



# THE HIDDEN WORLD WITHIN: EXPLORING THE MYCOBIOTA

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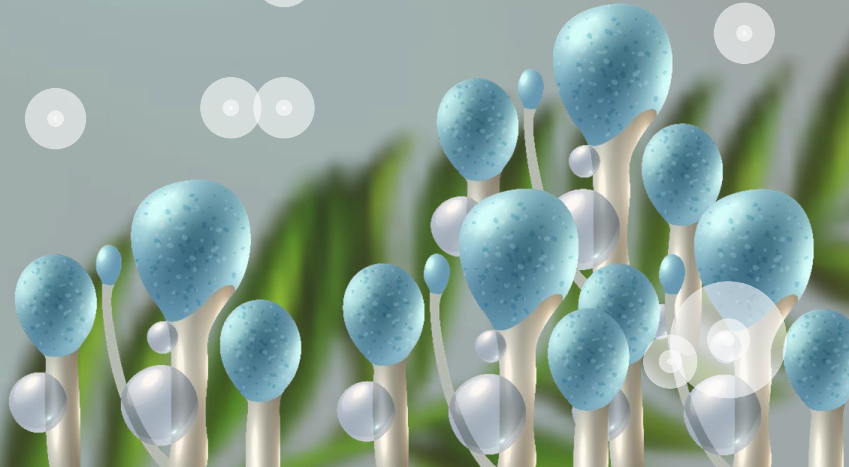


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01

# INTRODUCTION

*what is the Mycobiota?*



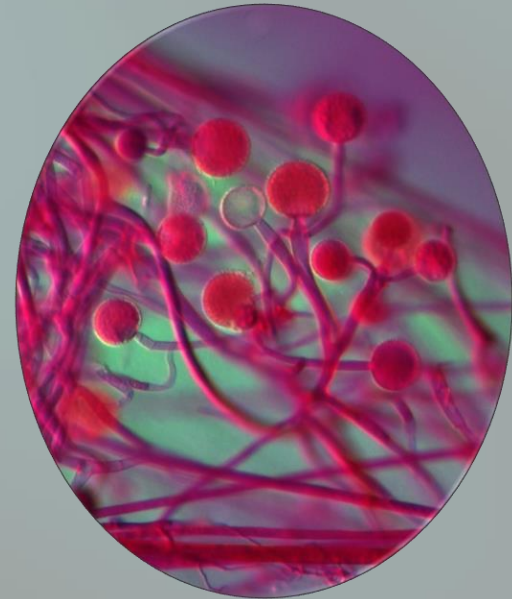
- The term “microbiota” invokes images of mucosal surfaces densely populated with bacteria.
- However, research from this past decade has started to complete the picture by focusing on largely neglected components of the microbiota: **archaea, fungi, protozoa, & viruses.**
- The community of commensal fungi, the **mycobiota**, interacts with commensal bacteria & the host, influencing overall body health and homeostasis.



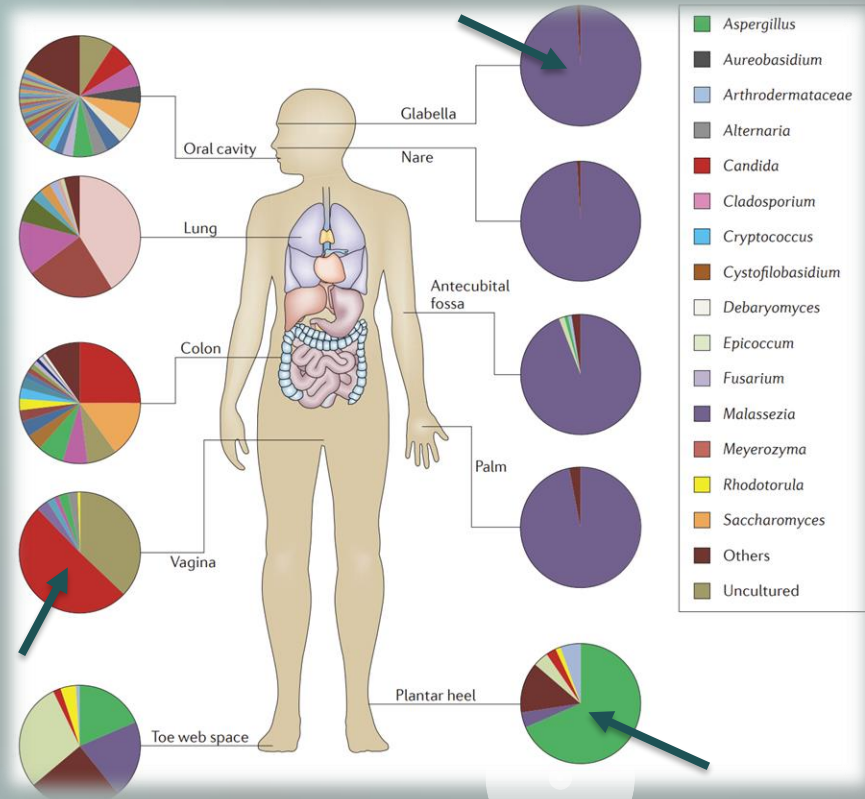
- Fungi are **microeukaryotes** which their presence in humans was historically thought to be only associated with pathogenesis.
- It was recently proved they can be **isolated** from humans in the **absence of disease**.
- Investigation of intestinal commensal-host symbiosis places emphasis on gut bacteria while neglecting gut fungi due to their **lower abundance** (**0.01–0.1%** of gut microbiome).
- In the period of 2008–2018, there have been almost 100 times more peer-reviewed publications on microbiota than on mycobiota.



- Notably, despite relatively small number of gut fungi, they profoundly affect intestinal homeostasis & barrier function.
- They also interact with the host immune system, impacting mucosal immune responses & inflammation.
- Though there is still relatively **poor understanding** of the influence of gut mycobiota on host's health & disease, imbalance in gut mycobiota has been linked to various **gastrointestinal & systemic diseases**.



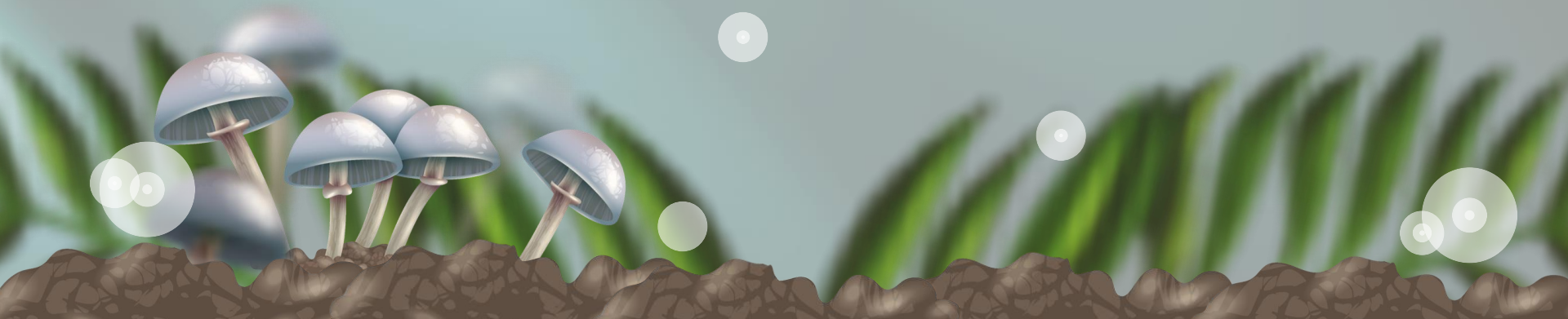
- Complex populations of fungi have been found associated with the **skin & all mucosal surfaces** of the healthy human body, especially the **GIT**.
- The fungal populations that are found on mucosal surfaces tend to be more diverse than those on the skin.
- In general, ***Malassezia spp.***, ***Aspergillus spp.***, & ***Candida spp.*** are among the most fungal Mycobiota isolated from healthy individuals.



# FACTORS INFLUENCING THE MYCOBIOME



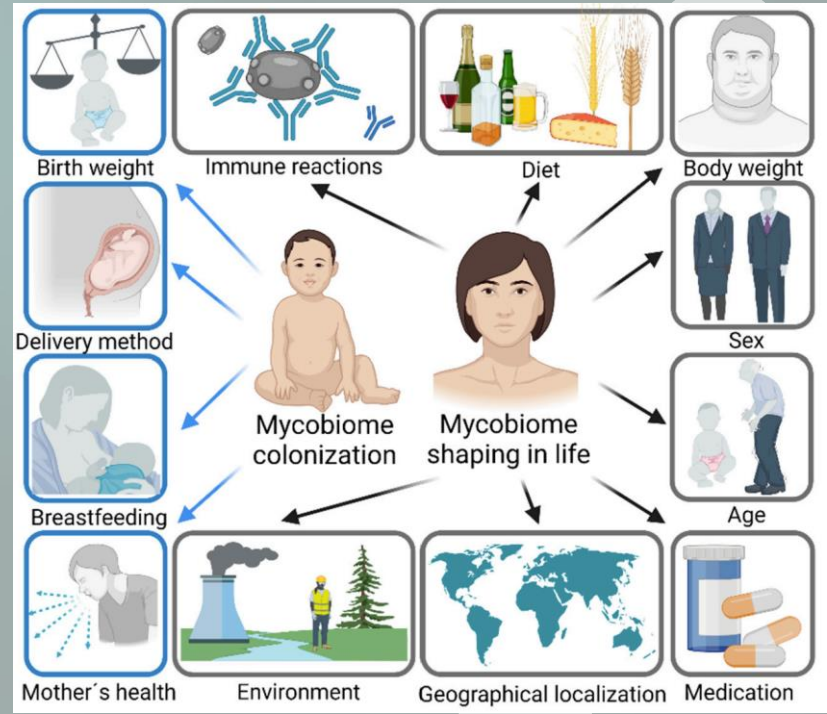
02





- Compared to the bacterial microbiome, the mycobiome seems to be **less consistent & less stable over time.**

- The mycobiome is primarily shaped by **delivery mode, diet, body weight, sex, age, medication, immune responses, the environment & geographical localization.**



**Table 1** Factors affecting the composition of gut mycobiota

Factors		Composition of gut mycobiota	References
Delivery method	➔ Natural birth	Fungi from mother's genital tract ↑ Russulales ↑	[37, 40–42]
	➔ C-section	Fungi from maternal skin and surroundings ↑ Saccharomycetales ↑	
Gestational age	➔ Preterm infants	Fungal diversity ↓ Saccharomycetales ↑ <i>Candida</i> ↑	[37]
	➔ Term infants	Polyporales ↑ Russulales ↑ <i>Stereum</i> ↑ <i>Malassezia</i> ↑	
Environment	Mice from Jackson Laboratory's & Services (JAX)	Basidiomycota ↑	[18, 43]

Season

- Naturally born infants are more likely to get *Candida spp.* from maternal genital tract, whereas infants born after cesarean delivery are more likely to get *Malassezia spp.* from maternal skin.
- Preterm delivery is specifically associated with *Candida spp.*, while term delivery is associated with increased *Malassezia spp.* colonization.

Diet and nutrition

N

**Table 2.** The list of food products colonized or contaminated by food-borne microscopic fungi.

Food Product	Microscopic Fungi	References
<b>Fruit and vegetables</b>		
Fresh citrus and grape	<i>Candida prunicola</i> , <i>Pichia fermentans</i>	[66]
Fresh apple, plum and pear	<i>Saccharomyces cerevisiae</i> , <i>Pichia kluyveri</i> , <i>Pichia kudriavzevii</i> , <i>Galactomyces candidus</i> , <i>Hanseniaspora uvarum</i> , <i>Hanseniaspora guilliermondii</i>	[67]
Peeled fruit salads	<i>Candida</i> sp., <i>Debaryomyces</i> sp., <i>Rhodotorula</i> sp., <i>Penicillium</i> sp., <i>Cladosporium</i> sp.	[68]
Dried fruit	<i>Cladosporium</i> sp., <i>Aspergillus niger</i> , <i>Aspergillus tubingensis</i> , <i>Penicillium palitans</i>	[68,69]
Various fresh vegetables (salad, tomato, cucumber, green onion, lettuce, spinach, etc.)	<i>Geotrichum</i> sp., <i>Alternaria</i> sp., <i>Cladosporium</i> sp., <i>Penicillium</i> sp.	[68,70]
<b>Dairy</b>		
Various cheeses (Blue cheese, Camembert, Cheddar)	<i>Penicillium</i> sp., <i>Candida</i> sp., <i>Scopulariopsis</i> sp.	[64]
Acidophilus milk	<i>Saccharomyces fragilis</i> , <i>Candida pseudotropicalis</i>	[71,72]
<b>Meat</b>		
Various meats (fermented sausage, dried meat, salami, ham)	<i>Debaryomyces</i> sp., <i>Penicillium</i> sp.	[64]
<b>Beverages</b>		
Wine	<i>Hanseniaspora</i> sp., <i>Saccharomyces</i> sp.	[73,74]
Beer	<i>Brettanomyces</i> sp., <i>Saccharomyces</i> sp.	[73,74]
Sake	<i>Aspergillus</i> sp., <i>Saccharomyces</i> sp.	[73]
<b>Other</b>		
Various nuts (pecan, almond, walnut, pine nut)	<i>Aspergillus</i> sp., <i>Penicillium</i> sp., <i>Alternaria</i> sp., <i>Cladosporium</i> sp., <i>Rhizopus</i> sp., <i>Fusarium</i> sp.	[69]
Koji	<i>Aspergillus</i> sp., <i>Rhizopus</i> sp.	[75]
Soy sauce	<i>Aspergillus</i> sp., <i>Hansenula</i> sp., <i>Zygosaccharomyces</i> sp.	[73]
Steamed pastry	<i>Wickerhamomyces anomalus</i>	[76,77]

M

O

Gender

Metabolic disorder

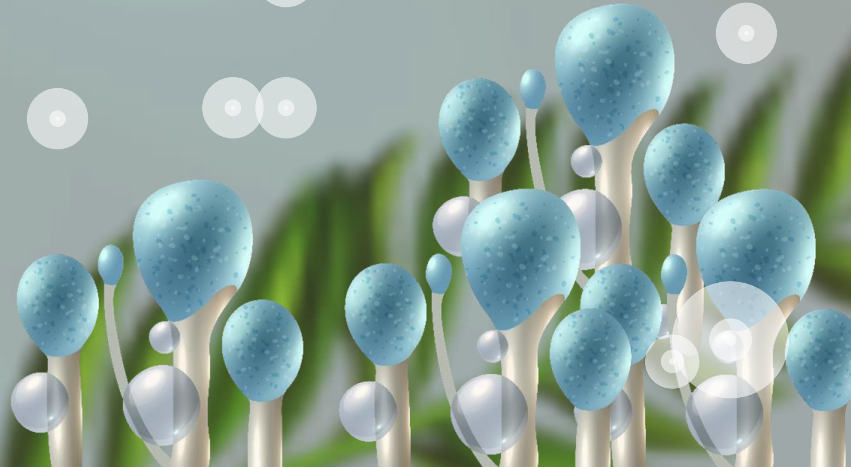
Maternal antibiotic exposure

Species

decreases  
the gut.  
positively  
tively with

03

# METHODOLOGIES FOR STUDYING MYCOBIOTA



- Methodologies for studying gut mycobiome are divided into culture-dependent & culture-independent methods.

- Traditionally, fungal diversity was assessed using **culture-dependent methods**, using various culture media as SDA & CHROMagar™ *Candida* medium used for *Candida* isolation & differentiation.

- ID fungi plate culture with MALDI-TOF MS is suitable for identification of filamentous fungi.



Device for rapid identification of molds and dermatophytes by MALDI-TOF

- Though cultivation of fungi is the most direct method with visualization of fungal morphology and colony color, there are some limitations in its application:

- ✓ During cultivation, the **environmental fungi may contaminate culture** & easily affect the precision of results.
- ✓ It is **difficult to distinguish** specific species and genus of similarly looking fungi even by microscope.
- ✓ Some fungi **cannot be cultured**.
- ✓ Culture methods are very **time-consuming**.




- **Culture-independent methods** depends on recent advances in deep-sequencing technologies and bioinformatics analysis, which are based on the analysis of genomic DNA, shedding light on the complexity of the gut fungal communities.
- Generally, many culture-independent methods have been developed, such as sequencing for 18s ribosomal DNA, ITS-1 and 2, & RFLP.
- The advent of sequencing technology allowed us to answer important questions about fungi:
  - ✓ Which fungi do commensal communities comprise?
  - ✓ Are they transiently present or do they stably colonize?
  - ✓ What are their functions?
- Overall, there is **no consensus on the optimal methodology** for characterizing mycobiome.



The background features a soft, light blue gradient. On the left, there is a green fern frond and a cluster of brown soil with several blue mushrooms. Scattered throughout the scene are numerous white, semi-transparent circles of varying sizes, creating a bokeh effect.

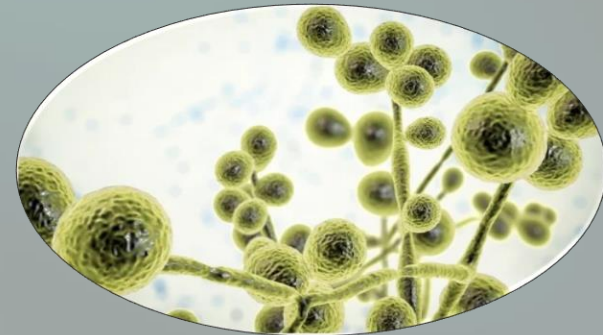
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# THE ORAL MYCOBIOTA



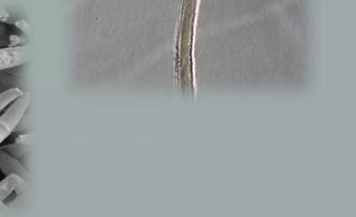
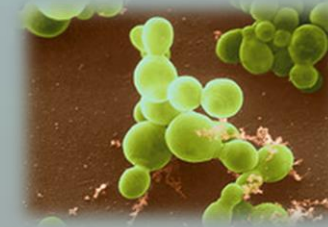
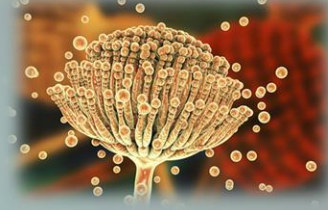


- *Ghannoum et al.* identified a total of **101 species** in the oral cavities of 20 healthy individuals.
- The oral mycobiome appears to be more **subject specific** than the oral bacteriome.
- Oral mycobiota comprises **active & transient colonizers.**



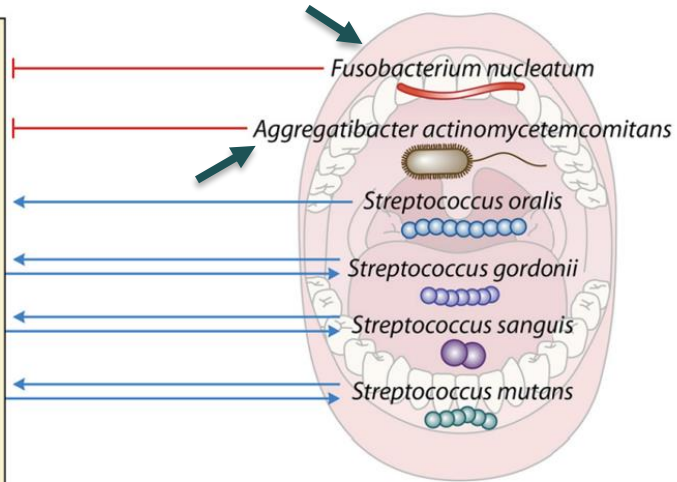
# Members of the Oral Mycobiota

- Among the most found fungi in the oral cavity are ***Aspergillus spp.*** & ***Candida spp.***
- *Candida* infections of the oral cavity are very common. On the other hand, pathological conditions due to *Aspergillus* are rare in the oral cavity.
- This discrepancy might be due to the possibility that ***Aspergillus* is a transient member** of the oral mycobiome, acquired via diet intake or inhalation.
- Other fungi of the oral mycobiota, such as ***Saccharomyces***, ***Penicillium***, ***Malassezia***, ***Cladosporium***, & ***Fusarium*** also represent active members of the oral microbiota.

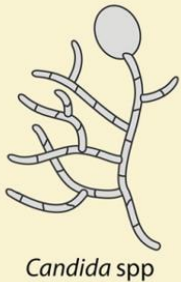


# Fungal-Bacterial Interactions in the Oral Cavity

## Protective Interactions

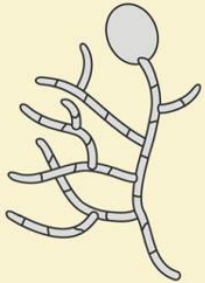
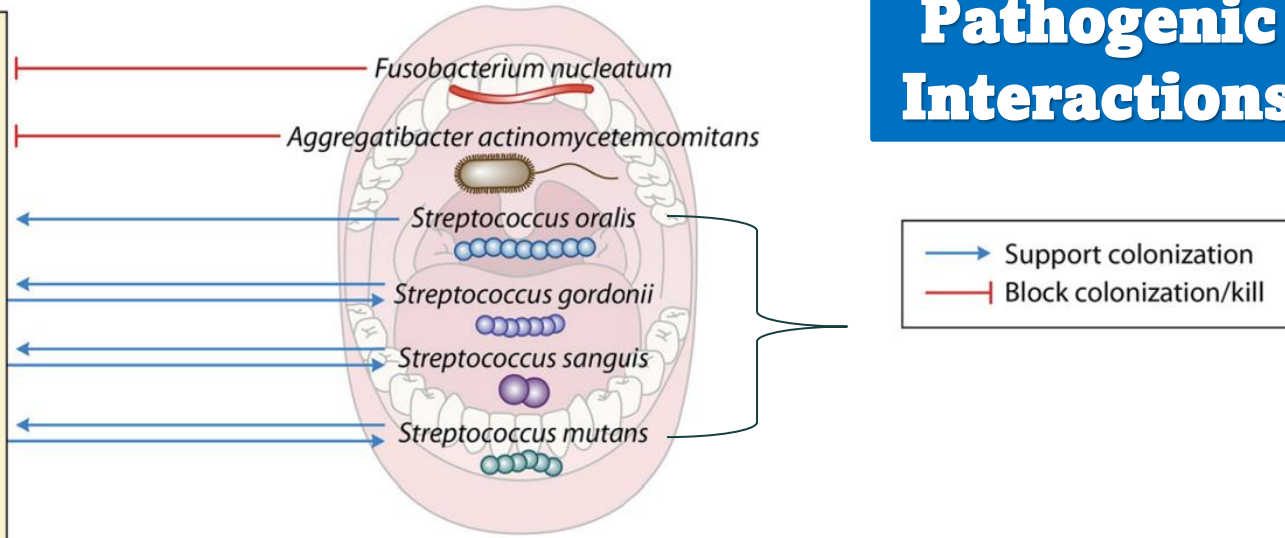


→ Support colonization  
—| Block colonization/kill



- The oral commensal *Fusobacterium spp.* has been shown to adhere to both the yeast and hyphal forms of *C. albicans*, limiting its ability of hyphal formation, thus reducing its ability to kill macrophages.
- The commensal *Aggregatibacter spp.* inhibits biofilm production by *C. albicans* through the secretion of the quorum-sensing molecules.

# Pathogenic Interactions

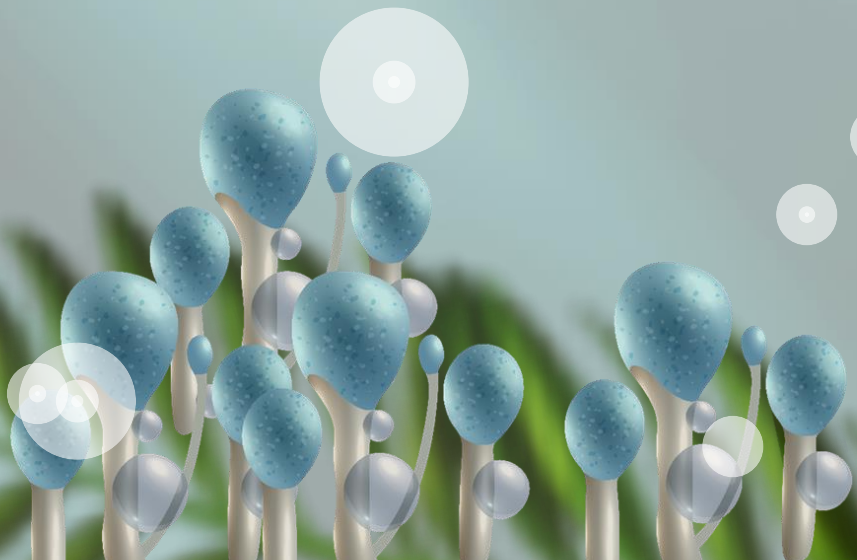


*Candida* spp

- Various studies have investigated mutualistic interactions between *C. albicans* & *Streptococcus spp.* that promote infection by taking an active part in biofilm formation and plaque virulence.
- This is mediated by cell wall polysaccharides, salivary proteins, adhesins on the surface of Streptococci & receptors on surface of Candida.

05

# THE GUT MYCOBIOTA



# Development of GUT Mycobiota



- *Willis et al.* recently suggested that fungal species might be present prior to birth & that *C. albicans* specifically could be associated with **preterm delivery**.
- Additional studies have shown that **vaginal delivery** allows vertical transmission of *Candida spp.* from mother to infant.
- Infants born by **C-section** harbor a bacterial microbiome similar to the mother's skin microbiome, therefore they also harbor higher *Malassezia spp.* in their GIT.



- *Boix-Amorós et al.* found a core breast milk mycobiome, composed of *Malassezia*, *Cladosporium*, & *Penicillium*.
- Accordingly, the infant gut mycobiome is **initially dominated by *Malasseziales***, most likely taken up through lactation.



- After the first 6 months of age, the infant gut mycobiome undergoes a dramatic change and is no longer dominated by *Malasseziales* but by ***Saccharomycetales*** instead.
- This change in mycobiome coincides with a change from breast milk to solid food.



- The gut microbiota further changes and matures during the development from childhood to adulthood.
- These changes are most likely **driven by the development of the immune system** and by the microorganisms that humans are exposed to through their **diet and environment**.

# Members of GUT Mycobiota

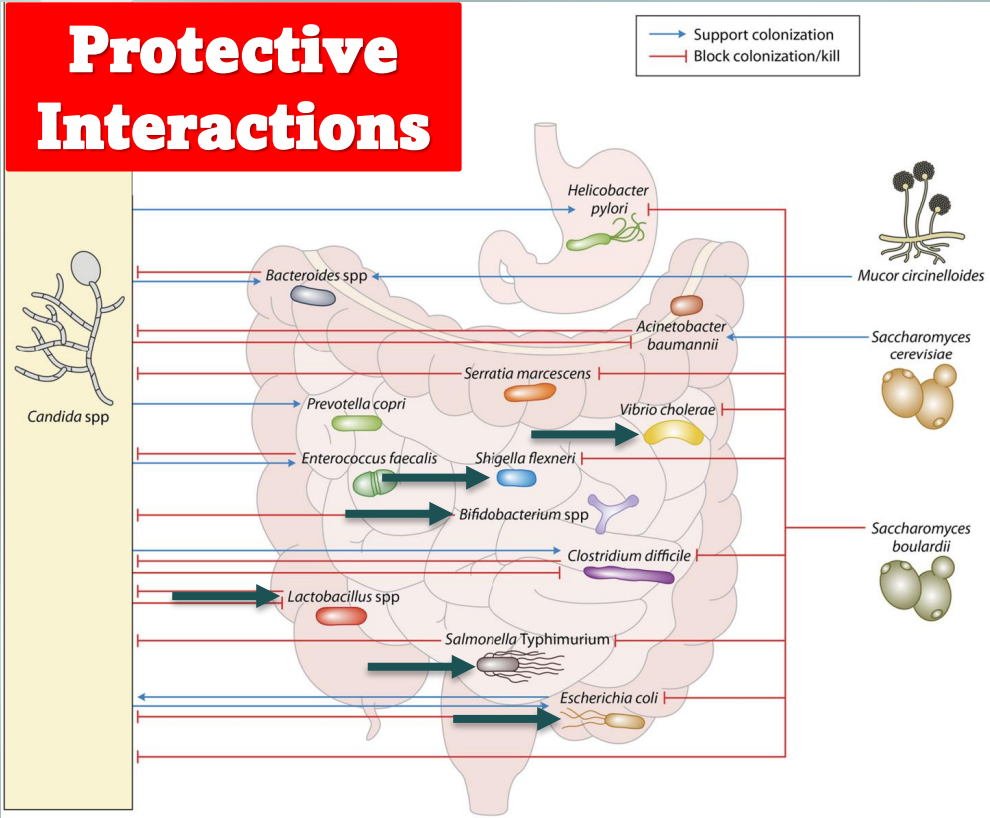
- Similar to the oral mycobiome, GUT mycobiota comprises active & transient colonizers.
- Several studies determined ***Saccharomyces***, ***Malassezia***, & ***Candida*** as the three most abundant genera present in the human gut .
  - ✓ *Saccharomyces* is ubiquitously present in the human diet.
  - ✓ *Malassezia* is the most abundant fungus colonizing the human skin.
  - ✓ *Candida* is the most identified fungus in the oral cavity.





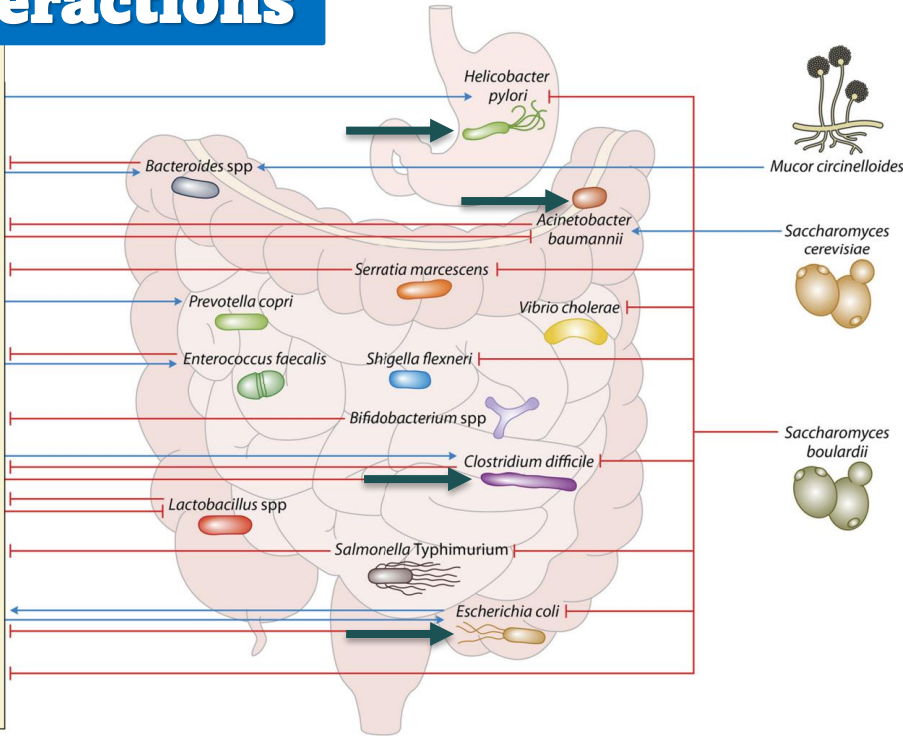
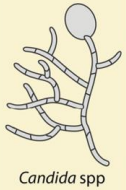
# Fungal-Bacterial Interactions in the GUT

## Protective Interactions



- *Saccharomyces* spp. & *C. albicans* have been extensively studied as a potential probiotics due to its protective effect against various bacterial GI pathogens.
- Probiotic bacterial strains *Lactobacillus* & *Bifidobacterium* spp. have shown efficacy in limiting the severity of *C. albicans* infection:
  - ✓ Inhibit the transition to invasive hyphal form
  - ✓ Inhibit biofilm formation

# Pathogenic Interactions



- **Enterohemorrhagic E.coli** enhances **C. albicans** invasion of intestinal epithelial cells in vitro.
- **C. albicans** allows the growth of the strict anaerobe **C. difficile** under aerobic culture conditions due to the rapid reduction of dissolved oxygen in the vicinity of the yeast.
- **H. pylori** was found within vacuoles in **C. albicans** cells which provides an environment that **H. pylori** can use to survive the low pH of the stomach.
- **S. cerevisiae** enhances the growth of the opportunistic **Acinetobacter baumannii** by producing ethanol.

The background features a soft-focus scene of several mushrooms with light blue caps and brown stems growing from a mound of dark brown soil. The scene is set against a light blue background with a bokeh effect of white and light blue circles of varying sizes. A green fern frond is visible in the upper left corner. The text '06' is centered in a large, light blue circle, and the title 'Mycobiota at Other Body Sites' is written in a dark blue, serif font below it, with a light blue double-headed arrow underneath.

06

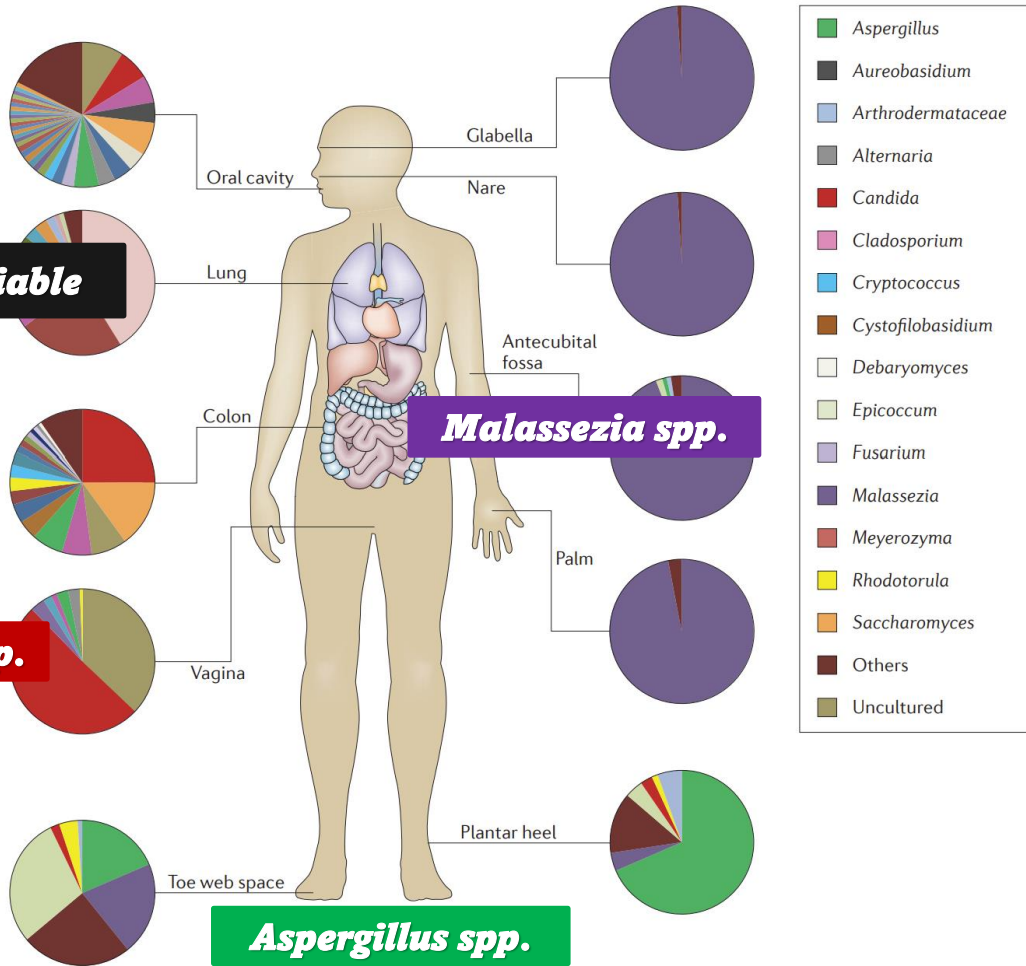
*Mycobiota at  
Other Body Sites*

**Complex & Variable**

**Candida spp.**

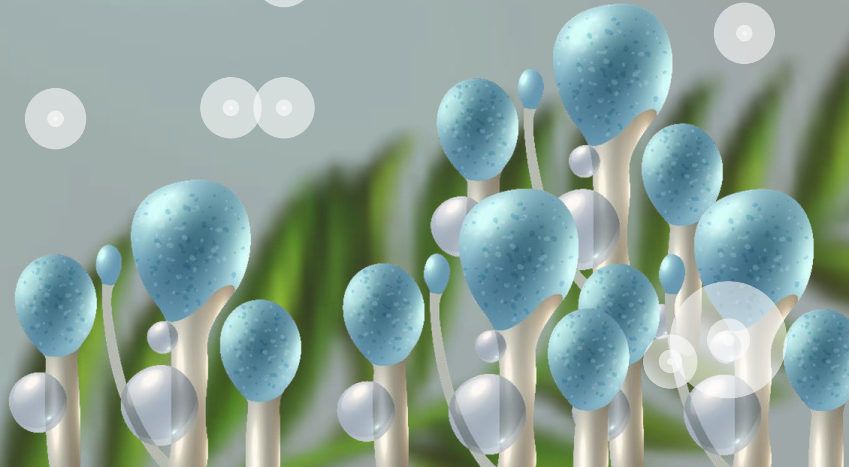
**Malassezia spp.**

**Aspergillus spp.**

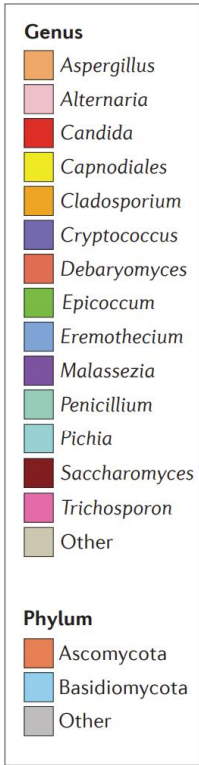


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# MYCOBIOME DYSBIOSIS

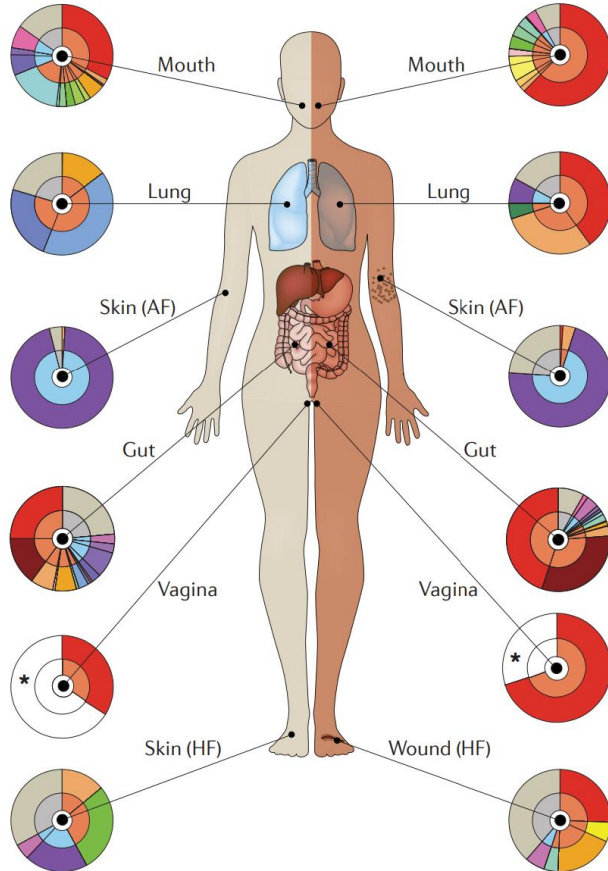


**a**



**Healthy mycobiota**

**Dysbiotic mycobiota**



**b Factors contributing to dysbiosis**

In the mouth, HIV-mediated immunodeficiency causes severe dysbiosis, which correlates with decreased numbers of CD4<sup>+</sup> T cells

**CF >>> ↑ *P. aeruginosae*  
>>> ↑ *Candida***  
yeast-to-hypha transition

**Th17 ↓ >>> CMC**

**↑ *Candida* >>> IBD  
CD  
CRC**  
including glycogen and oestrogen produced during pregnancy, HIV-mediated immunodeficiency and depletion of lactobacilli

Temporally stable dysbiotic fungal communities occupy chronic wounds and can interfere with the skin-healing process

**AIRE  
STAT 3  
IL-17**

**Table 3** Association of enteral and parenteral diseases with gut mycobiota

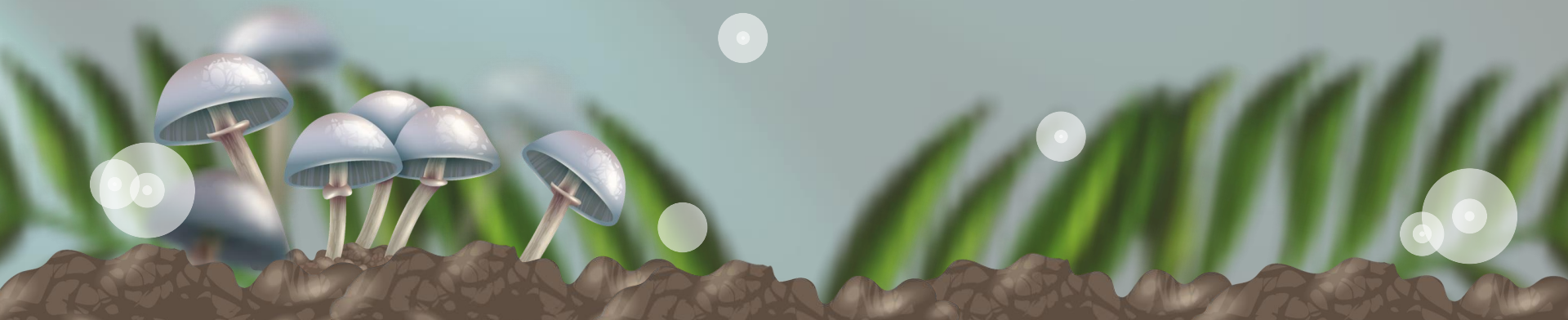
Targets		Diseases	Related fungi	Reference
Intestinal tract		→ Inflammatory bowel disease (IBD)	Basidiomycota ↑ Ascomycota ↓ <u>Candida</u> ↑ <u>S. cerevisiae</u> ↓	[115–118]
		→ Celiac disease	<u>Candida</u> ↑	[119, 120]
		→ Colon cancer	<u>C. tropicalis</u> ↑	[121, 122]
Extra-intestinal tract	Lung	Fluconazole induced Allergic airway disease (AAD)	<u>Candida</u> ↓ Aspergillus ↑ Wallemia ↑ Epicoccum ↑	[11, 114]
		Pulmonary infection	<i>Histoplasma capsulatum</i>	[123]
	Liver	Cirrhosis	Fungal detection ↑	[124]
	Kidney (possible)	Sepsis	<i>C. albicans</i>	[125, 126]
	Pancreas	→ Pancreatic ductal adenocarcinoma (PDA)	<u>Malassezia</u> ↑	[127]
	Brain	→ Multiple sclerosis (MS)	<u>Candida</u>	[128]
		→ Schizophrenia (SCs)	<u>Chaetomium</u> ↑	[129]

“↑” indicates increase and “↓” indicates decrease

# CONCLUDING REMARKS

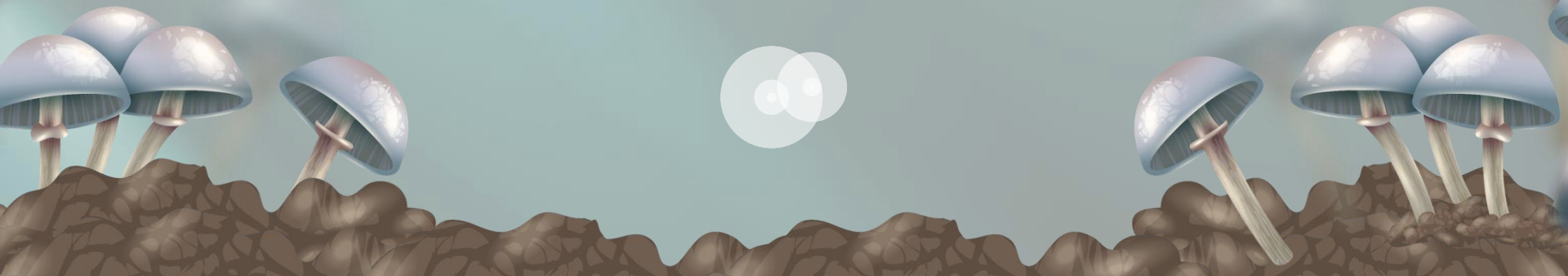


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- Mycobiome research is a **rapidly expanding field**, yet many questions are currently still unanswered.
- Due to the high **inter- and intra-individual variability**, it is unclear if core mycobiomes can be defined.
- Future research will expand our knowledge on which fungi are **resident** and which are **transiently present** in the gastrointestinal tract.





# THANK YOU!

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