

Resource Summary Report

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MIPS Ustilago maydis Database

RRID:SCR_007563

Type: Tool

Proper Citation

MIPS Ustilago maydis Database (RRID:SCR_007563)

Resource Information

URL: <http://mips.gsf.de/genre/proj/ustilago/>

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Description: The MIPS Ustilago maydis Genome Database aims to present information on the molecular structure and functional network of the entirely sequenced, filamentous fungus Ustilago maydis. The underlying sequence is the initial release of the high quality draft sequence of the Broad Institute. The goal of the MIPS database is to provide a comprehensive genome database in the Genome Research Environment in parallel with other fungal genomes to enable in depth fungal comparative analysis. The specific aims are to: 1. Generate and assemble Whole Genome Shotgun sequence reads yielding 10X coverage of the U. maydis genome 2. Integrate the genomic sequence assembly with physical maps generated by Bayer CropScience 3. Perform automated annotation of the sequence assembly 4. Align the strain 521 assembly with the FB1 assembly provided by Exelixis 5. Release the sequence assembly and results of our annotation and analysis to public Ustilago maydis is a basidiomycete fungal pathogen of maize and teosinte. The genome size is approximately 20 Mb. The fungus induces tumors on host plants and forms masses of diploid teliospores. These spores germinate and form haploid meiotic products that can be propagated in culture as yeast-like cells. Haploid strains of opposite mating type fuse and form a filamentous, dikaryotic cell type that invades plant tissue to reinitiate infection. Ustilago maydis is an important model system for studying pathogen-host interactions and has been studied for more than 100 years by plant pathologists. Molecular genetic research with U. maydis focuses on recombination, the role of mating in pathogenesis, and signaling pathways that influence virulence. Recently, the fungus has emerged as an excellent experimental model for the molecular genetic analysis of phytopathogenesis, particularly in the characterization of infection-specific morphogenesis in response to signals from host plants. Ustilago maydis also serves as an important model for other basidiomycete plant pathogens that are more difficult to work with in the laboratory, such as the rust and bunt fungi. Genomic sequence of U. maydis will also be valuable for comparative analysis of other fungal genomes, especially with respect to understanding the host range of fungal phytopathogens. The analysis of U. maydis would provide a framework for studying the hundreds of other Ustilago species that attack

important crops, such as barley, wheat, sorghum, and sugarcane. Comparisons would also be possible with other basidiomycete fungi, such as the important human pathogen *C. neoformans*. Commercially, *U. maydis* is an excellent model for the discovery of antifungal drugs. In addition, maize tumors caused by *U. maydis* are prized in Hispanic cuisine and there is interest in improving commercial production. The complete putative gene set of the Broad Institute's second release is loaded into the database and in addition all deviating putative genes from a putative gene set produced by MIPS with different gene prediction parameters are also loaded. The complete dataset will then be analysed, gene predictions will be manually corrected due to combined information derived from different gene prediction algorithms and, more important, protein and EST comparisons. Gene prediction will be restricted to ORFs larger than 50 codons; smaller ORFs will be included only if similarities to other proteins or EST matches confirm their existence or if a coding region was postulated by all prediction programs used. The resulting proteins will be annotated. They will be classified according to the MIPS classification catalogue receiving appropriate descriptions. All proteins with a known, characterized homolog will be automatically assigned to functional categories using the MIPS functional catalog. All extracted proteins are in addition automatically analysed and annotated by the PEDANT suite.

Synonyms: MUMDB

Resource Type: data or information resource, database

Keywords: drug, environment, filamentous, functional, fungal, fungal genome databases, fungus, gene, genetic, basidiomycete, cell, codon, culture, dikaryotic, diploid, genome, genomic, germinate, haploid, host, human, infection, maize, mating, meiotic, model, molecular, morphogenesis, network, orf, pathogen, pathologist, phytopathogen, phytopathogenesis, plant, protein, recombination, sequence, signal, spore, strain, structure, teliospore, teosinte, tissue, tumor, ustilago maydis, virulence, yeast

Resource Name: MIPS Ustilago maydis Database

Resource ID: SCR_007563

Alternate IDs: nif-0000-21276

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260905T133140+0000

Ratings and Alerts

No rating or validation information has been found for MIPS Ustilago maydis Database.

No alerts have been found for MIPS Ustilago maydis Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Bäcker N, et al. (2025) Peroxisomal core structures segregate diverse metabolic pathways. Nature communications, 16(1), 1802.

Elías-Villalobos A, et al. (2015) The Hos2 Histone Deacetylase Controls *Ustilago maydis* Virulence through Direct Regulation of Mating-Type Genes. PLoS pathogens, 11(8), e1005134.

Martínez-Salgado JL, et al. (2013) Analysis of the regulation of the *Ustilago maydis* proteome by dimorphism, pH or MAPK and GCN5 genes. Journal of proteomics, 79, 251.

Steinberg G, et al. (2012) Cytoplasmic fungal lipases release fungicides from ultra-deformable vesicular drug carriers. PloS one, 7(5), e38181.

Teertstra WR, et al. (2011) Absence of repellents in *Ustilago maydis* induces genes encoding small secreted proteins. Antonie van Leeuwenhoek, 100(2), 219.

Pérez-Martín J, et al. (2009) DNA-damage response in the basidiomycete fungus *Ustilago maydis* relies in a sole Chk1-like kinase. DNA repair, 8(6), 720.

Mao N, et al. (2009) Role of Blm and collaborating factors in recombination and survival following replication stress in *Ustilago maydis*. DNA repair, 8(6), 752.

König J, et al. (2009) The fungal RNA-binding protein Rrm4 mediates long-distance transport of *ubi1* and *rho3* mRNAs. The EMBO journal, 28(13), 1855.

Mao N, et al. (2007) Ortholog of BRCA2-interacting protein BCCIP controls morphogenetic responses during DNA replication stress in *Ustilago maydis*. DNA repair, 6(11), 1651.