

GEPHE SUMMARY

Mac1 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+Mac1+Gephebase-summary-title)	Gephebase Gene	GP00000560	GepheID
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category+Physiology+Gephebase-summary-title)	Trait Category		
Virulence (https://www.gephebase.org/search-criteria?/and+Trait+Virulence+Gephebase-summary-title)	Trait		
Cryptococcus neoformans	Trait State in Taxon A		
Cryptococcus neoformans	Trait State in Taxon B		
Data not curated	Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Intraspecific+Gephebase-summary-title)	Taxonomic Status		
	Taxon A		Taxon B
	Latin Name		Latin Name
Cryptococcus neoformans (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Cryptococcus+neoformans+Gephebase-summary-title)	Common Name	Cryptococcus neoformans (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Cryptococcus+neoformans+Gephebase-summary-title)	Common Name
-	Synonyms	-	Synonyms
Blastomyces neoformans; Debaryomyces neoformans; Lipomyces neoformans; Saccharomyces neoformans; Torula neoformans; Torulopsis neoformans; Cryptococcus neoformans (San Felice) Vuill. 1901; ATCC 32045; ATCC:32045; BCRC:20528; CCRC 20528; CCRC:20528; DBVPG 6010; DBVPG:6010; IFO 0608; IFO:0608; IGC 3957; IGC:3957; NRRL Y-2534; NRRL Y-8347; NRRL:Y:2534; NRRL:Y:8347; UM-161; UM:161; Filobasidiella neoformans; Filobaxidiella neoformans	Rank	Blastomyces neoformans; Debaryomyces neoformans; Lipomyces neoformans; Saccharomyces neoformans; Torula neoformans; Torulopsis neoformans; Cryptococcus neoformans (San Felice) Vuill. 1901; ATCC 32045; ATCC:32045; BCRC:20528; CCRC 20528; CCRC:20528; DBVPG 6010; DBVPG:6010; IFO 0608; IFO:0608; IGC 3957; IGC:3957; NRRL Y-2534; NRRL Y-8347; NRRL:Y:2534; NRRL:Y:8347; UM-161; UM:161; Filobasidiella neoformans; Filobaxidiella neoformans	Rank
species	Lineage	species	Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Tremellomycetes; Tremellales; Cryptococcaceae; Cryptococcus; Cryptococcus neoformans species complex	Parent	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Tremellomycetes; Tremellales; Cryptococcaceae; Cryptococcus; Cryptococcus neoformans species complex	Parent
Cryptococcus neoformans species complex () - (Rank: species group) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1897064)	NCBI Taxonomy ID	Cryptococcus neoformans species complex () - (Rank: species group) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1897064)	NCBI Taxonomy ID
5207 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5207)	is Taxon A an Intraspecies?	5207 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5207)	is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

CGB_D8050W	Generic Gene Name	UniProtKB Cryptococcus gattii serotype B (strain WM276 / ATCC MYA-4071) E6R4R6 (http://www.uniprot.org/uniprot/E6R4R6)	GenebankID or UniProtKB
CGB_D8050W	Synonyms	()	
36775.XP_003193861.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=36775.XP_003193861.1)	String		
-	Sequence Similarities		
-	GO - Molecular Function		
GO:0005509 : calcium ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005509)	GO - Biological Process		
-			

-	
Unknown (<a +unknown`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Presumptive+Null=">https://www.gephebase.org/search-criteria?/and+Presumptive Null=`Unknown`#gephebase-summary-title)	Presumptive Null
Unknown (<a +unknown`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Molecular+Type=">https://www.gephebase.org/search-criteria?/and+Molecular Type=`Unknown`#gephebase-summary-title)	Molecular Type
Unknown (<a +unknown`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Aberration+Type=">https://www.gephebase.org/search-criteria?/and+Aberration Type=`Unknown`#gephebase-summary-title)	Aberration Type
unknown	Molecular Details of the Mutation
Linkage Mapping (<a +linkage+mapping`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=">https://www.gephebase.org/search-criteria?/and+Experimental Evidence=`Linkage Mapping`#gephebase-summary-title)	Experimental Evidence
Virulence attributes and hyphal growth of <i>C. neoformans</i> are quantitative traits and the MAT α allele enhances filamentation. (2006) (https://pubmed.ncbi.nlm.nih.gov/17112316)	Main Reference
Lin X; Huang JC; Mitchell TG; Heitman J	Authors
	Abstract
<p><i>Cryptococcus neoformans</i> is a fungal human pathogen with a bipolar mating system. It undergoes a dimorphic transition from a unicellular yeast to hyphal filamentous growth during mating and monokaryotic fruiting. The traditional sexual cycle that leads to the production of infectious basidiospores involves cells of both alpha and a mating type. Monokaryotic fruiting is a modified form of sexual reproduction that involves cells of the same mating type, most commonly alpha, which is the predominant mating type in both the environment and clinical isolates. However, some a isolates can also undergo monokaryotic fruiting. To determine whether mating type and other genetic loci contribute to the differences in fruiting observed between alpha and a cells, we applied quantitative trait loci (QTL) mapping to an inbred population of F2 progeny. We discovered that variation in hyphal length produced during fruiting is a quantitative trait resulting from the combined effects of multiple genetic loci, including the mating type (MAT) locus. Importantly, the alpha allele of the MAT locus enhanced hyphal growth compared with the a allele. Other virulence traits, including melanization and growth at 39 degrees C, also are quantitative traits that share a common QTL with hyphal growth. The Mac1 transcription factor, encoded in this common QTL, regulates copper homeostasis. MAC1 allelic differences contribute to phenotypic variation, and mac1Delta mutants exhibit defects in filamentation, melanin production, and high temperature growth. Further characterization of these QTL regions will reveal additional quantitative trait genes controlling biological processes central to fungal development and pathogenicity.</p>	
	Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS