

## GEPHE SUMMARY

	Gephebase Gene	GephelD
Mac1 ( <a href="https://www.gephebase.org/search-criteria/?and+Gene">https://www.gephebase.org/search-criteria/?and+Gene</a> Gephebase="Mac1">#gephebase-summary-title)	GP00000560	
	Entry Status	Main curator
Published	Martin	

## PHENOTYPIC CHANGE

	Trait Category		
Physiology ( <a href="https://www.gephebase.org/search-criteria/?and+Trait">https://www.gephebase.org/search-criteria/?and+Trait</a> Category="Physiology">#gephebase-summary-title)	Trait		
Virulence ( <a href="https://www.gephebase.org/search-criteria/?and+Trait=^Virulence^#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Trait=^Virulence^#gephebase-summary-title</a> )	Trait State in Taxon A		
Cryptococcus neoformans	Trait State in Taxon B		
Cryptococcus neoformans	Ancestral State		
Data not curated	Taxonomic Status		
Intraspecific ( <a href="https://www.gephebase.org/search-criteria/?and+Taxonomic">https://www.gephebase.org/search-criteria/?and+Taxonomic</a> Status="Intraspecific">#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Cryptococcus neoformans ( <a href="https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Cryptococcus+neoformans^#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Cryptococcus+neoformans^#gephebase-summary-title</a> )		Cryptococcus neoformans ( <a href="https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Cryptococcus+neoformans^#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Cryptococcus+neoformans^#gephebase-summary-title</a> )	
-	Common Name	-	Common Name
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	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	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Tremellomycetes; Tremellales; Cryptoccaceae; Cryptococcus; Cryptococcus neoformans species complex	Lineage	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Tremellomycetes; Tremellales; Cryptoccaceae; Cryptococcus; Cryptococcus neoformans species complex	Lineage
Cryptococcus neoformans species complex () - (Rank: species group) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1897064">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1897064</a> )	Parent	Cryptococcus neoformans species complex () - (Rank: species group) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1897064">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1897064</a> )	Parent
NCBI Taxonomy ID 5207 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5207">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5207</a> )		NCBI Taxonomy ID 5207 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5207">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5207</a> )	
is Taxon A an Infraspecies?		is Taxon B an Infraspecies?	
No		No	

## GENOTYPIC CHANGE

CGB_D8050W	Generic Gene Name	UniProtKB Cryptococcus gattii serotype B (strain WM276 / ATCC MYA-4071) E6R4R6 ( <a href="http://www.uniprot.org/uniprot/E6R4R6">http://www.uniprot.org/uniprot/E6R4R6</a> )
CGB_D8050W	Synonyms	GenebankID or UniProtKB 0
367775.XP_003193861.1 ( <a href="http://string-db.org/newstring_cgi/show_network_section.pl?identifier=367775.XP_003193861.1">http://string-db.org/newstring_cgi/show_network_section.pl?identifier=367775.XP_003193861.1</a> )	String	
-	Sequence Similarities	
GO - Molecular Function GO:0005509 : calcium ion binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005509">https://www.ebi.ac.uk/QuickGO/term/GO:0005509</a> ) GO - Biological Process		

Unknown ( <a href="https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^Unknown">#gephebase-summary-title)</a>	Presumptive Null
Unknown ( <a href="https://www.gephebase.org/search-criteria?/and+Molecular+Type=^Unknown">#gephebase-summary-title)</a>	Molecular Type
Unknown ( <a href="https://www.gephebase.org/search-criteria?/and+Aberration+Type=^Unknown">#gephebase-summary-title)</a>	Aberration Type
unknown	Molecular Details of the Mutation
Linkage Mapping ( <a href="https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Linkage+Mapping">#gephebase-summary-title)</a>	Experimental Evidence
Virulence attributes and hyphal growth of <i>C. neoformans</i> are quantitative traits and the MATalpha allele enhances filamentation. (2006) ( <a href="https://pubmed.ncbi.nlm.nih.gov/17112316/">https://pubmed.ncbi.nlm.nih.gov/17112316/</a> )	Main Reference
Lin X; Huang JC; Mitchell TG; Heitman J	Authors
Cryptococcus neoformans 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 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.	Abstract
	Additional References

## RELATED GEPHE

No matches found.	Related Genes
No matches found.	Related Haplotypes

## EXTERNAL LINKS

## COMMENTS