



**GLYOXYLATE CYCLE AND ALTERNATIVE CARBON METABOLISM IN  
METABOLIC FLEXIBILITY AND PATHOGENICITY OF  
*Candida glabrata***

**CHEW SHU YIH**

**FPSK(p) 2020 19**



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*Candida glabrata*

By  
CHEW SHU YIH

Thesis submitted to the School of Graduate Studies, Universiti Putra  
Malaysia, in fulfilment of the requirements for the Degree of Doctor of  
Philosophy

November 2019

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Abstract of thesis presented to the Senate of Universiti Putra Malaysia in  
fulfilment of the requirement for the degree of Doctor of Philosophy

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**November 2019**

**Chairman : Leslie Than Thian Lung, PhD**  
**Faculty : Medicine and Health Sciences**

Distinct microenvironments in the host can differ significantly (e.g. nutrients availability) and that *Candida glabrata*, in order to be an effective human pathogen, must transit between these niches and adapt to the differences. In addition, most of the immune cells also actively deprive nutritional resources from invading pathogens, which makes the survival of intracellular pathogens even more challenging. *Candida glabrata* appears to utilise unique stealth, evasion and persistence strategies in subverting the onslaught of host immune response during systemic infection. In fact, it is surprising that *C. glabrata* triggers its own engulfment by macrophages. Considering the glucose-deficient condition within the macrophages, *C. glabrata* must be able to assimilate endogenous resources such as alternative carbon sources for their survival. The present study concentrated on the impact of alternative carbon metabolism in the metabolic flexibility and pathogenicity of *C. glabrata*. Growth on alternative carbon sources such as acetate, lactate, ethanol and oleic acid induced alteration in several fitness and pathogenic attributes of *C. glabrata*. These include the reduction in planktonic growth, biofilm formation, and oxidative stress resistance. Alternative carbon sources also modulated the cell wall architecture of *C. glabrata*, as demonstrated by the reduction of  $\beta$ -glucan and chitin layer, and the increase of mannan layer. Furthermore, the antifungal resistance of *C. glabrata* grown in alternative carbon sources was significantly enhanced. The metabolic regulation of alternative carbon metabolism in *C. glabrata* was subsequently explored using high-throughput transcriptomic and proteomic analyses in response to acetate, an alternative carbon source that has been proven to be

relevant *in vivo*. Collectively, both transcriptome and proteome data revealed that the regulation of alternative carbon metabolism in *C. glabrata* substantially resembled human fungal pathogens such as *Candida albicans* and *Cryptococcus neoformans*, with up-regulation of many proteins and transcripts from the glyoxylate cycle and gluconeogenesis, namely isocitrate lyase (*ICL1*), malate synthase (*MLS1*), phosphoenolpyruvate carboxykinase (*PCK1*) and fructose 1,6-biphosphatase (*FBP1*). In the absence of glucose, *C. glabrata* shifted its metabolism to hexose anabolism from the available carbon source. The results essentially suggest that the gluconeogenic metabolism are possibly critical for the survival of phagocytosed *C. glabrata* within the glucose-deficient macrophages. The importance of the glyoxylate cycle enzyme gene *ICL1* in the metabolic flexibility and pathogenicity of *C. glabrata* was further substantiated by the comprehensive analyses of *icl1Δ* mutant strains. Indeed, disruption of *ICL* rendered *C. glabrata* unable to assimilate several alternative carbon sources, as well as reduced its biofilm formation capability. In addition, *ICL1* is also pivotal for the survival of phagocytosed *C. glabrata*, as the *icl1Δ* mutant strains were significantly more susceptible to macrophage killing relative to wild-type strain. Finally, evaluation of *icl1Δ* mutant strains in a mouse model of invasive candidiasis showed that *ICL1* is essentially required for the full virulence of *C. glabrata* *in vivo*. In conclusion, the present study demonstrated that alternative carbon metabolism and the glyoxylate cycle is crucial for the metabolic flexibility and pathogenicity of *C. glabrata* *in vitro* and *in vivo*. The findings implicate *ICL1* as a promising target in the development of novel and innovative treatments for a better management of invasive candidiasis.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia  
sebagai memenuhi keperluan untuk ijazah Doktor Falsafah

**KITAR GLIOKSILAT DAN METABOLISME KARBON ALTERNATIF  
DALAM FLEKSIBILITI METABOLIK DAN KEPATOGENAN**  
*Candida glabrata*

Oleh

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Persekutuan mikro dalam perumah boleh berbeza dengan ketara (ketersediaan nutrien) dan *Candida glabrata*, untuk menjadi patogen manusia yang berkesan, mesti transit antara nic perumah dan menyesuaikan diri dengan perbezaan ini. Tambahan pula, kebanyakkan sel-sel imun juga melucutkan sumber pemakanan secara aktifnya daripada pathogen penyerang, dan ini menjadikan survival pathogen intraselular lebih mencabar. *Candida glabrata* menggunakan strategi penyelinapan, pengelakan dan pengekalan yang unik untuk melawan gerak balas imun perumah semasa jangkitan sistemik. Malah, *C. glabrata* juga mencetuskan fagositosisnya oleh sel makrofaj. Memandangi keadaan kekurangan glukosa dalam sel makrofaj, *C. glabrata* mesti mengasimilasi sumber endogen seperti sumber karbon alternatif untuk menjamin survival mereka. Penyelidikan ini bertujuan untuk mengkaji kesan metabolisme karbon alternatif terhadap fleksibiliti metabolismik dan kepatogenan *C. glabrata*. Pertumbuhan dalam sumber karbon alternatif seperti asetat, laktat, etanol dan asid oleik membawa perubahan kepada beberapa sifat kecergasan dan patogen *C. glabrata*. Ini termasuk pengurangan pertumbuhan planktonik, pembentukan biofilm, dan rintangan oksidatif. Sumber karbon alternatif juga memodulasi seni bina dinding sel *C. glabrata*, seperti yang ditunjukkan dalam pengurangan lapisan  $\beta$ -glukan dan kitin, dan peningkatan lapisan manan. Tambahan pula, rintangan antikulat *C. glabrata* dalam sumber karbon alternatif juga telah dipertingkatkan dengan ketara. Pengawalaturan metabolisme karbon alternatif *C. glabrata* dalam asetat dikaji dengan menggunakan analisis transkrip dan protein keupayaan celusan tinggi. Secara keseluruhannya, data transkrip dan protein menunjukkan bahawa pengawalaturan metabolisme karbon alternatif *C. glabrata* menyerupai

patogen kulat manusia seperti *Candida albicans* dan *Cryptococcus neoformans*, dengan peningkatan pengawalaturan protein dan transkrip dari kitaran glioksilat dan glukoneogenesis, termasuk isositrat liase (*ICL1*), malat sintase (*MLS1*), fosfoenolpiruvat karboksikinase (*PCK1*) dan fruktosa 1,6-bifosfat (*FBP1*). Semasa ketidakhadiran glukosa, *C. glabrata* mengalih metabolismenya ke anabolisme glukosa dengan menggunakan sumber karbon yang sedia ada. Hasil kajian mencadangkan bahawa kitaran glioksilat dan glukoneogenesis berkemungkinan kritikal kepada survival *C. glabrata* dalam sel makrofaj yang kekurangan glukosa. Kepentingan kitaran glioksilat dalam fleksibiliti metabolik dan kepatogenan *C. glabrata* juga dibuktikan oleh analisis komprehensif strain mutan *icl1Δ*. Penghapusan gen *ICL1* menghalang *C. glabrata* daripada mengasimilasi beberapa sumber karbon alternatif, dan juga mengurangi keupayaannya dalam pembentukan biofilm. Di samping itu, *ICL1* adalah penting untuk survival fagositosis *C. glabrata*, kerana strain mutan *icl1Δ* lebih mudah terdedah kepada pembunuhan makrofaj berbanding dengan strain jenis liar. Akhir sekali, penilaian strain mutan *icl1Δ* dalam model tikus kandidiasis invasif menunjukkan bahawa *ICL1* diperlukan untuk virulensi *C. glabrata in vivo*. Kesimpulannya, kajian ini menunjukkan bahawa metabolisme karbon alternatif dan kitaran glioksilat adalah penting untuk fleksibiliti metabolik dan kepatogenan *C. glabrata in vitro* dan *in vivo*. Penemuan ini mencadangkan *ICL1* sebagai sasaran berpotensi dalam perkembangan rawatan baru dan inovatif untuk pengurusan kandidiasis yang lebih baik.

## **ACKNOWLEDGEMENTS**

First and foremost, I wish to express my sincere and deepest appreciation to my respectful supervisor Associate Professor Dr Leslie Than Thian Lung for his continuous support, invaluable guidance, advice and unfailing help throughout my entire research project. His immeasurable kindness and patience are commendable.

To all my co-supervisors, namely Professor Dr Alistair J.P. Brown, Professor Dr Cheah Yoke Kqueen, and Associate Professor Dr Ho Kok Lian, thanks for all the humble thoughts, guidance, suggestions and supports throughout my study.

Not forgetting also to my dedicated colleagues, labmates and friends namely Der Jiun, Tzu Shan, Premmala, Sulin, Hadiza, Hassan, Fish, Amri, Zaim, Wallace, Yi-Linn, Angela, Theysshana and many others whom I did not mention here. I would like to thank them for their endless supports, helps and guidance. I am forever grateful to all of them for sharing their experience and knowledge with me throughout the highs and lows of my research project.

Finally, I would like to extend my acknowledgements to Dr. Benjamin Lau from Malaysian Palm Oil Board (MPOB) and all the members from Department of Medical Microbiology and Parasitology for their kind assistances. Also, to all others who have attributed and involved one way another to the successful completion of my study, they are conferred with my sincere appreciation. Finally, a special thanks to my beloved parents, brother and sister for their relentless love, understanding and utmost moral support throughout my study.

This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfilment of the requirement for degree of Doctor of Philosophy. The members of the Supervisory Committee were as follows:

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## LIST OF ABBREVIATIONS

ABC	ATP-binding cassette
ABPA	Allergic bronchopulmonary aspergillosis
AFB1	Aflatoxin B1
AGC	Automatic gain control
AIDS	Acquired immunodeficiency syndrome
ATCC	American Type Culture Collection
BLAST	Basic local alignment search tool
BSI	Bloodstream infection
CDS	Coding sequences
CFU	Colony-forming-unit
CHAPS	3-[(3-Cholamidopropyl)dimethylammonio]-1-propanesulfonate
CLSI	Clinical and Laboratory Standards Institute
CNA	Chronic necrotising aspergillosis
CNS	Central nervous systems
CO <sub>2</sub>	Carbon dioxide
CoA	Coenzyme A
COMeT	Comparative Medicine and Technology Unit
CSRE	Carbon source-responsive element
CT	Cycle threshold
CWPs	Cell wall proteins
DAVID	Database for Annotation, Visualization, and Integrated Discovery
DEGs	Differential expressed genes
DEPs	Differential expressed proteins
DHA	Drug:H <sup>+</sup> antiporter
DHAP	Dihydroacetone phosphate
DMEM	Dulbecco's Modified Eagle's Medium
DTT	Dithiothreitol
EASE	Expression analysis systematic explorer
ECM	Extracellular matrix
EDTA	Ethylenediaminetetraacetic acid
ELISA	Enzyme-linked immunosorbent assay
FBS	Foetal bovine serum
FDR	False discovery rate
FPKM	Fragments per kilobase of transcript per million mapped fragments
GFP	Green fluorescent protein
GI	Gastrointestinal
GM-CFS	Granulocyte-macrophage colony-stimulating factor
GO	Gene ontology
GPI	Glycosylphosphatidylinositol
H <sub>2</sub> O <sub>2</sub>	Hydrogen peroxide
HAART	Highly active anti-retroviral therapy

HCC	Hepatocellular carcinoma
HCD	High-energy collisional dissociation
HIV	Human immunodeficiency virus
HSCT	Haematopoietic stem-cell transplantation
IACUC	Institutional Animal Care and Use Committee
ICR	Institute of Cancer Research
ICU	Intensive care unit
IPA	Invasive pulmonary aspergillosis
iTRAQ	Isobaric tags for relative and absolute quantitation
ITS	Internal transcribed spacer
KEGG	Kyoto Encyclopedia of Genes and Genomes
LOS	Length of stay
m/z	Mass-to-charge ratio
MAPK	Mitogen-activated protein kinase
MDR	Multidrug-resistance
MFS	Major facilitator superfamily
MIC	Minimum inhibitory concentration
MOI	Multiplicity of infection
MPO	Myeloperoxidase
MPOB	Malaysian Palm Oil Board
MTL	Mating type-like locus
NADPH	Nicotinamide adenine dinucleotide phosphate
NCAC	Non-albicans <i>Candida</i> species
NCBI	National Centre for Biotechnology Information
NGS	Next generation sequencing
OD	Optical density
OPC	Oropharyngeal candidiasis
OTC	Over-the-counter
PAS	Periodic acid-Schiff
PATH	Prospective antifungal therapy
PBS	Phosphate buffered saline
PCP	<i>Pneumocystis</i> pneumonia
PCR	Polymerase chain reaction
PDB	Protein Data Bank
PMN	Polymorphonuclear neutrophils
PRR	Pattern recognition receptor
qPCR	Quantitative real-time PCR
RIN	RNA integrity number
ROS	Reactive oxygen species
RPMI	Roswell Park Memorial Institute
SC	Synthetic complete
SCFAs	Short chain fatty acids
SD	Standard deviations
SDA	Sabouraud dextrose agar
SDS	Sodium dodecyl sulphate
SEM	Scanning electron microscopy
SOT	Solid organ transplantation

SPE	Solid phase extraction
SV	Spin/vacuum
TBE	Tris-Borate-EDTA
TCA	Tricarboxylic acid
TCEP	Tris(2-carboxyethyl)phosphine
TEM	Transmission electron microscopy
UHPLC	Ultra-high-performance liquid chromatography
UV	Ultraviolet
VVC	Vulvovaginal candidiasis
WT	Wild type
XTT	2, 3-bis-(2-methoxy-4-nitro-5-sulfophenyl)-2H tetrazolium-5-carboxanilide
YNB	Yeast nitrogen base
YPD	Yeast-peptone-dextrose

# CHAPTER 1

## INTRODUCTION

### 1.1 Introduction

Nearly 150 million of human populations are affected by potentially life-threatening fungal infections worldwide (Bongomin et al., 2017). However, these fungal diseases are as yet a disregarded issue by public health authorities even though most deaths caused by fungal infections are preventable (Bongomin et al., 2017). Invasive candidiasis, a systemic fungal infection caused by *Candida* species arises regularly among hospitalised individuals in the developed countries and is widely acknowledged as the cause of high morbidity and mortality (>50,000 deaths annually), primarily due to delay in diagnosis and commencement of fitting antifungals (Kullberg and Arendrup, 2015; Ben-Ami, 2018). Invasive candidiasis is one of the most common invasive mycoses and comprises of bloodstream infection (candidaemia) and deep-seated infection (Kullberg and Arendrup, 2015; Calandra et al., 2016). Also, candidaemia is associated with longer length of stay (LOS) and high financial burden up to USD 40,000 per person (Zaoutis et al., 2005; Strollo et al., 2017).

Approximately 10 - 20% of the *Candida* species discovered, including common species such as *Candida albicans*, *Candida glabrata*, *Candida krusei*, *Candida tropicalis*, and *Candida parapsilosis* have been implicated to cause invasive candidiasis in human (Pfaller et al; 2014; Yapar, 2014). Distribution of *Candida* species that cause infection has been changing throughout the last decade, with a diminishing prevalence of *C. albicans* and emergence of non-*albicans* *Candida* species (NCAC) (Lamoth et al., 2018). Notably, *C. glabrata* has been recognised as either second or third commonest cause of invasive candidiasis after *C. albicans*, and similar epidemiology have also been highlighted in multiple global surveillance programmes such as SENTRY, ARTEMIS and TRANSNET (Messer et al., 2006; Messer et al., 2009; Pfaller et al., 2010; Andes et al., 2016). Invasive candidiasis caused by *C. glabrata* is most commonly associated with patients with solid tumours and solid organ transplantation (Pfaller et al., 2014). Furthermore, *C. glabrata* candidaemia often has a longer LOS and imposes higher costs when compared to candidaemia caused by *C. albicans* (Moran et al., 2010).

Host immunity and pathogenicity of *Candida* are believed to be crucial for establishment of candidiasis (Silva et al., 2012). For instance, fitness and pathogenic attributes such as biofilm formation, phenotypic switching, secretion of hydrolytic enzymes, drug resistance and enhanced metabolic flexibility are all associated with the virulence of *Candida* species (Sardi et al., 2013). Relative to *C. albicans*, the fitness and pathogenic attributes of *C. glabrata* are not well-studied,

particularly in their natural niche. It has been shown that higher proportion of *C. glabrata* candidaemia shows increased resistance to antifungals such as azoles and echinocandins (Lee et al., 2009; Perlin, 2015) compared to *C. albicans*. However, *C. glabrata* is incapable to form hyphae and produce tissue-damaging hydrolytic enzymes (Silva et al., 2012), which explains the relatively less aggressive nature of this particular fungal pathogen.

Compared to the aggressive *C. albicans*, *C. glabrata* elicits a weaker polymorphonuclear neutrophils (PMN) activation that could trigger the recruitment of monocytic cells to the site of infection and subsequent monocytic engulfment (Duggan et al., 2015). Since *C. glabrata* is able to survive within macrophages, but not within neutrophils, this fungal pathogen could use monocytes or macrophages as potential “Trojan horses” to gain protection against the host defence system, especially neutrophils attack (Seider et al., 2011; Seider et al., 2014; Duggan et al., 2015). *Candida glabrata* clearly pursues a different immune evasion and persistence strategies to *C. albicans*, as escape from the macrophages upon engulfment is not the priority of this fungal pathogen. In fact, *C. glabrata* persists and propagates within the microenvironment of macrophages without causing any significant damage to the host, but eventually leads to cell burst and release the fungal progenies.

While trapped within macrophages, *C. glabrata* relies on endogenous resources for survival as the microenvironment is often depicted as glucose-deficient (Lorenz et al., 2004; Kaur et al., 2007). It has been shown that the ability of *C. glabrata* in mobilisation of the intracellular resources through autophagy serves as a major contributor to sustain viability of this pathogen during glucose deprivation (Roetzer et al., 2010; Shimamura et al., 2019). Besides recycling the intracellular resources via autophagy, the ability to utilise alternative carbon sources other than glucose could also potentially assist in the survival of engulfed *C. glabrata*. In fact, fundamental metabolic pathways involved in alternative carbon metabolism, including  $\beta$ -oxidation of fatty acids, the glyoxylate cycle and gluconeogenesis have been shown to be highly induced in phagocytosed-*C. albicans* (Lorenz et al., 2004), signifying that glucose deprivation and the availability of alternative carbon sources are indeed relevant *in vivo*. The principle function of these interconnected pathways is the generation of key metabolic intermediates from alternative carbon sources for growth and survival of the pathogen *in vivo*.

Besides, the key metabolic enzyme genes from  $\beta$ -oxidation of fatty acids (*FOX2*, encoded for  $\beta$ -oxidation multifunctional protein), the glyoxylate cycle (*ICL1*, encoded for isocitrate lyase) and gluconeogenesis (*FBP1*, encoded for fructose-1,6-biphosphatase) have been proven to be essential for the full virulence of *C. albicans* (Ramírez and Lorenz, 2007), as disruption of these genes confers a severe attenuation in the virulence in a mouse model of invasive candidiasis. All these

findings suggest that enhanced metabolic flexibility through alternative carbon metabolism could be a virulence determinant in *Candida* species.

To date, little is known about the alternative carbon metabolism of *C. glabrata* in their natural niche. The contribution of alternative carbon metabolism in the physiological and pathogenic attributes of *C. glabrata*, as well as the regulation of transcriptional and proteomic network still remain unresolved. In addition, the essential role of one of the metabolic pathways, the glyoxylate cycle (*ICL1*) in the metabolic flexibility and virulence of *C. glabrata* also warrants further investigation. It is envisaged that the knowledge generated from investigating the glyoxylate cycle and alternative carbon metabolism of *C. glabrata* will provide insights into devising novel and innovative strategies for reducing the severity of invasive candidiasis worldwide.

## 1.2 Objectives

### **General objective:**

To investigate the role of alternative carbon metabolism and the glyoxylate cycle in the metabolic flexibility and pathogenicity of *C. glabrata*.

### **Specific objectives:**

1. To investigate the impact of alternative carbon metabolism on the fitness attributes of *C. glabrata*.
2. To decipher the impact of alternative carbon metabolism on the transcriptional and proteomic landscapes of *C. glabrata*.
3. To investigate the essential role of glyoxylate cycle gene *ICL1* in the metabolic flexibility and virulence of *C. glabrata*.

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