, database

Keywords: gene, annotation, compendium, contig, distance, drosophila, genome, mitochondrial, neurospora crassa, plasmid, region, rna, sequence, trna, untranslated

Availability: Free, Freely available,

Resource Name: Neurospora crassa Database

Resource ID: SCR_001372

Alternate IDs: nif-0000-20965

Alternate URLs: <http://www.broadinstitute.org/annotation/genome/neurospora/Home.html>

Record Creation Time: 20220129T080207+0000

Record Last Update: 20260729T044010+0000

Ratings and Alerts

No rating or validation information has been found for Neurospora crassa Database.

No alerts have been found for Neurospora crassa Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Grum-Grzhimaylo AA, et al. (2021) Somatic deficiency causes reproductive parasitism in a fungus. Nature communications, 12(1), 783.

Sun Y, et al. (2012) Large-scale introgression shapes the evolution of the mating-type chromosomes of the filamentous ascomycete Neurospora tetrasperma. PLoS genetics, 8(7), e1002820.

Gudimella R, et al. (2010) Fungome: Annotating proteins implicated in fungal pathogenesis. *Bioinformation*, 5(5), 202.

Ischebeck T, et al. (2010) At the poles across kingdoms: phosphoinositides and polar tip growth. *Protoplasma*, 240(1-4), 13.