Magnaporthe comparative Database

RRID:SCR_003079
Type: Tool

Proper Citation

Magnaporthe comparative Database (RRID:SCR_003079)

Resource Information

URL:
http://www.broadinstitute.org/annotation/genome/magnaporthe_comparative/MultiHome.html

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Description: The Magnaporthe comparative genomics database provides accesses to multiple fungal genomes from the Magnaporthaceae family to facilitate the comparative analysis. As part of the Broad Fungal Genome Initiative, the Magnaporthe comparative project includes the finished M. oryzae (formerly M. grisea) genome, as well as the draft assemblies of Gaeumannomyces graminis var. tritici and M. poae. It provides users the tools to BLAST search, browse genome regions (to retrieve DNA, find clones, and graphically view sequence regions), and provides gene indexes and genome statistics. We were funded to attempt 7x sequence coverage comprising paired end reads from plasmids, Fosmids and BACs. Our strategy involves Whole Genome Shotgun (WGS) sequencing, in which sequence from the entire genome is generated and reassembled. Our specific aims are as follows: 1. Generate and assemble sequence reads yielding 7X coverage of the Magnaporthe oryzae genome through whole genome shotgun sequencing. 2. Generate and incorporate BAC and Fosmid end sequences into the genome assembly to provide a paired-end of average every 2 kb. 3. Integrate the genome sequence with existing physical and genetic map information. 4. Perform automated annotation of the sequence assembly. 5. Distribute the sequence assembly and results of our annotation and analysis through a freely accessible, public web server and by deposition of the sequence assembly in GenBank.

Abbreviations: Broad MGG

Synonyms: M. oryzae Database, Magnaporthe comparative genomics database

Resource Type: analysis service resource, database, data analysis service, data or information resource, service resource, production service resource

Keywords: genome, gene, sequencing, magnaporthe, m. grisea genome, m. oryzae

Funding: USDA ;
NSF

Resource Name: Magnaporthe comparative Database

Resource ID: SCR_003079

Alternate IDs: nif-0000-03095

Old URLs: http://www.broad.mit.edu/annotation/genome/magnaporthe_grisea/Home.html

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250411T054827+0000

Ratings and Alerts

No rating or validation information has been found for Magnaporthe comparative Database.

No alerts have been found for Magnaporthe comparative Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Liu X, et al. (2016) Carbamoyl Phosphate Synthetase Subunit MoCpa2 Affects Development and Pathogenicity by Modulating Arginine Biosynthesis in Magnaporthe oryzae. Frontiers in microbiology, 7, 2023.

Zhong K, et al. (2016) MoDnm1 Dynamin Mediating Peroxisomal and Mitochondrial Fission in Complex with MoFis1 and MoMdv1 Is Important for Development of Functional Appressorium in Magnaporthe oryzae. PLoS pathogens, 12(8), e1005823.

Rodríguez-Romero J, et al. (2015) Multilayer regulatory mechanisms control cleavage factor I proteins in filamentous fungi. Nucleic acids research, 43(1), 179.

Zhang Z, et al. (2015) An S-(hydroxymethyl)glutathione dehydrogenase is involved in conidiation and full virulence in the rice blast fungus Magnaporthe oryzae. PloS one, 10(3), e0120627.

Takeda I, et al. (2014) Motif-independent prediction of a secondary metabolism gene cluster using comparative genomics: application to sequenced genomes of Aspergillus and ten other filamentous fungal species. DNA research : an international journal for rapid publication of reports on genes and genomes, 21(4), 447.

Perez-Nadales E, et al. (2014) Fungal model systems and the elucidation of pathogenicity determinants. Fungal genetics and biology : FG & B, 70(100), 42.

Zeng XQ, et al. (2014) Crosstalk between SNF1 pathway and the peroxisome-mediated lipid metabolism in Magnaporthe oryzae. PloS one, 9(8), e103124.

Li L, et al. (2014) MoPex19, which is essential for maintenance of peroxisomal structure and woronin bodies, is required for metabolism and development in the rice blast fungus. PloS one, 9(1), e85252.

Chen G, et al. (2013) Involvement of MoVMA11, a Putative Vacuolar ATPase c' Subunit, in Vacuolar Acidification and Infection-Related Morphogenesis of Magnaporthe oryzae. PloS one, 8(6), e67804.

Wang J, et al. (2013) PTS1 peroxisomal import pathway plays shared and distinct roles to PTS2 pathway in development and pathogenicity of Magnaporthe oryzae. PloS one, 8(2), e55554.