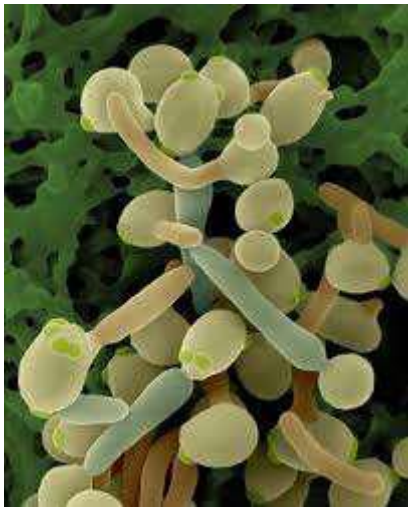
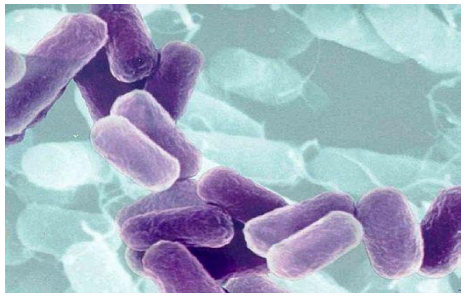
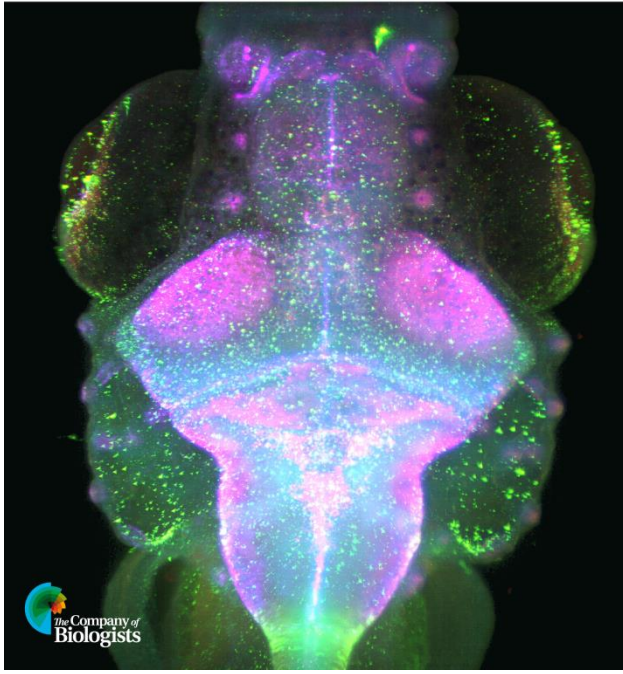




Μυκοβίωμα



Σαμπατάκου Ελένη
Αναπληρώτρια Καθηγήτρια
ΕΚΠΑ

Lita Proctor
HMP

Μυκοβίωμα εντέρου

>10^{14} μικροοργανισμοί στο ΓΕΣ (90% bugs και 10% “us”!) η χλωρίδα
Mycobiota= η κοινότητα των μυκήτων
Mycobiome=το σύνολο των γονιδίων αυτών
“Dysbiosis”= δυσλειτουργία. Συχνή σε πολλά νοσήματα, περιλαμβανομένου ΣΔ, Ca παχέως εντέρου και ιδιοπαθής φλεγμονώδης νόσος εντέρου

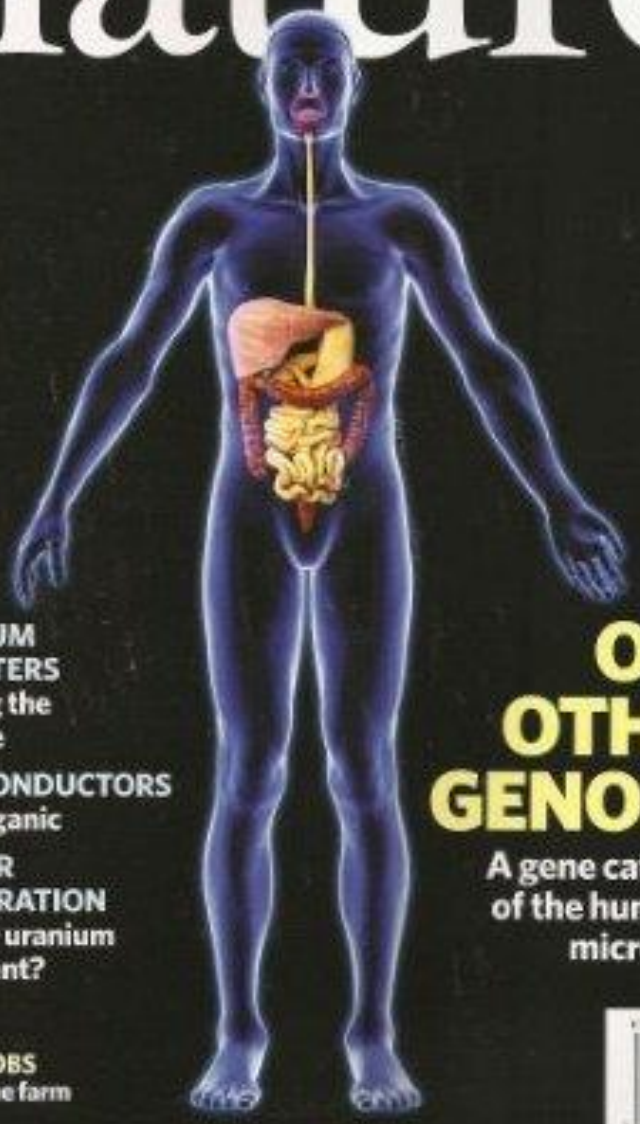
Site specific mycobiota

Αν και μελέτες υποδεικνύουν κεντρικό ρόλο των μυκήτων στην ομοιόσταση του εντέρου και στην συστηματική ανοσολογία, <0.4% της βιβλιογραφίας του μικροβιώματος αναφέρεται στην κοινότητα των μυκήτων (*Hernández-Santos and Klein, 2017*).
Πρόσφατα ευρήματα υποστηρίζουν την ύπαρξη ανταγωνισμού μεταξύ βακτηρίων και μυκήτων στο έντερο.

4 March 2010 | www.nature.com/nature | $10

THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE

nature



QUANTUM COMPUTERS
Choosing the hardware

SUPERCONDUCTORS
Going organic

NUCLEAR PROLIFERATION
Ban laser uranium enrichment?

NATUREJOBS
Down on the farm

OUR OTHER GENOME

A gene catalogue of the human gut microbiome

Critical Issues in Mycobiota Analysis

B Halwachs, et al. Frontiers in Microbiology 2017 | Volume 8

- Εξαρτώμενο από τον ξενιστή, οι μύκητες συνιστούν το **<0.1%** των μικροοργανισμών στο **ΓΕΣ** και έως **10%** στο **δέρμα** (*Belkaid and Naik,2013*).
- Το μυκητιακό κύτταρο είναι **100 φορές** μεγαλύτερο από το βακτηριακό, επηρεάζοντας την φυσιολογία του ξενιστή (*Underhill and Iliev, 2014*).
- **Το μυκοβίωμα του ΓΕΣ αλληλεπιδρά με το ανοσοποιητικό,** όπως μέσω του υποδοχέα της Dectin-1, αμβλύνοντας την φλεγμονή του ΓΕΣ (*Iliev et al., 2012*).

This is from2014!

New mushrooms found in porcini packet

SHARE SHARE SHARE SHARE

DNA sequencing of mushrooms in a shop-bought packet of porcini results in the description of three species new to science.

Contents of a commercial packet of dried porcini containing three species new to science (Photo: B. Dentinger)

OXFORD

FEDERATION OF EUROPEAN MICROBIOLOGICAL SOCIETIES
FEMS JOURNALS
investing in science

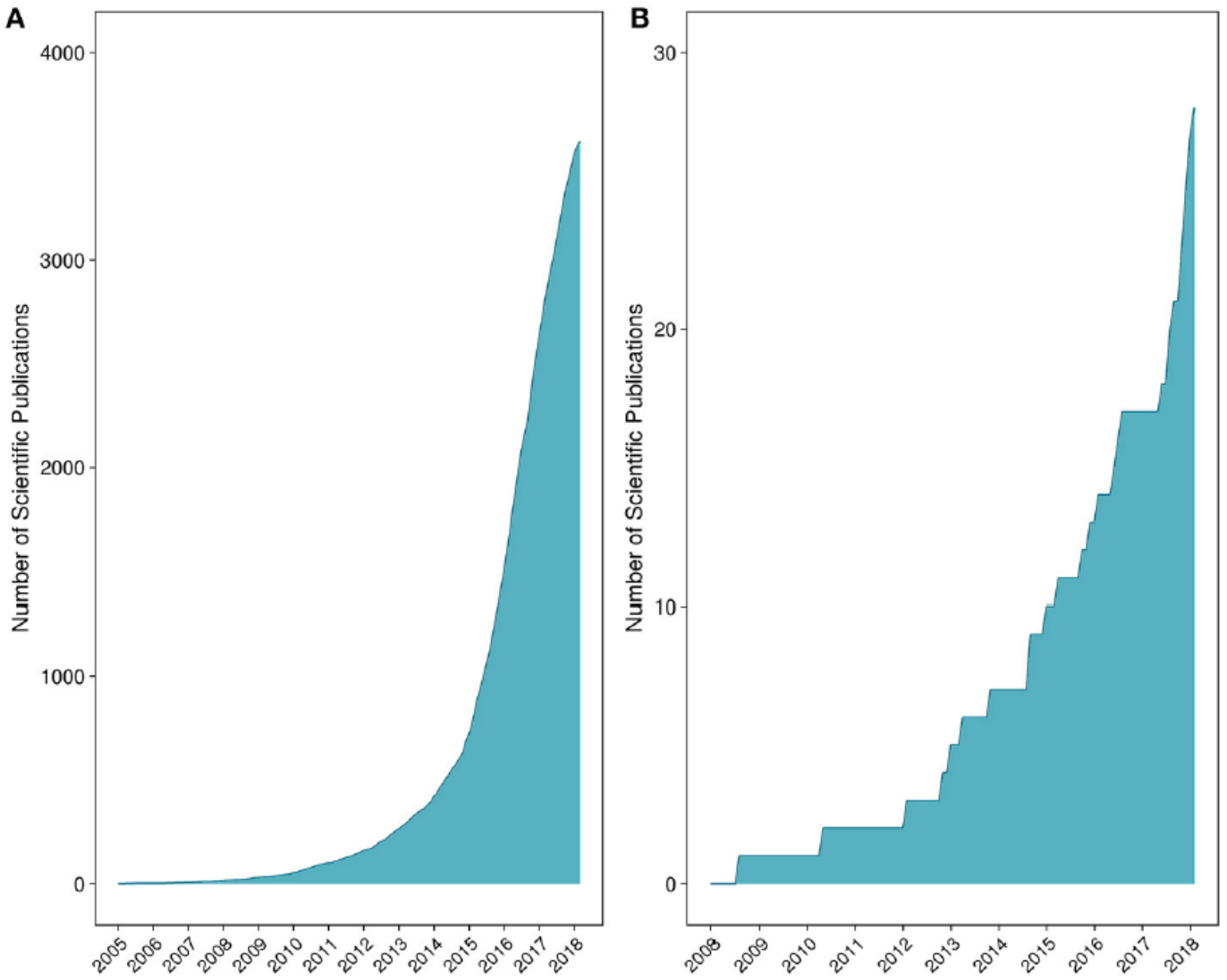
REVIEW ARTICLE

Forgotten fungi—the gut mycobiome in human health and disease

Chloe E. Huseyin[1,2,3], Paul W. O'Toole[2,3], Paul D. Cotter[1,2] and Pauline D. Scanlan[2,*]

FEMS Microbiology Reviews, fuw047, 41, 2017, 479–511

Number of peer-reviewed scientific publications for (A) microbiome and (B) mycobiome studies



First publication in 2009*,
Pubmed search for Mycobiota
10 results in 2013
At least **70 results** as of July 2016
24 September 2018, **370 results**
Filter "Humans" In the last 5 Years **49 results**
167 results in 2020
16 Reviews

**Gillevet, P.M, et al. Fungal Ecol. 2009, 2, 160–167*

An Emerging Need For Reference Materials in Mycobiome Research

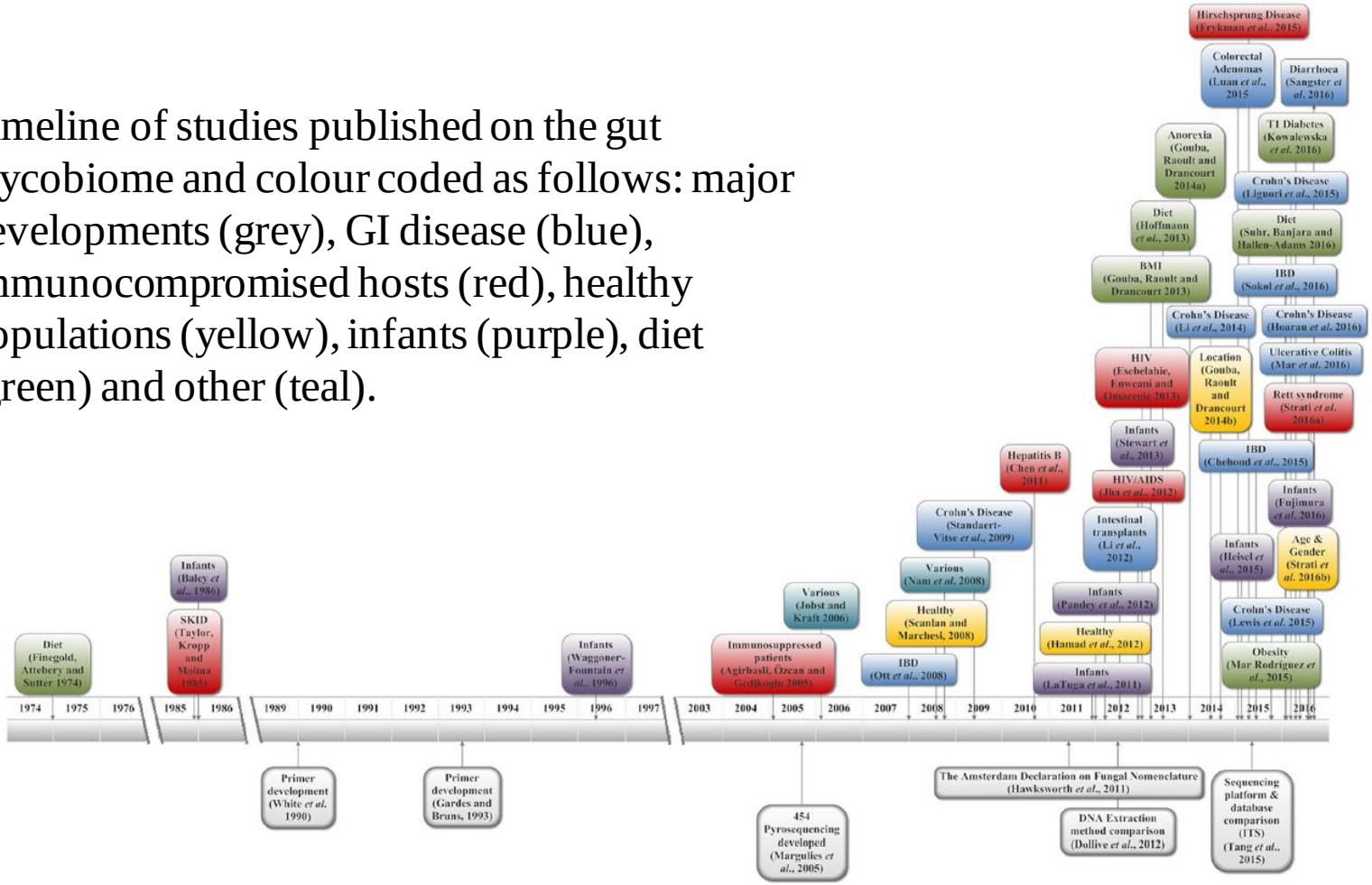
REVIEW ARTICLE

Forgotten fungi—the gut mycobiome in human health and disease

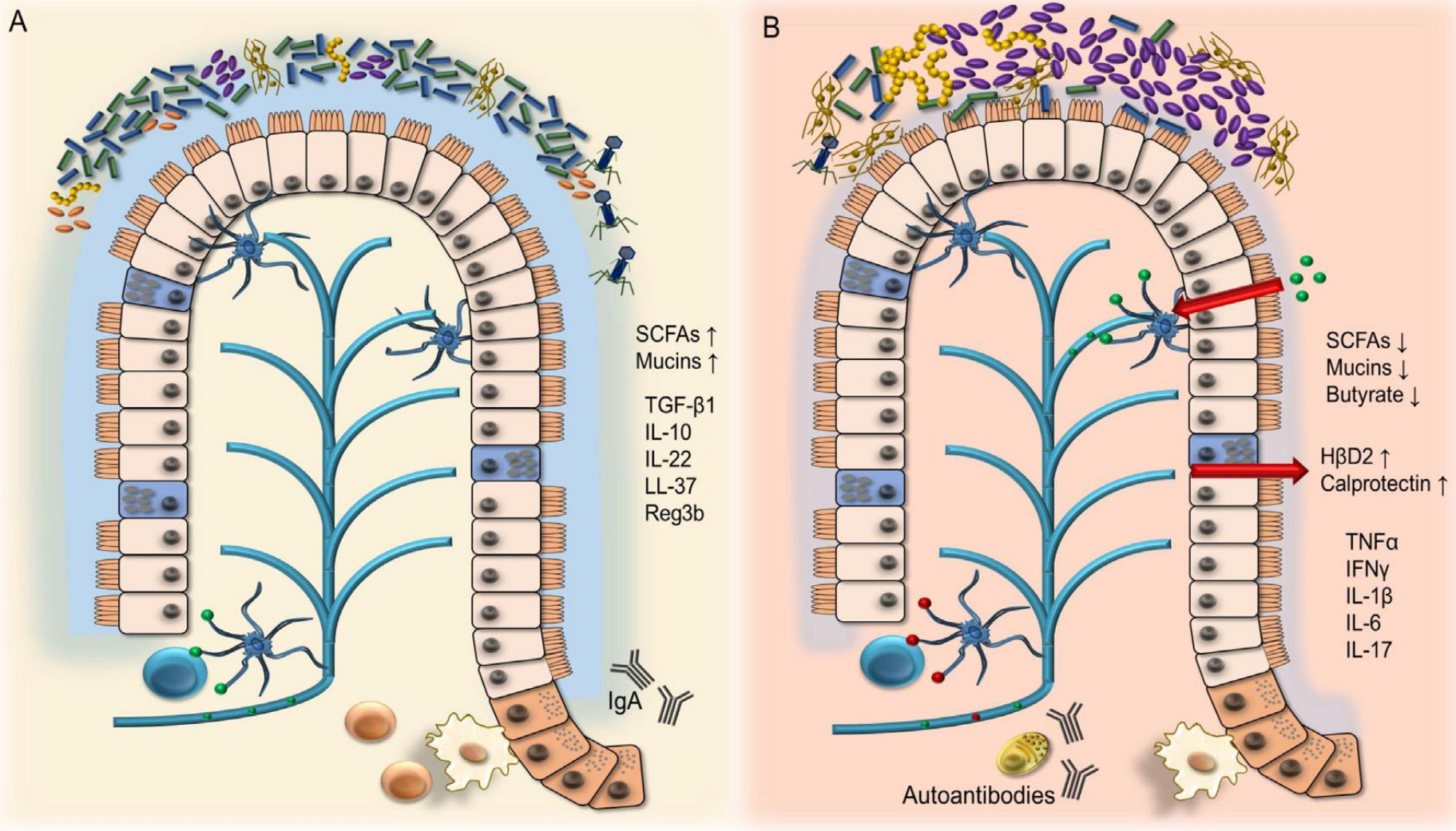
Chloe E. Huseyin[1,2,3], Paul W. O'Toole[2,3], Paul D. Cotter[1,2] and Pauline D. Scanlan[2,*]

FEMS Microbiol Rev. 2017 Jul 1;41(4):479-511.

Timeline of studies published on the gut mycobiome and colour coded as follows: major developments (grey), GI disease (blue), immunocompromised hosts (red), healthy populations (yellow), infants (purple), diet (green) and other (teal).



Healthy intestinal environment (A) compared to dysbiosis (B) that leads to intestinal inflammation and emerging of autoimmunity



Μυκοβίωμα υποεκτίμηση?

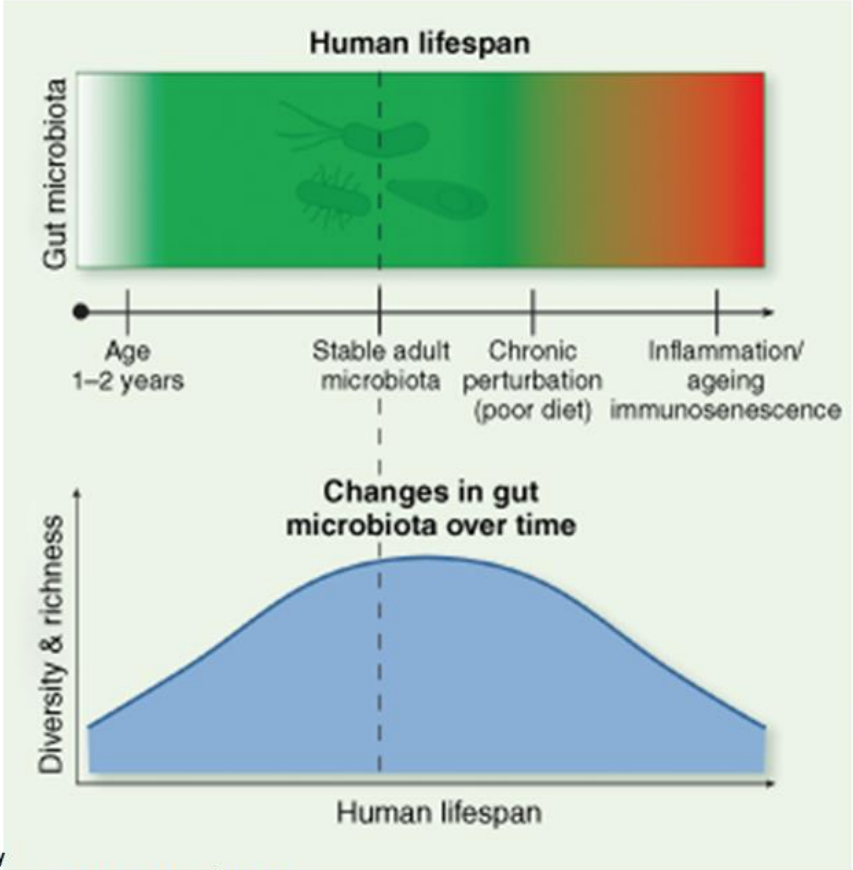
Αριθμός σημαντικών μελετών του μυκοβιώματος βασίζεται σε μοριακές μεθόδους.

Αφορούν κυρίως μελέτες παθήσεων του ΓΕΣ (*Ott et al. 2008; Iliev et al. 2012; Lewis et al. 2015;Hoarau et al. 2016; Mar et al. 2016)* καθώς και μελέτες επίπτωσης μυκήτων σε ανοσοκατασταλμένους (*Chen et al. 2011;Mukherjee et al. 2014)*.

Το μυκοβίωμα επηρεάζεται από την ηλικία (*Gewolb et al. 1999; Strati et al.2016b*), περιλαμβανομένων παιδιών (*Heisel et al. 2015)* και ενηλίκων *(Scanlan and Marchesi 2008*), φύλο (*Strati et al. 2016b)*, γεωγραφική περιοχή (*Nam et al. 2008; Hamad et al. 2012)*, διαβήτη, παχυσαρκία (*Gouba, Raoult and Drancourt 2013; Mar Rodrıguez et al. 2015; Kowalewska et al. 2016)* και διατροφή, anorexia nervosa (*Gouba, Raoult and Drancourt 2014a*) και περιοχή σώματος (Zhang *et al. 2011; Nguyen, Viscogliosi and* Delhaes 2015)

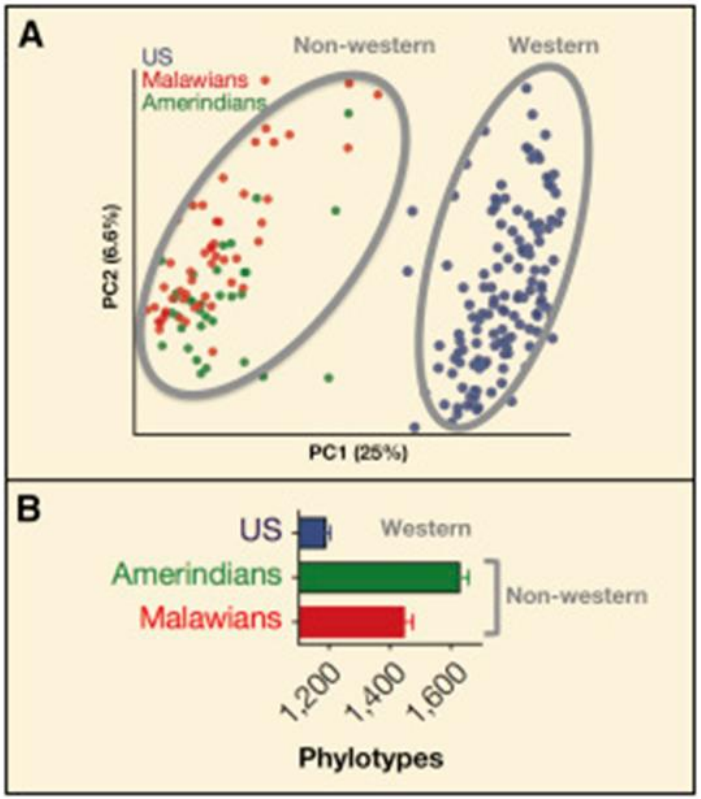
Τεχνικές Shotgun metagenomics sequencing υπολογίζουν τους μύκητες στο 0.1% του εντερικού μικροβιώματος (*Qin et al., 2010*)

The gut microbiota during the human lifespan



Clinical & Experimental Immunology
Volume 179, Issue 3, pages 363-377, 16 FEB 2015 DOI: 10.1111/cei.12474
http://onlinelibrary.wiley.com/doi/10.1111/cei.12474/full#cei12474-fig-0001

The Western Microbiota Diverges from That of Non-Western Populations

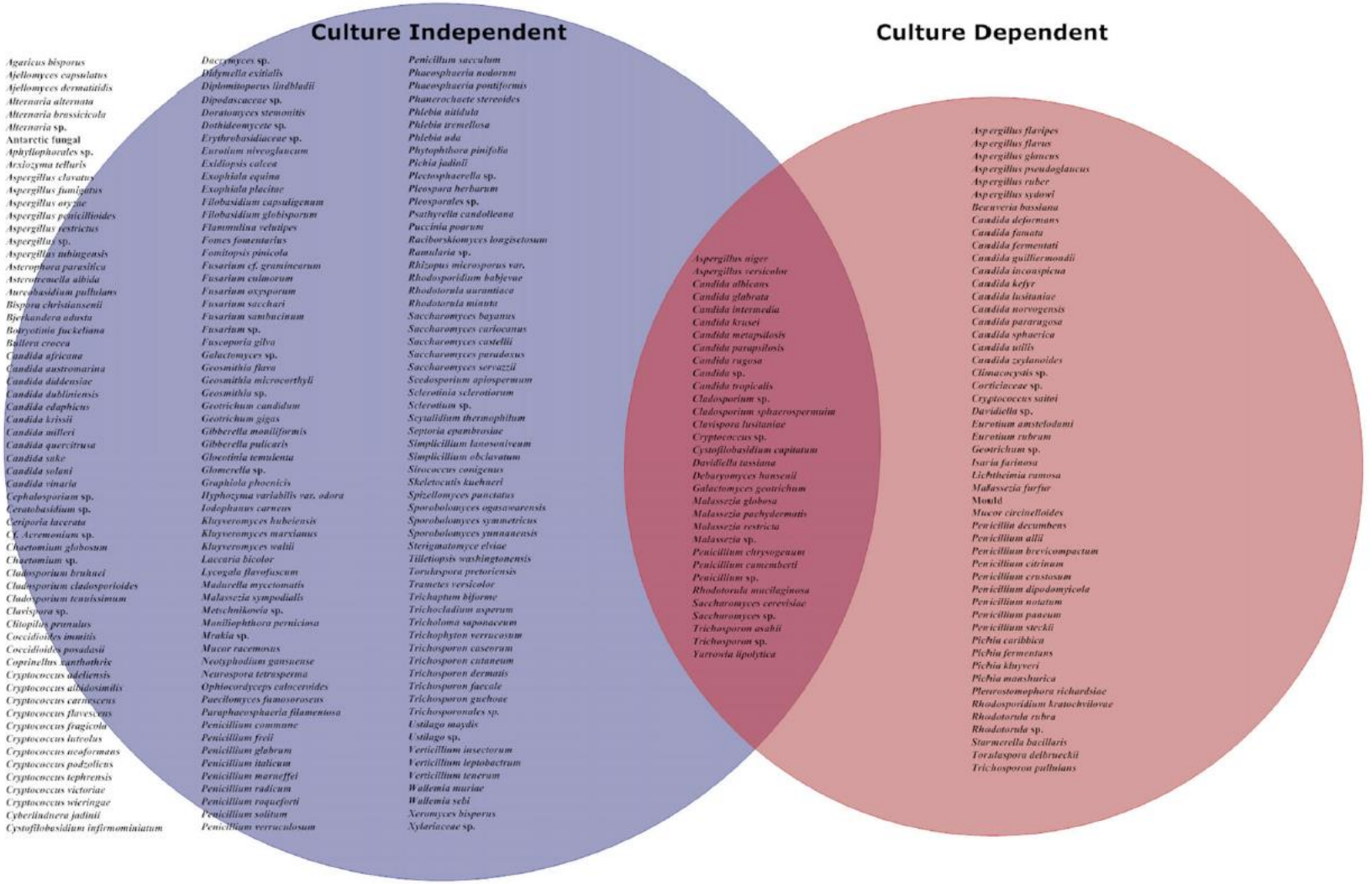


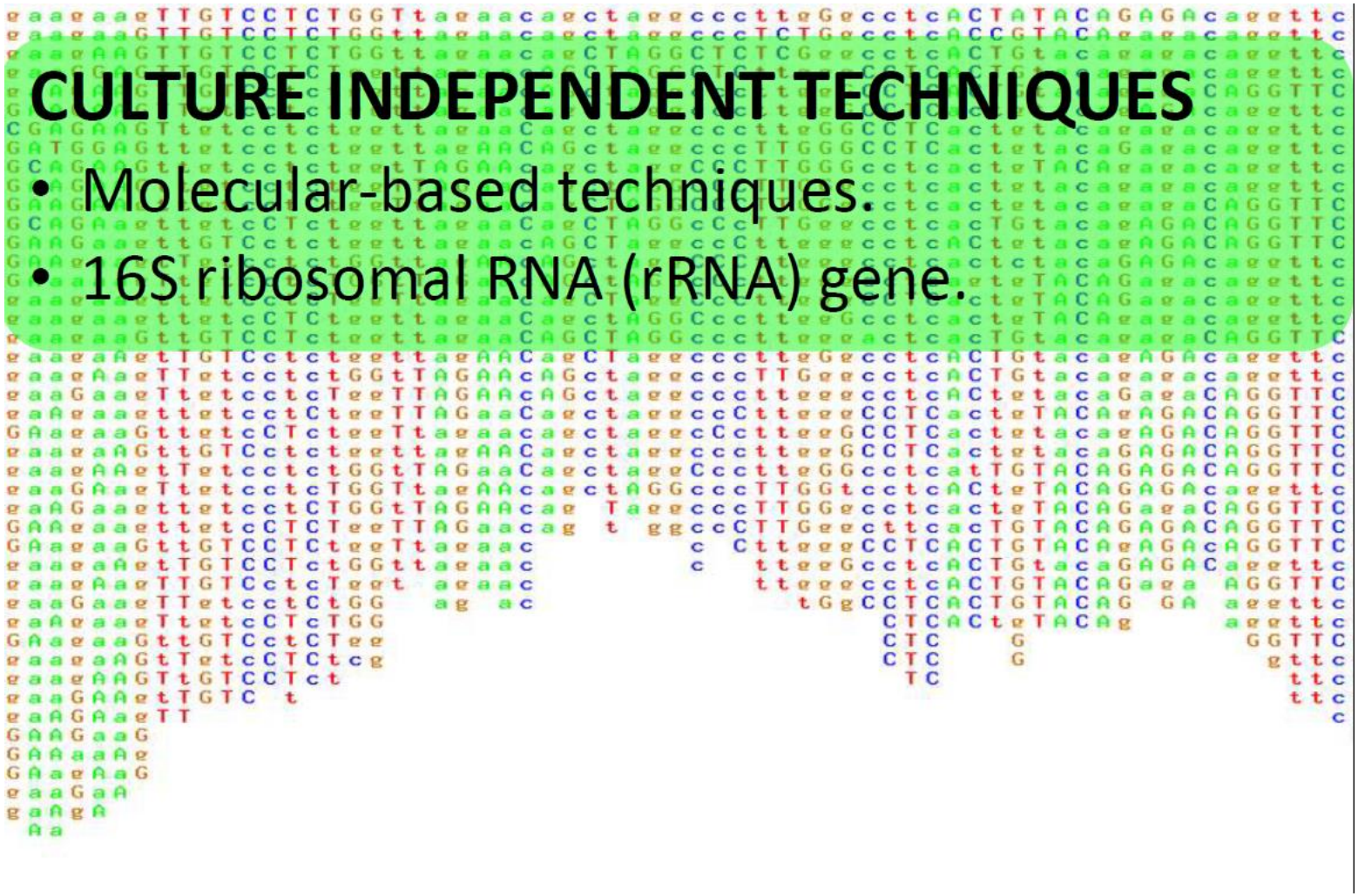
Starving our Microbial Self: The Deleterious Consequences of a Diet Deficient in Microbiota-Accessible Carbohydrates

Cell Metabolism, Volume 20, Issue 5, 2014, 779–786

GUT MYCOBIOME

Huseyin C, et al. FEMS Microbiol Rev. 2017 Jul 1;41(4):479-511.

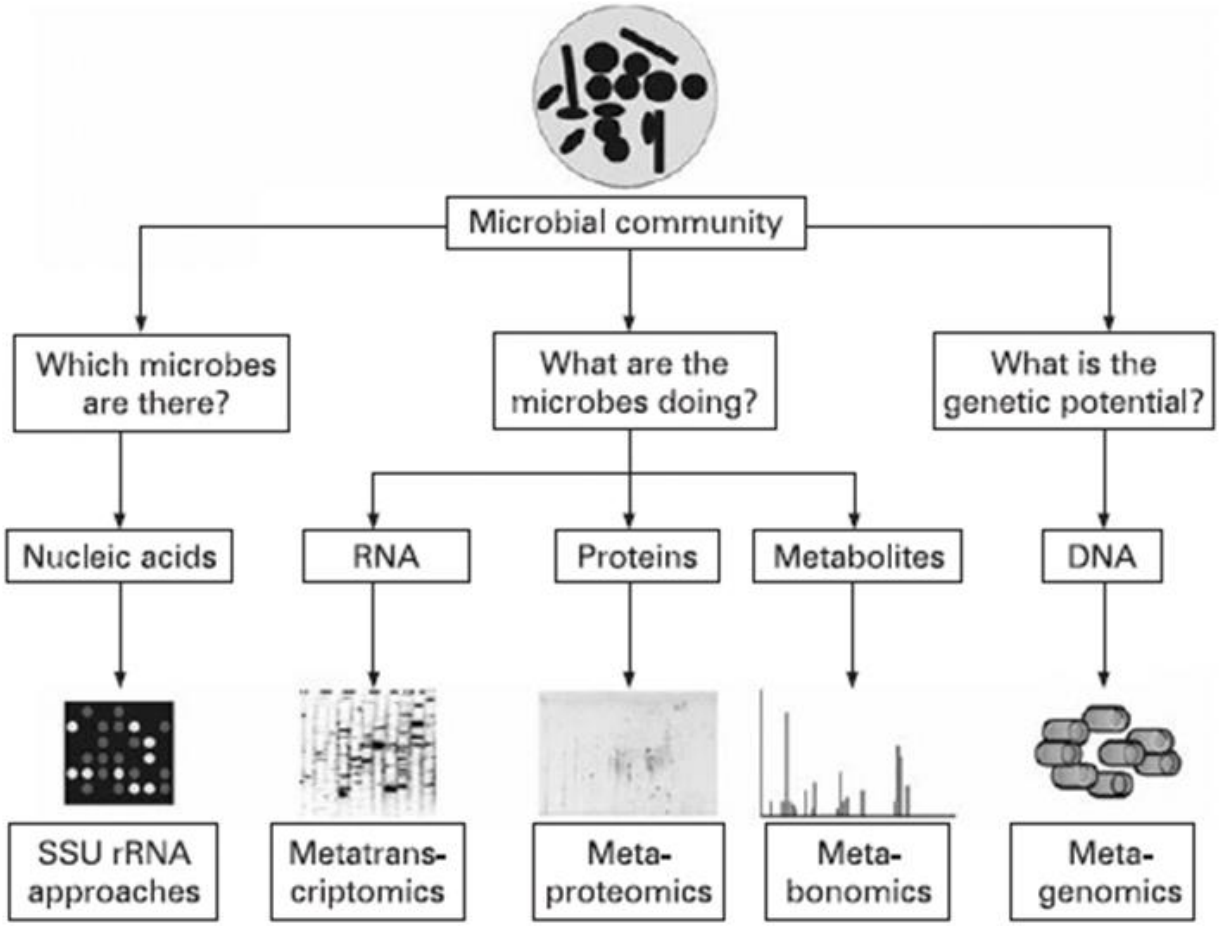




CULTURE INDEPENDENT TECHNIQUES

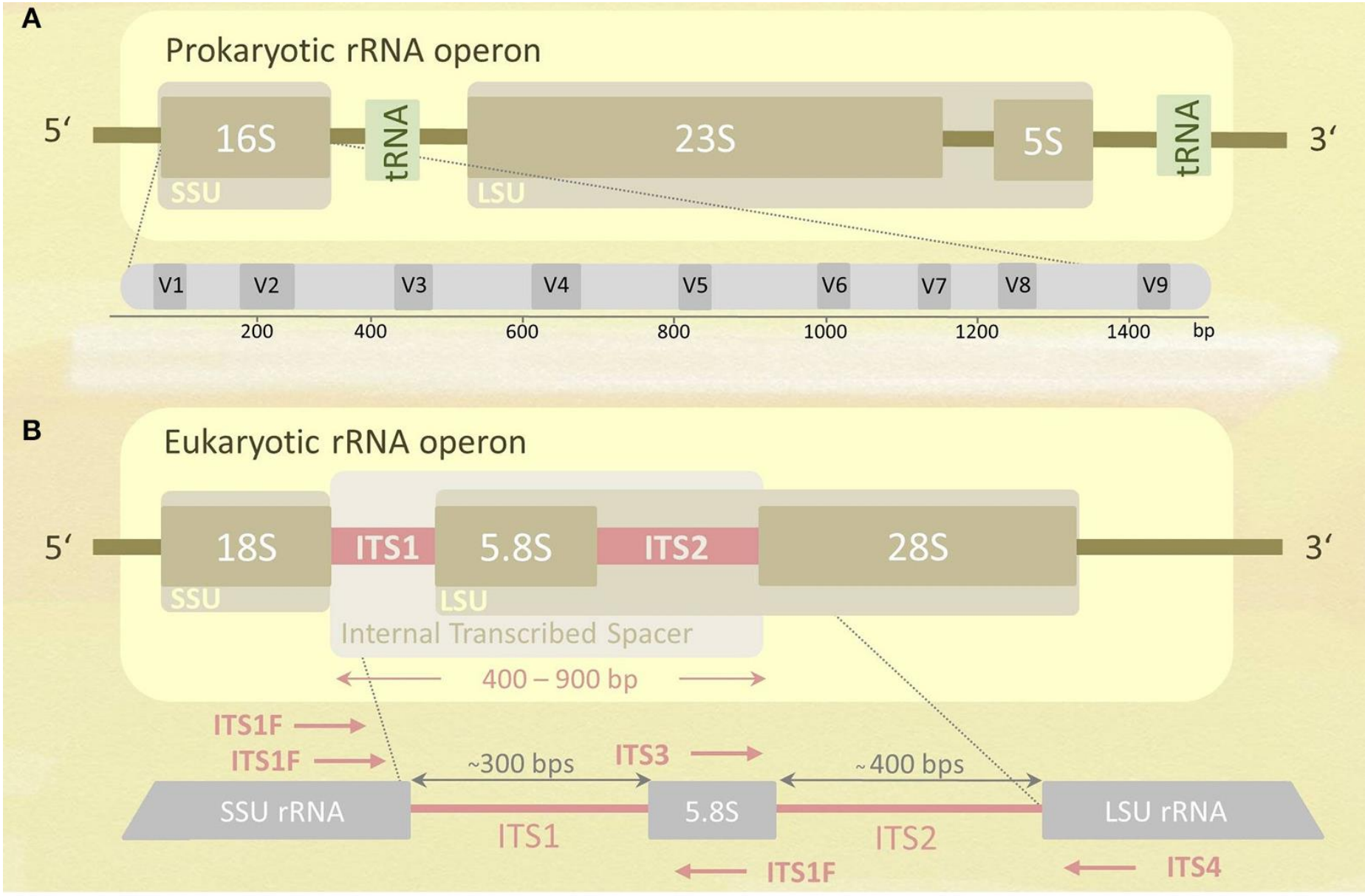
- Molecular-based techniques.
- 16S ribosomal RNA (rRNA) gene.

Methods to study the microbiome

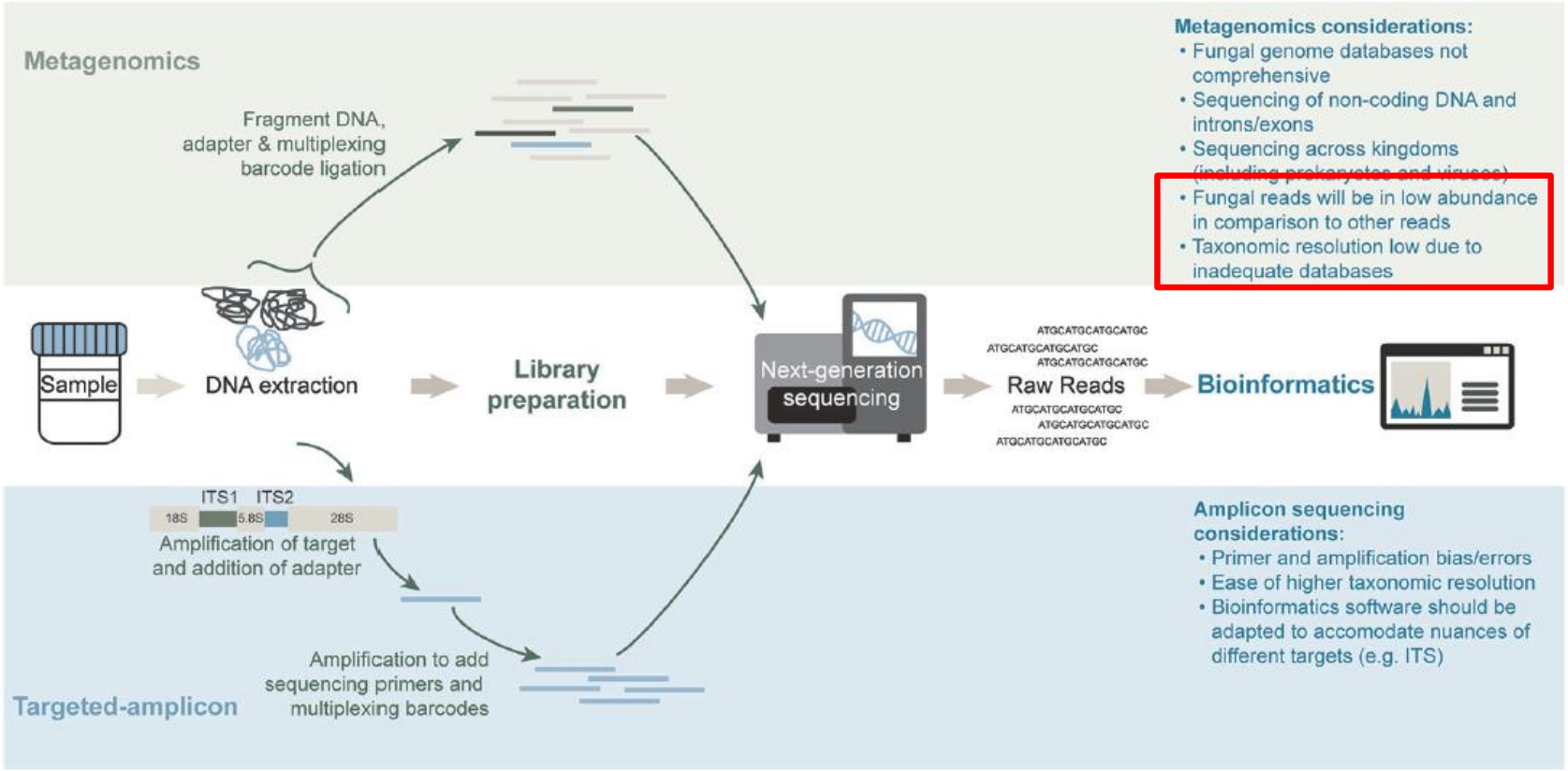


Zoetendal, Gut 2008

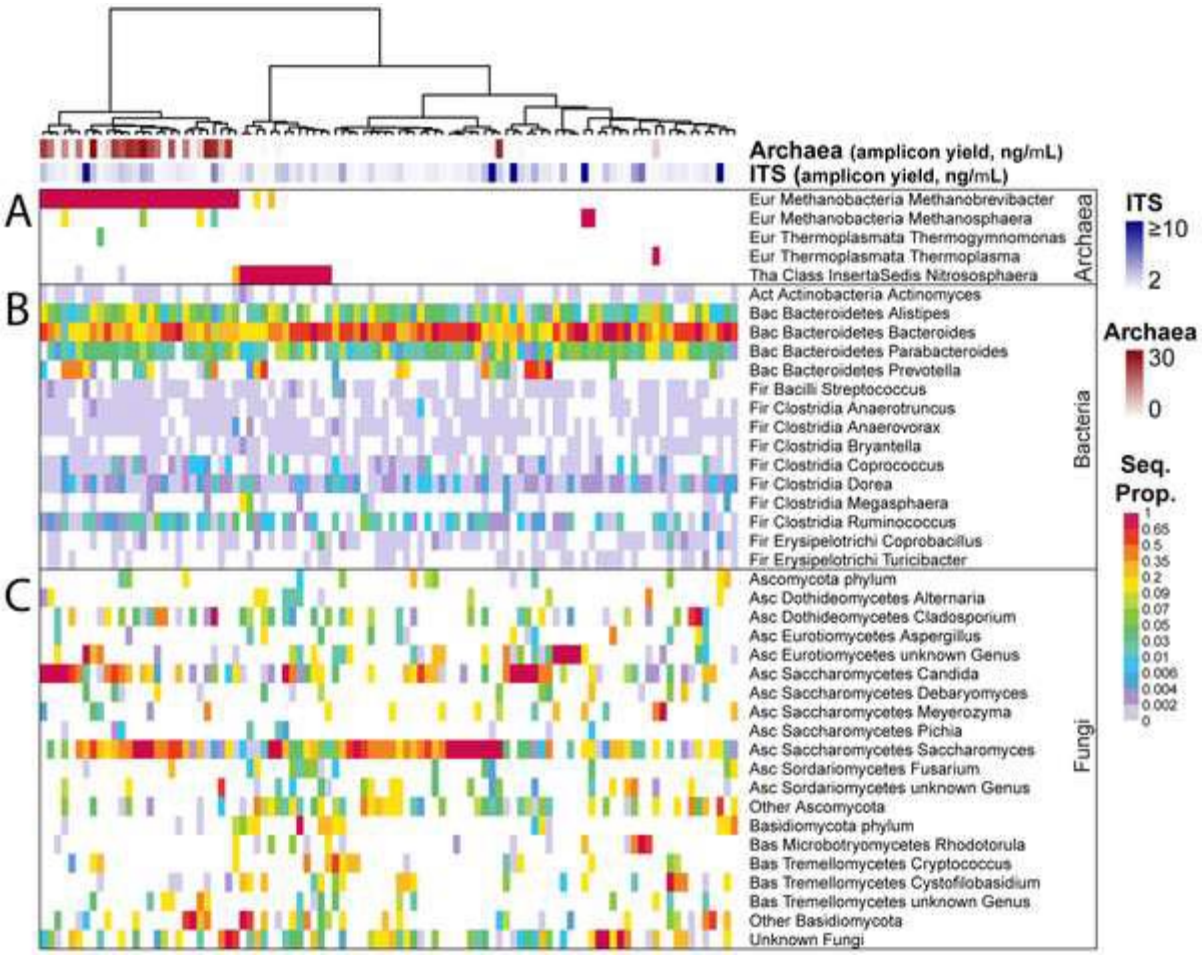
Amplicon-based next generation sequencing : Schematic representations of rRNA operons and their variability assessed by multiple sequence alignments (MSA)



Mycobiota characterization of a shotgun metagenomics and targeted-amplicon sequencing of a phylogenetically informative fungal marker.



The archaeal and fungal components of the human gut microbiome



UPDATE CLASSIFICATION

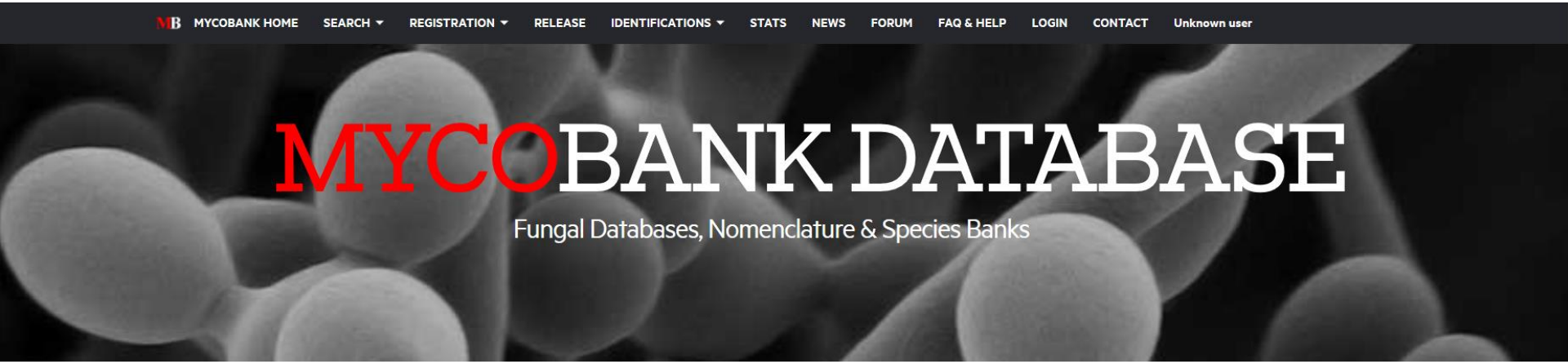
Mycobank

http://www.mycobank.org/

Index Fungorum

http://www.indexfungorum.org/names/names.asp

Hoffmann C, Dollive S, Grunberg S, Chen J, Li H, et al. (2013) Archaea and Fungi of the Human Gut Microbiome: Correlations with Diet and Bacterial Residents. PLOS ONE 8(6): e66019.



MycoBank in short

MycoBank is an on-line database aimed as a service to the mycological and scientific community by documenting mycological nomenclatural novelties (new names and combinations) and associated data, for example descriptions and illustrations. Pairwise sequence alignments and polyphasic identifications of fungi and yeasts against curated references databases are proposed. More information here.

An Excel version of the list of taxa present in MycoBank (export date: 31st of July 2019) can be downloaded here.

REVIEW ARTICLE

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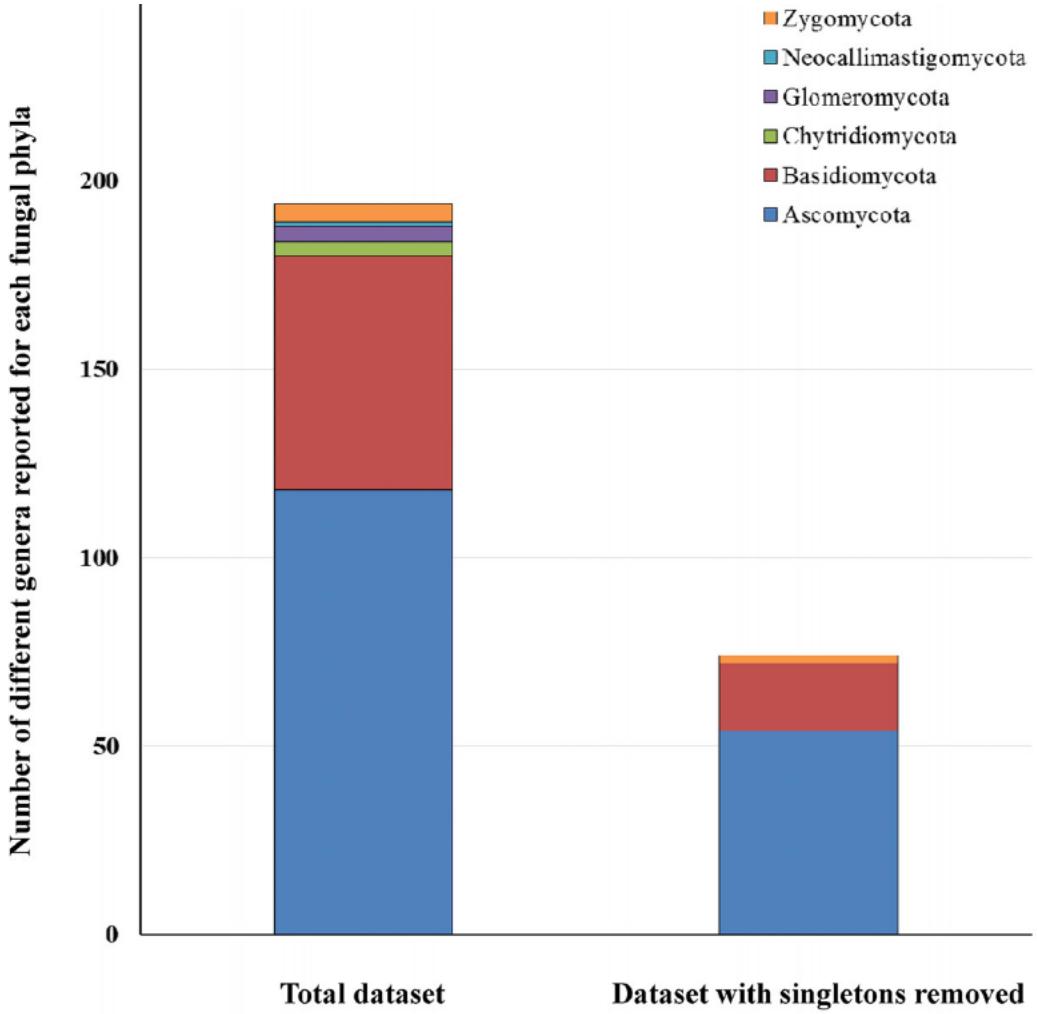
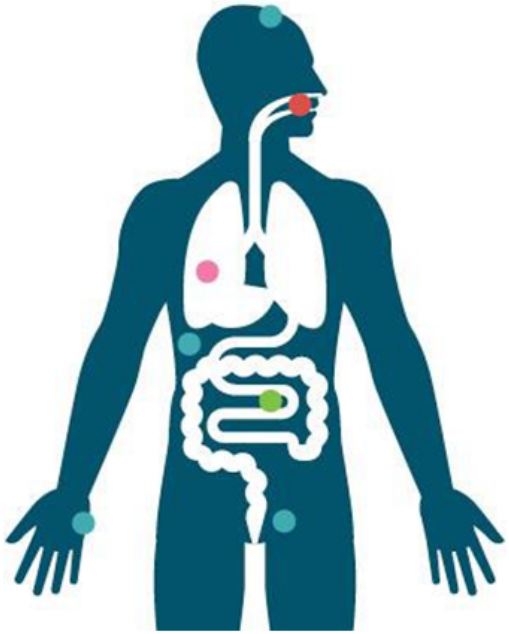
Chloe E. Huseyin[1,2,3], Paul W. O'Toole[2,3], Paul D. Cotter[1,2] and Pauline D. Scanlan[2,*]

FEMS Microbiol Rev. 2017 Jul 1;41(4):479-511.



The Human Mycobiome



ORAL CAVITY

- *Alternaria*
- *Aspergillus*
- *Aureobasidium*
- *Candida*
- *Cladosporium*
- *Cryptococcus*
- *Fusarium*
- *Gibberella*
- *Glomus*
- *Pichia*
- *Saccharomyces*
- *Teratosphaeria*

LUNGS

- *Aspergillus*
- *Candida*
- *Cladosporium*
- *Penicillium*
- *Cryptococcus*

GASTRO-INTESTINAL

- *Aspergillus*
- *Candida*
- *Cladosporium*
- *Cryptococcus*
- *Fusarium*
- *Penicillium*
- *Pneumocystis*
- *Mucor*
- *Saccharomyces*

SKIN

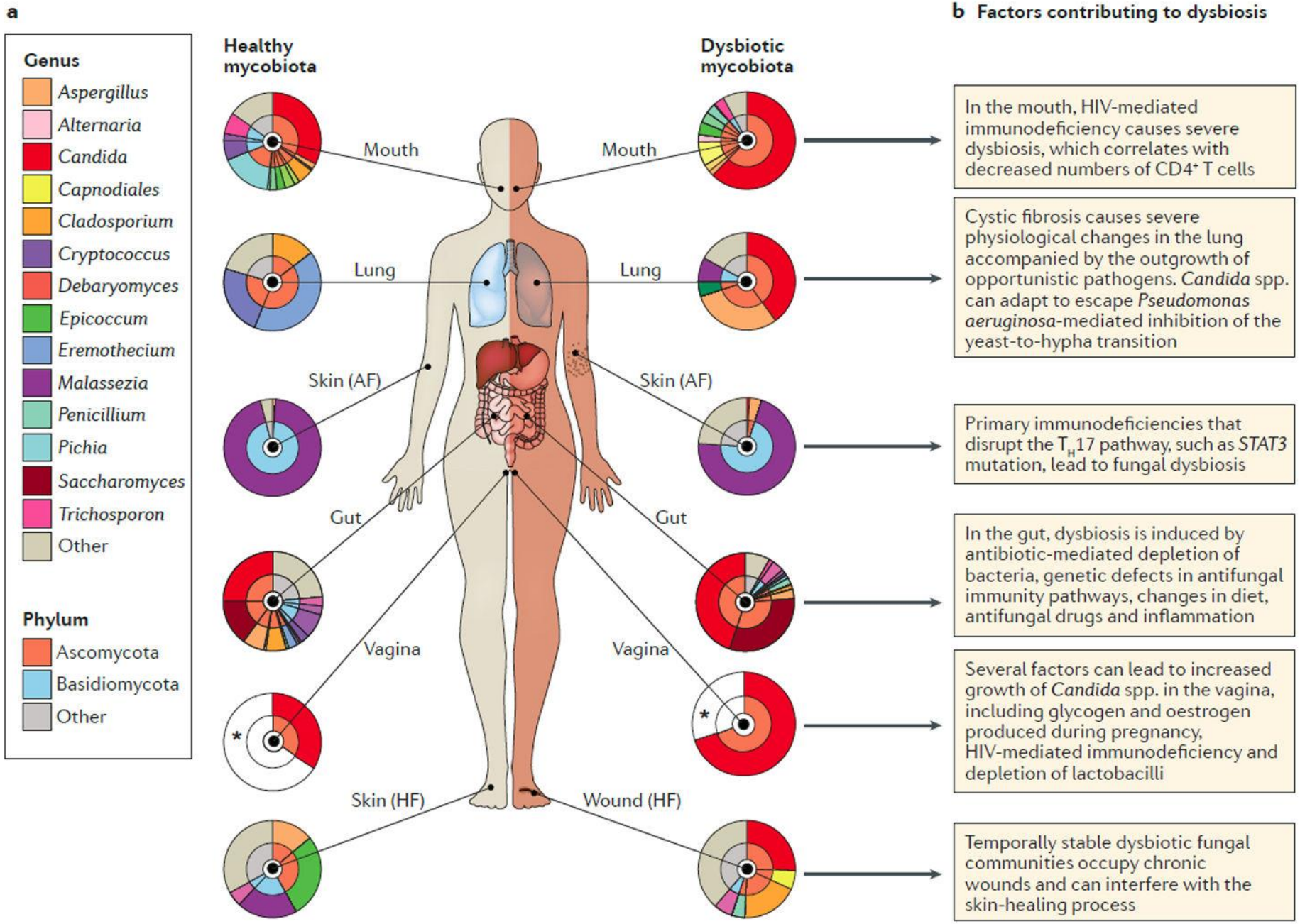
- *Candida*
- *Cryptococcus*
- *Debaryomyces*
- *Epidermophyton*
- *Malassezia*
- *Microsporum*
- *Rhodotorula*
- *Trichophyton*
- *Aspergillus*
- *Chrysosporium*
- *Epicoccum*
- *Leptosphaerulina*
- *Penicillium*
- *Phoma*
- *Saccharomyces*
- *Ustilago*

*Potentially pathogenic lineages

- Early surveys have revealed several pathogenic species that may increase one's risk of disease when the healthy microbiome is disrupted.
- *Candida* and *Aspergillus* species are among the most common members of the human mycobiome.
- When the balance of a microbial community is disrupted, fungal species can flourish and cause disease

The Scientist. 02.2016. 37

The mycobiota during health and in dysbiosis

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ScienceDirect

Current Opinion in Microbiology

Gut mycobiota under scrutiny: fungal symbionts or environmental transients?

William D Fiers[1,2], Iris H Gao[1,2,4] and Iliyan D Iliev[1,2,3,4]

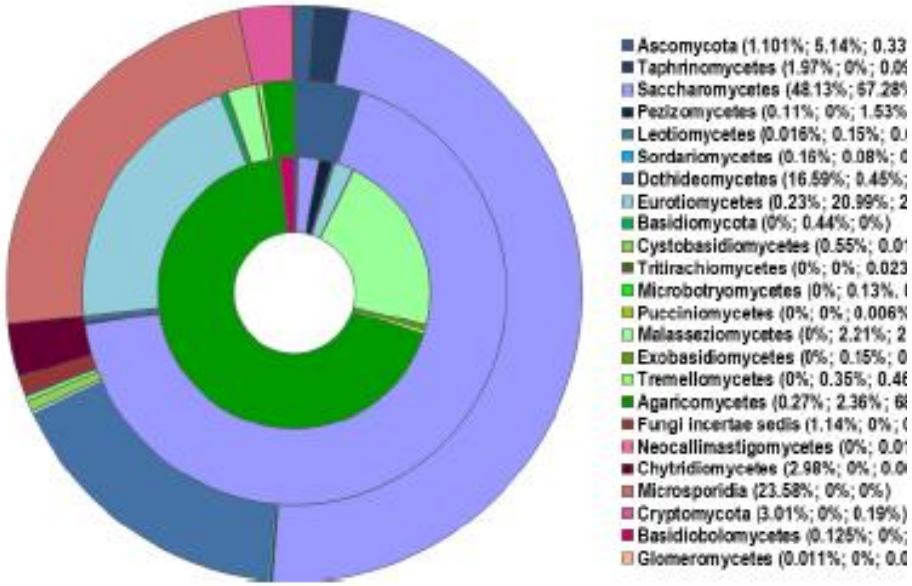
frontiers in MICROBIOLOGY

REVIEW ARTICLE
published: 13 February 2015
doi: 10.3389/fmicb.2015.00089

The lung mycobiome: an emerging field of the human respiratory microbiome

*Linh D. N. Nguyen[1], Eric Viscogliosi[1] and Laurence Delhaes[1,2]**

Cross talk between the intestinal and lung microbioma?



Distribution of fungal classes (% of relative abundance) in the sputum of **healthy individuals** (outerring) and patients with **CF** (middle ring) and **asthma** (innerring),based on published pyrosequencing investigations

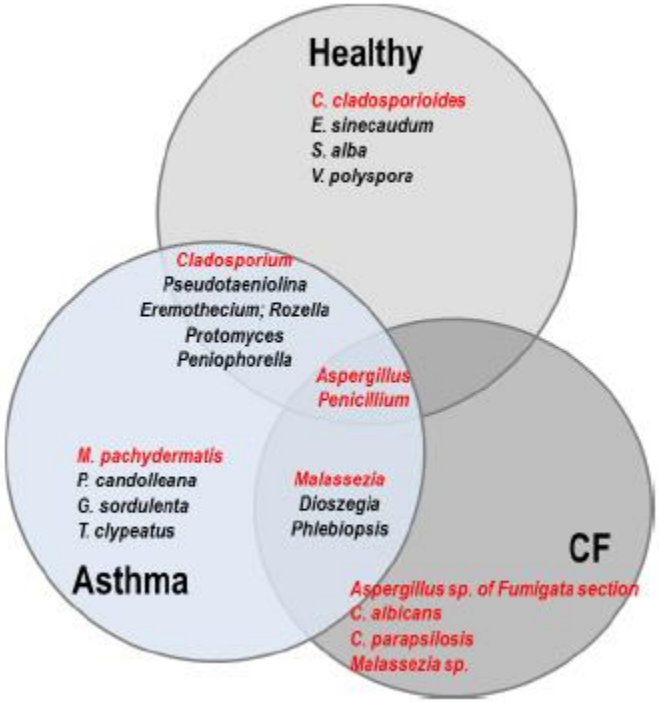


Diagram representing the comparison of the respiratory mycobiomes in healthy individuals, and patients with CF or asthma from published studies

RESEARCH ARTICLE

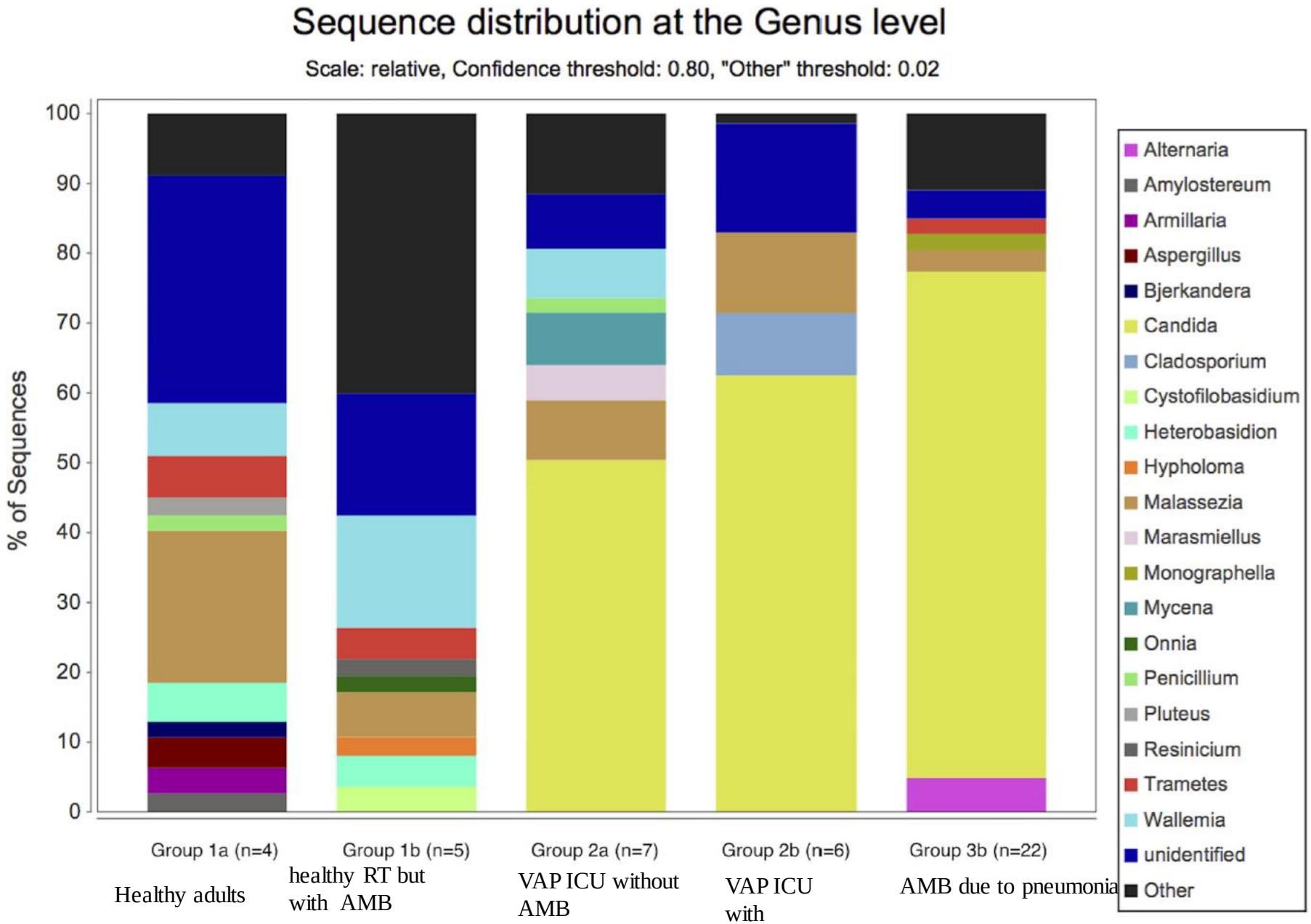
Characterisation of *Candida* within the Mycobiome/Microbiome of the Lower Respiratory Tract of ICU Patients

Robert Krause[1]*, Bettina Halwachs[2,3,4], Gerhard G. Thallinger[5], Ingeborg Klymiuk[6], Gregor Gorkiewicz[4], Martin Hoenigl[1], Jürgen Prattes[1], Thomas Valentin[1],

PLOS ONE | DOI:10.1371/journal.pone.0155033 May 20, 2016

	1a, healthy adults (n = 87)	1b, non-ICU, extrapulmonary infection, AB therapy (n = 18)	2a, ICU, no AB therapy (n = 8)	2b, ICU, extrapulmonary infection, AB therapy (n = 23)	3b, ICU, pneumonia, AB therapy (n = 34)[α]	4, candidemia (n = 32)	p-value
Intrahospital death	0	0	3 (38%)	9 (39%)	11 (32%)	10 (31%)	0.92
30-day mortality	0	0	3 (38%)	9 (39%)	11 (32%)	10 (31%)	0.92
Candida related death (related to total deaths)	0	0	0 (0%)	0 (0%)	0 (0%)	7 (70%)	0.074

Krause R, et al, PLOS ONE 2016



Healthy adults

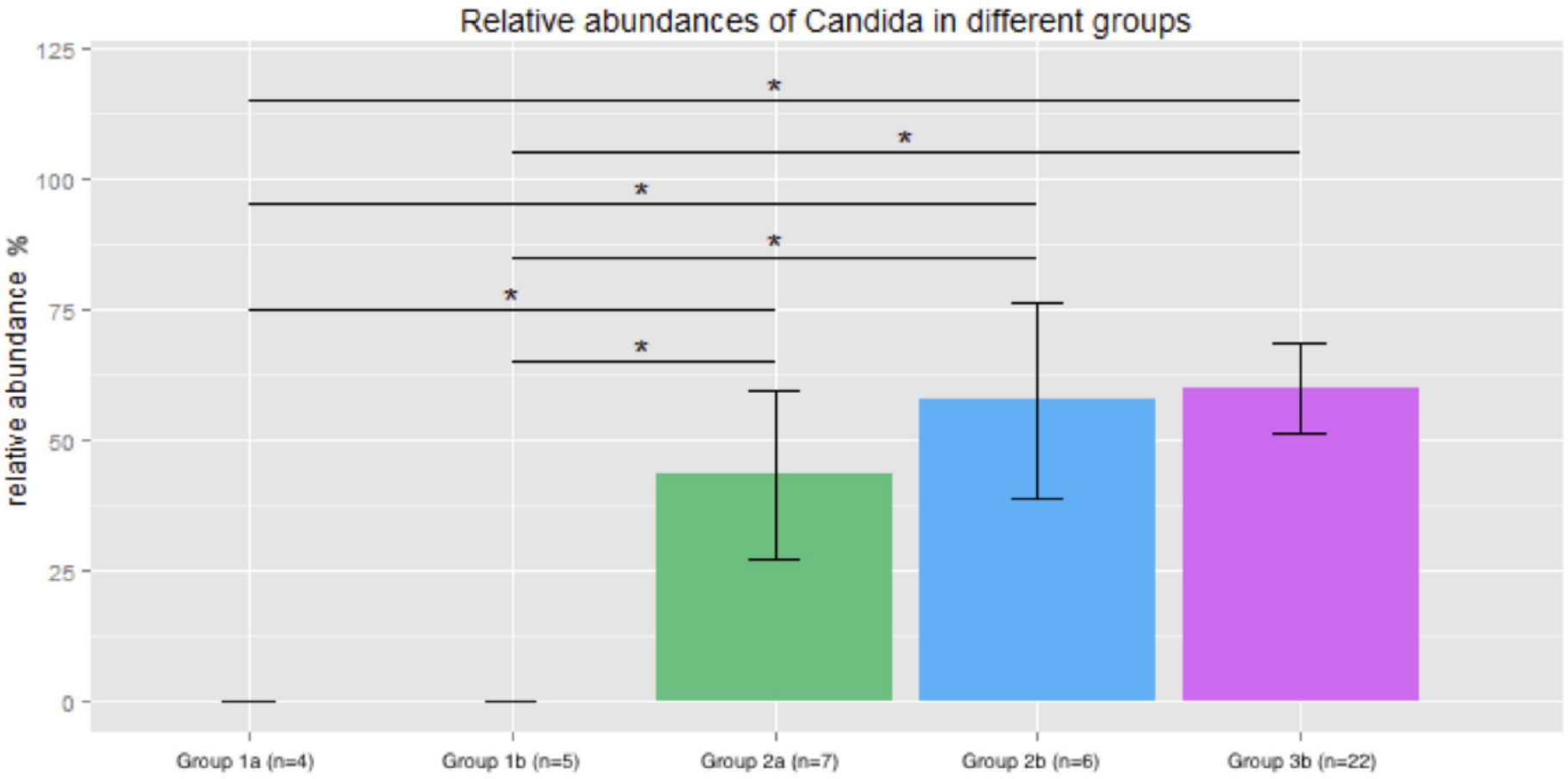
healthy RT but with AMB

VAP ICU without AMB

VAP ICU with

AMB due to pneumonia

Krause R, et al, PLOS ONE 2016



Healthy adults

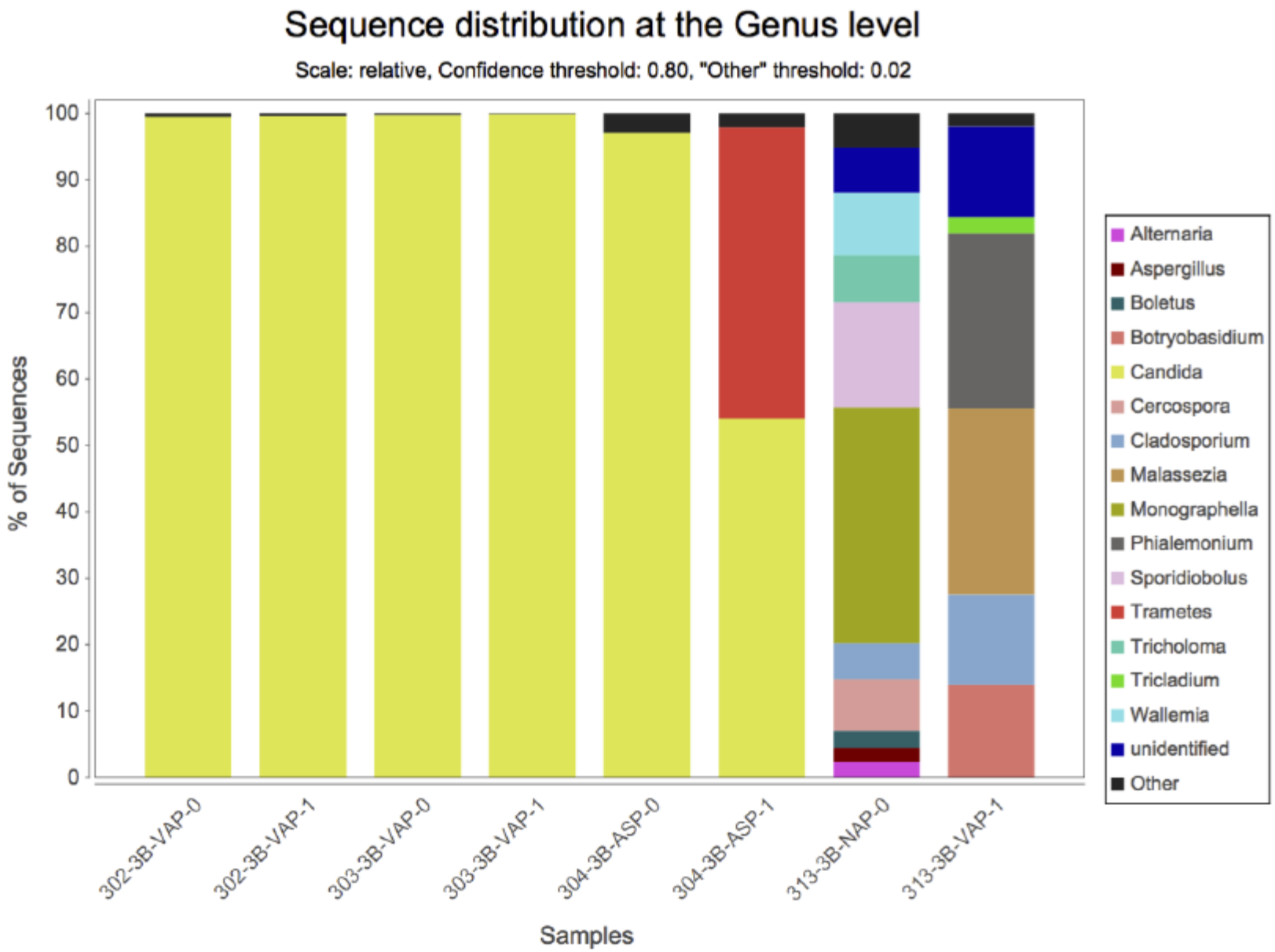
healthy RT but with AMB

VAP ICU without AMB

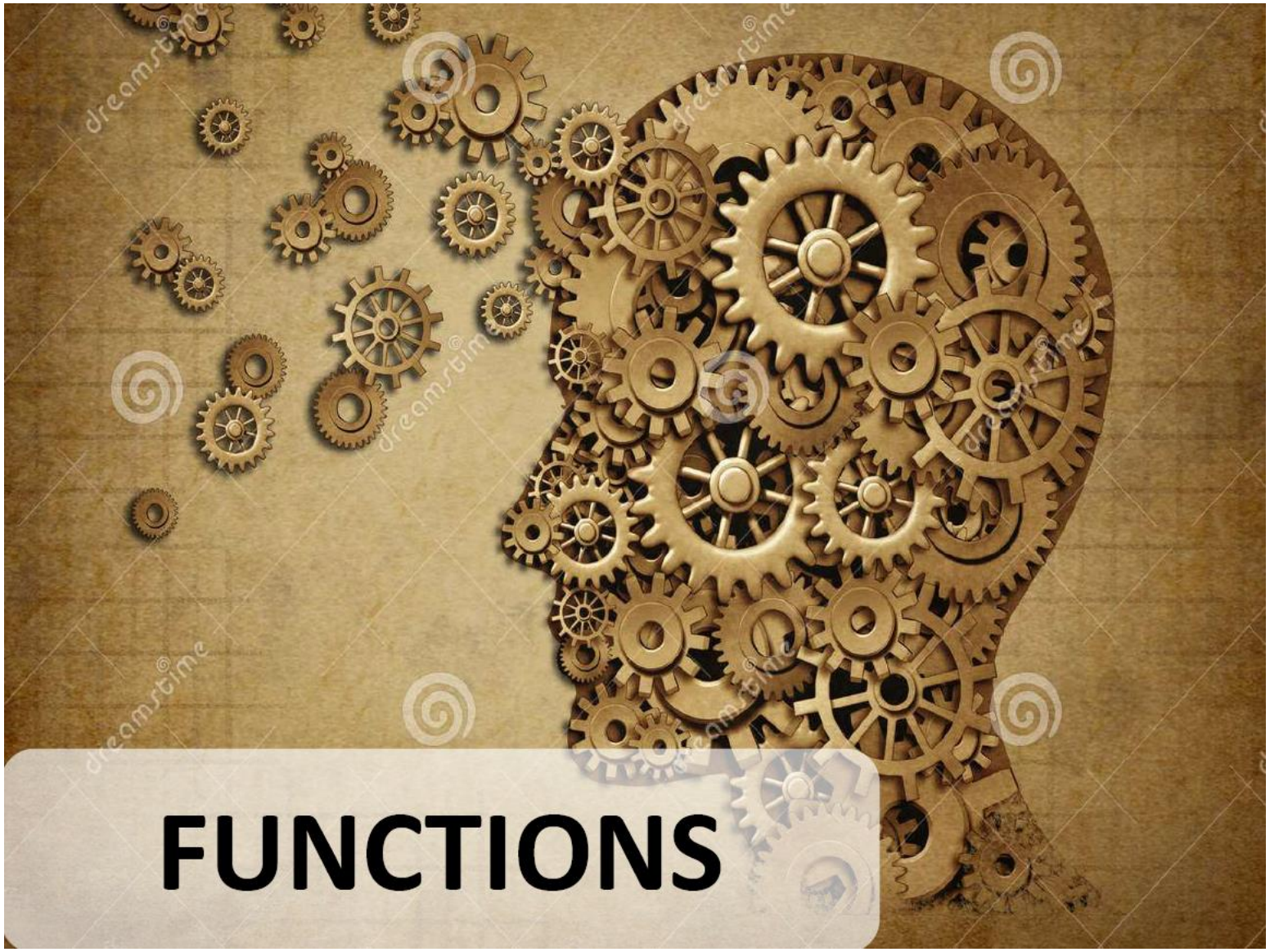
VAP ICU with AMB

AMB due to pneumonia

Krause R, et al, PLOS ONE 2016



Mycobiota



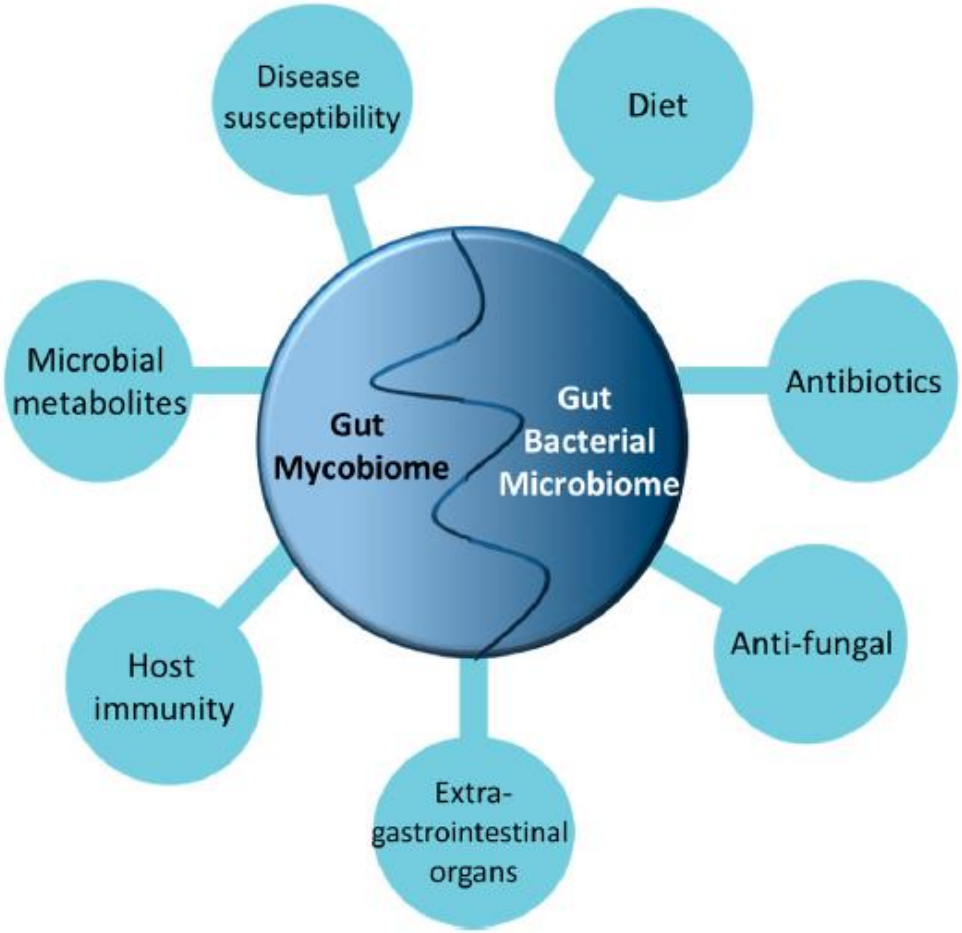
International Journal of
Molecular Sciences

MDPI

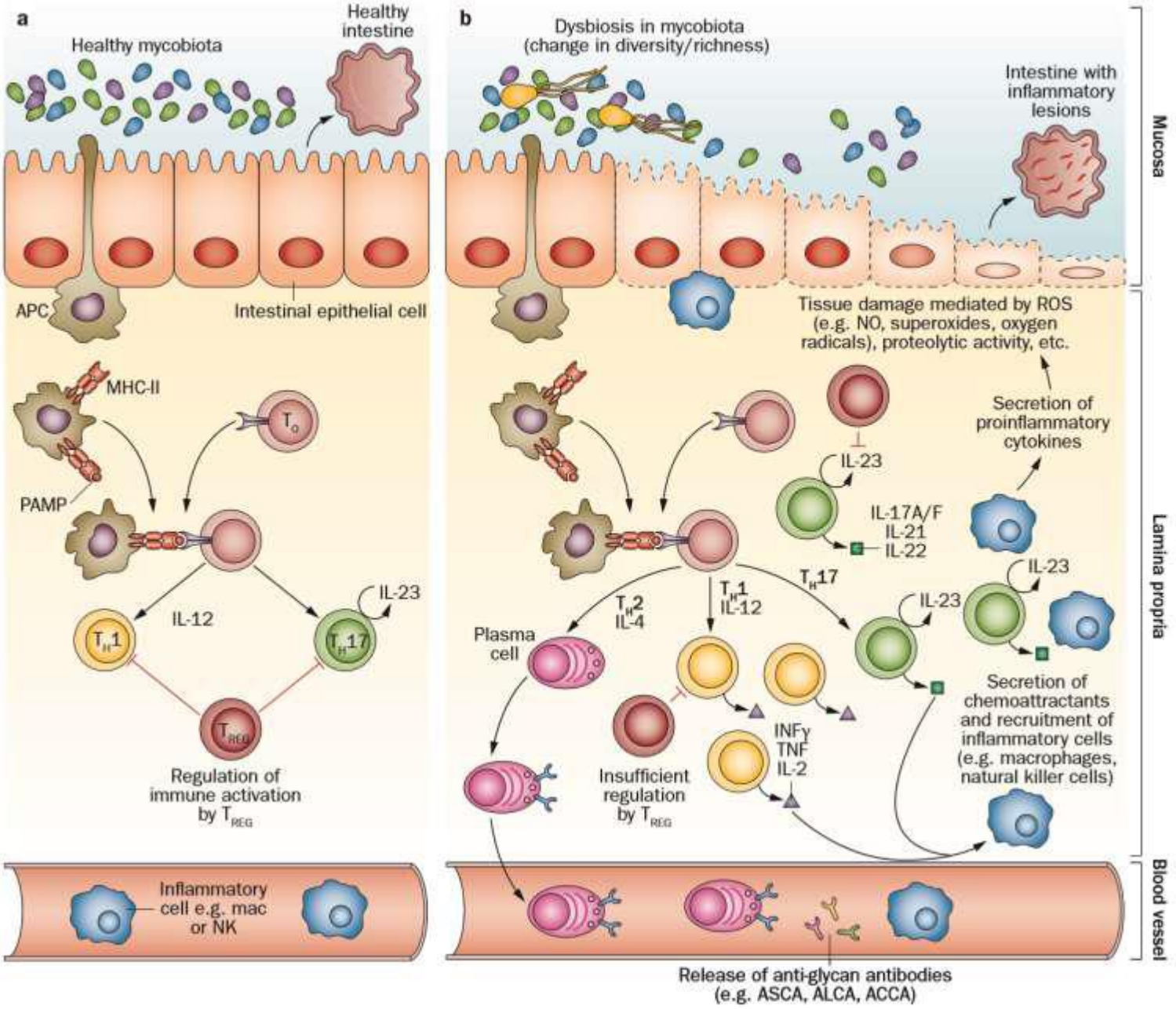
Review

The Fungal Mycobiome and Its Interaction with Gut Bacteria in the Host

Qi Hui Sam [1], Matthew Wook Chang [2,3] and Louis Yi Ann Chai [1,4,*]

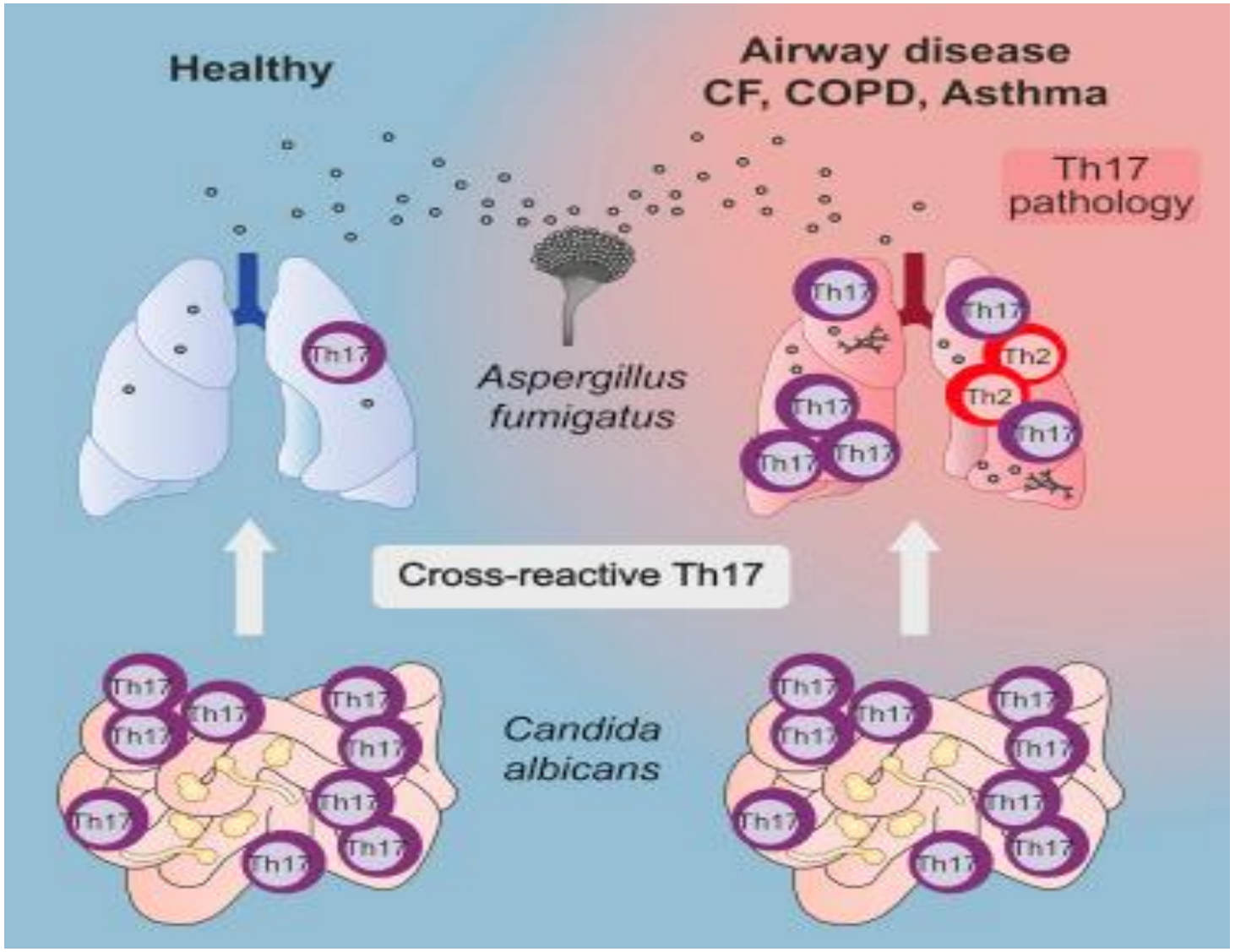


Mycobiota and immune system



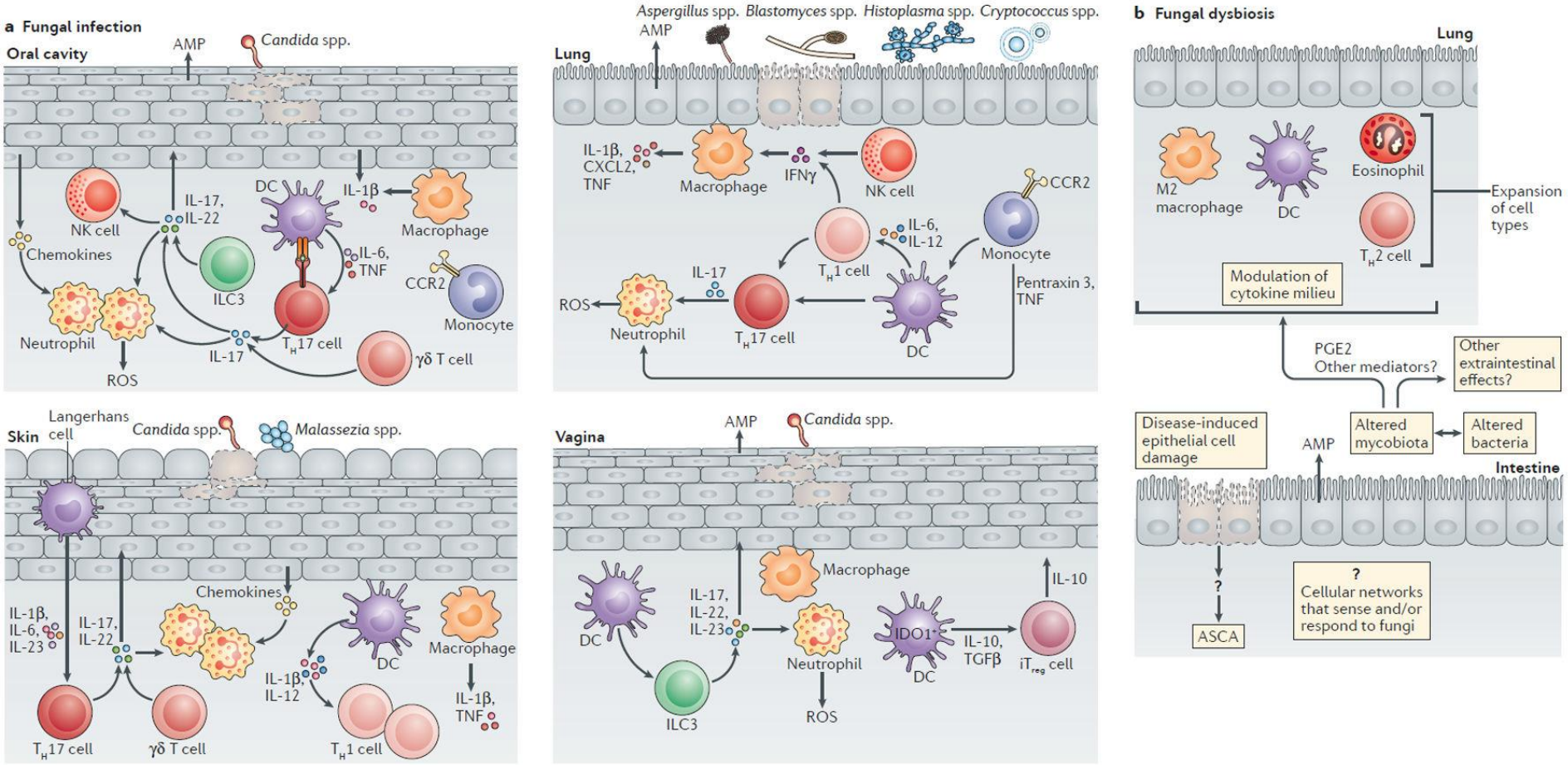
Bacher P, et al. Human anti-fungal Th17 immunity and pathology rely on cross-reactivity against Candida albicans

Cell 2019; 176(6):1340-1355



Examples of mucosal immune responses to fungal infection and dysbiosis

Iliev I, et al. Nat Rev Immunol. 2017 Oct;17(10):635-646



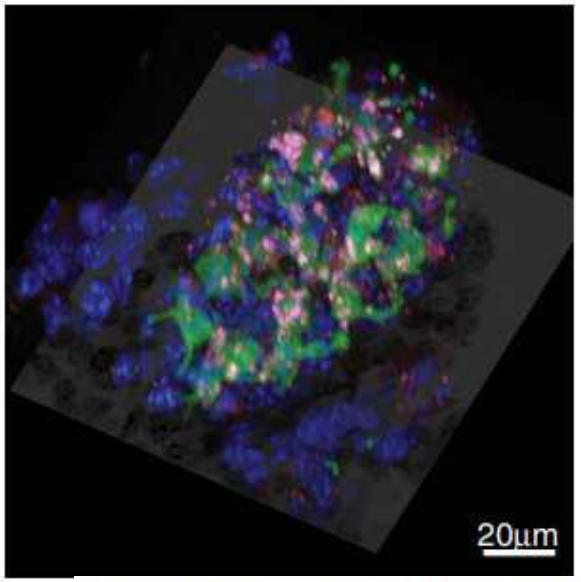
Leonardi et al., Science 2018; 359:232–236

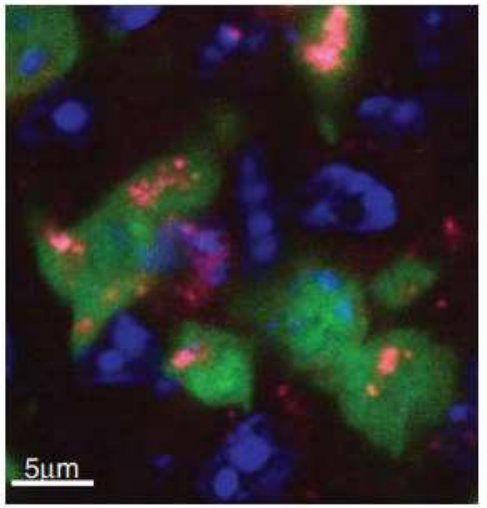
GUT IMMUNITY

CX3CR1^{+} mononuclear phagocytes control immunity to intestinal fungi

Irina Leonardi,[1,2] Xin Li,[1,2] Alexa Semon,[1,2] Dalin Li,[3] Itai Doron,[1,2] Gregory Putzel,[2] Agnieszka Bar,[1,2] Daniel Prieto,[4] Maria Rescigno,[5] Dermot P. B. McGovern,[3] Jesus Pla,[4] Iliyan D. Iliev[1,2,6]*

Intestinal fungi are an important component of the microbiota, and recent studies have unveiled their potential in modulating host immune homeostasis and inflammatory disease. Nonetheless, the mechanisms governing immunity to gut fungal communities (mycobiota) remain unknown. We identified CX3CR1^{+} mononuclear phagocytes (MNPs) as being essential for the initiation of innate and adaptive immune responses to intestinal fungi. CX3CR1^{+} MNPs express antifungal receptors and activate antifungal responses in a Syk-dependent manner. Genetic ablation of CX3CR1^{+} MNPs in mice led to changes in gut fungal communities and to severe colitis that was rescued by antifungal treatment. In Crohn's disease patients, a missense mutation in the gene encoding CX3CR1 was identified and found to be associated with impaired antifungal responses. These results unravel a role of CX3CR1^{+} MNPs in mediating interactions between intestinal mycobiota and host immunity at steady state and during inflammatory disease.





C. albicans-RFP

Curr Opin Gastroenterol. 2018 Sep 18. doi: 10.1097/MOG.0000000000000479. [Epub ahead of print]

Macrophage interactions with fungi and bacteria in inflammatory bowel disease.

Leonardi I[1,2], Li X[1,2], Iliev ID[1,2,3,4].

KEY POINTS

- At steady state, gut-resident macrophages are required for the establishment of an immunoregulatory response.
- In IBD patients, intestinal inflammation affects the maturation of infiltrating monocytes into tolerogenic macrophages and results in the accumulation of proinflammatory monocytes.
- Gut-resident macrophages are required to control intestinal fungi and bacteria.
- Defects in CX3CR1^{+} mononuclear phagocyte function worsens gut intestinal inflammation.
- Loss of function mutation in CX3CR1 affects the induction of humoral responses against intestinal fungi in Crohn's disease patients.

ΣΔ Ι, ΙΦΝΕ και εντερικό μυκοβίωμα

Τα κύρια ευρήματα μέχρι στιγμής σχετίζονται με *Saccharomyces cerevisiae* και *Candida* sp. Υπερανάπτυξη *Candida* spp.έχει διαπιστωθεί σε ασθενείς με ΣΔ Ι και φλεγμονώδη νόσο εντέρου.

Κακή ρύθμιση ΣΔ μπορεί να οδηγεί σε υπερανάπτυξη μυκήτων και ασθενείς με ΣΔ είναι πιο επιρρεπείς σε μυκητιακές λοιμώξεις [79].

Το ίδιο ισχύει και για ανοσοκατασταλμένους ασθενείς [2,3].

Σε νόσο Crohn έχει παρατηρηθεί ↑ αποικισμός από *Candida* sp, ↑ επίπεδα antifungal-antibodies against Saccharomyces cerevisiae (ASCA Ig) και ↓ *Saccharomyces cerevisiae* στο εντερικό μυκοβίωμα . Ο ↑ αποικισμός από *Candida* sp σε ΙΦΝΕ μπορεί να οφείλεται σε ανοσολογική διαταραχή και σε χρήση αντιφλεγμονωδών, AMB [4].

Η υπόθεση ότι το εντερικό μυκοβίωμα έχει επίπτωση σε εξωεντερική ανοσία υποστηρίζεται από ευρήματα σε επίμυες με πνευμονική αλλεργία επαγόμενη από AMB υπερανάπτυξη *Candida* [5].

Η μυκητιακή χλωρίδα μπορεί επίσης να επηρεάζει τον βλεννογονικό φραγμό, όταν το μικροβίωμα διαταράσσεται [6].

1. Nowakowska D, et al. J Infect 2004;48(4):339–46. 2. Li Q, et al. J Clin Gastroenterol 2014;48(6):513–23.
3. Chehoud C, et al. Inflamm Bowel Dis 2015;21(8):1948–56
4. Plantinga TS, et al. Clin Infect Dis 2009;49(5):724–32.
5. Noverr MC, et al. Infect Immun 2005;73(1):30–8.
6. Sokol H, et al. Gut 2017;66(6):1039–48.

Review Article

Diagnostic Markers for Nonspecific Inflammatory Bowel Diseases

ASCA, I2, and OmpC altogether can be found in 80% of patients with CD

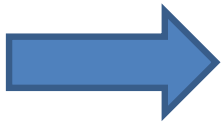


Table 1: The most important currently used markers for nonspecific inflammatory bowel diseases (IBD).

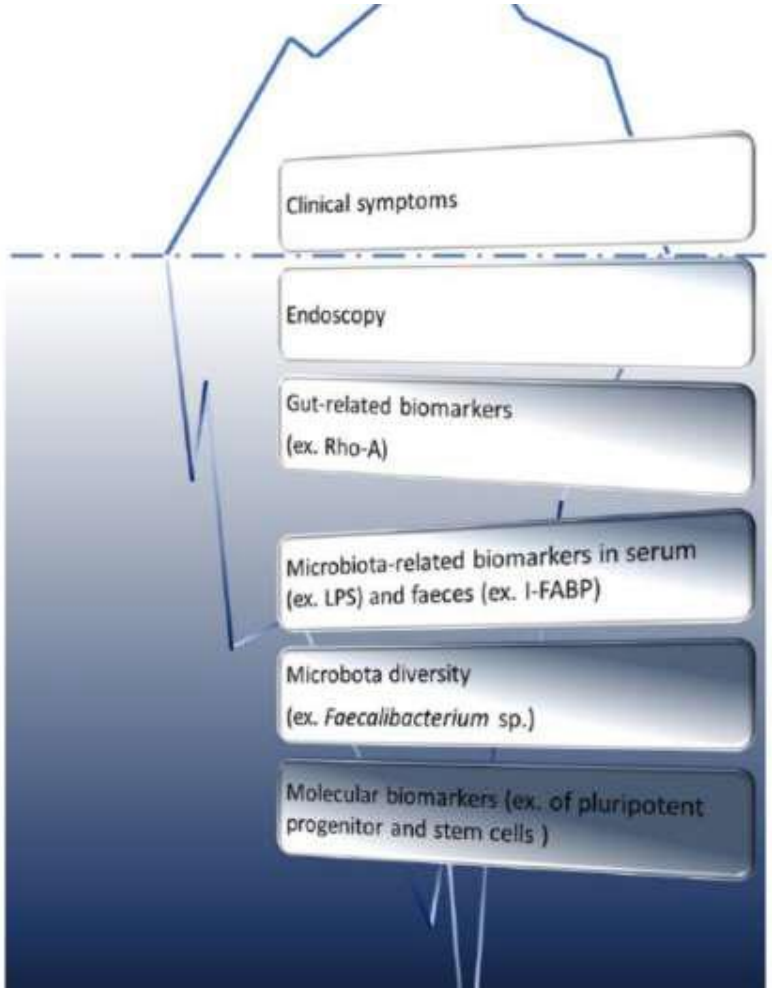
Marker	Name	Expression	Comments	References
Tests evaluating neutrophil activation				
ENA-78	Epithelial neutrophil activating peptide	Bowel epithelial cells; intestinal epithelial cells	Stimulates the chemotaxis of neutrophils, possesses *angiogenic* properties	[10, 21]
HLE	Human leucocytic elastase	Activated neutrophils	Plays a role in degenerative and inflammatory diseases through proteolysis of collagen-IV and elastin	[6]
MRP-8/MRP-14 or S100A8/A9	Calprotectin	Cytoplasm of neutrophils and monocytes	Antibacterial, antifungal, immunomodulatory, and antiproliferative action; a chemotactic factor for neutrophils; the fecal level is proportional to neutrophilic influx into the intestinal tract	[1, 77]
L	Lactoferrin	Neutrophils	Takes part in acute inflammatory response; exhibits high affinity to iron making iron inaccessible to bacteria; fecal L increases significantly with bowel infiltration by neutrophils	[10, 58]
N	Neopterine	Monocytes and macrophages	Inflammatory marker; may help predict the progress of the disease; useful to assess clinical activity of IBD	[9]
Serological markers				
ANCAs	Antineutrophil cytoplasmic antibodies	Antibodies against granules of neutrophil cytoplasm	High p-ANCA levels and antibodies to CBir1 have been associated with increased risk of pouchitis after colectomy in UC	[70]
cANCA	Cytoplasmic		Increase in UC	
sANCA	Speckled		Patients with CD and positive p-ANCA were less likely to respond to therapy with infliximab	
pANCA	Peripheral-antinuclear cytoplasmic antibody		Increase significantly in UC	[74]
ASCAs	Anti-*Saccharomyces cerevisiae* antibodies		The utility in diagnosing difficult cases of indeterminate colitis (IC)	[74]
Anti-OmpC	Antiouter membrane protein C antibody		OmpC pANCA, ASCA, and I2 altogether can be found in 80% of patients with CD	[10]
Hup-B	Mycobacterial histone H1 homologue		May represent the target antigen for pANCA	[10]
Anti-CBir1 flagellin	Antibodies to bacterial flagellin		May be a marker of Crohn's disease complicated by fistulas, perforations, or other serious problems	[10]
PAB	Pancreatic antibody (an antibody to a trypsin-sensitive protein in pancreatic secretions)		PAB is positive in 20%–40% of CD cases and 5% of UC cases; PAB expression may exhibit racial differences	[6]
Anti-I2	Antibodies to *Pseudomonas fluorescens*-associated sequence I2		IgA anti-I2 is positive in 55% of CD cases, 10% of UC cases, and 20% of non-IBD colitis cases; anti-I2 has also been found in patients with other inflammatory enteritis	[10]

Emerging concepts in non-invasive monitoring of Crohn's disease

Wojciech Marlicz, Karolina Skonieczna-Żydecka, Konstantinos John Dabos, Igor Łoniewski and Anastasios Koulaouzidis

Ther Adv Gastroenterol
2018, Vol. 11: 1–20
DOI: 10.1177/1756284818769076

The Basidiomycota:Ascomycota ratio and the Candida albicans count were found to be increased, while Saccharomyces cerevisiae abundance decreased.
Other species' numbers found elevated in CD included Gibberella moniliformis, Alternaria brassicicola and Cryptococcus neoformans.
It is of interest that fungal microbiota correlated with the CD activity index and the degree of inflammation expressed by C-reactive protein (CRP) concentration.



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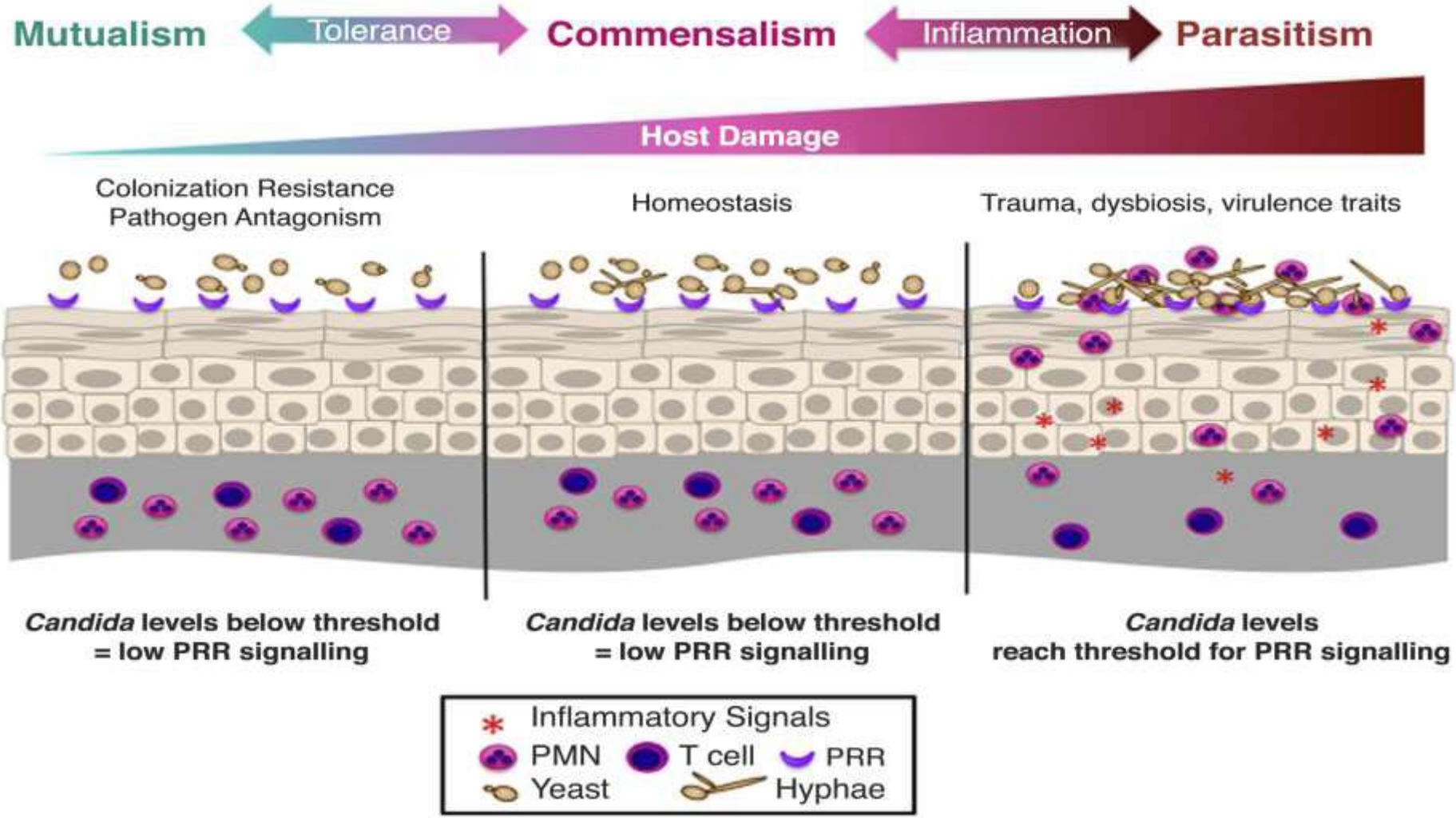
Current Opinion in Microbiology

Fungal interactions with the human host: exploring the spectrum of symbiosis

Rebecca A Hall[1,3] and Mairi C Noverr[2,3]



The Fungal Mycobiota: Small Numbers, Large Impacts

Carol A. Kumamoto[1,*]
[1]Department of Molecular Biology and Microbiology, Tufts University, 150 Harrison Avenue, Boston, MA 02111, USA
*Correspondence: carol.kumamoto@tufts.edu
http://dx.doi.org/10.1016/j.chom.2016.05.018

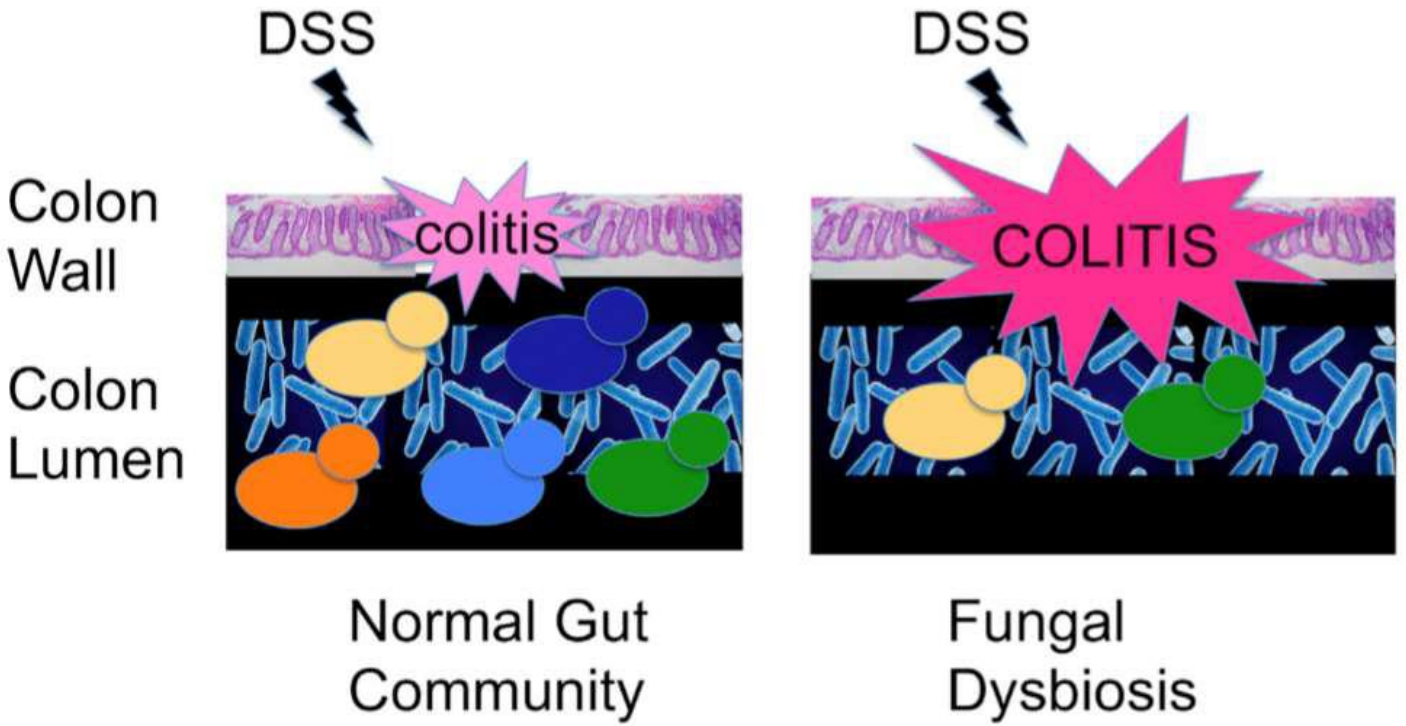


Figure 1. Effects of Fungal Dysbiosis on Colitis

A normal fungal community exhibits diversity (left panel). Long-term treatment with an antifungal drug such as fluconazole shifts the composition of the fungal community, producing fungal dysbiosis. In this situation, the host has an exaggerated response to dextran sodium sulfate (DSS)-induced colitis (right panel). Image of colonic tissue by E. Uthman, public domain. Image of bacteria, public domain FDA.

NATURE REVIEWS | GASTROENTEROLOGY & HEPATOLOGY

Mycobiota in gastrointestinal diseases

Pranab K. Mukherjee, Boualem Sendid, Gautier Hoarau, Jean-Frédéric Colombel, Daniel Poulain

Key points

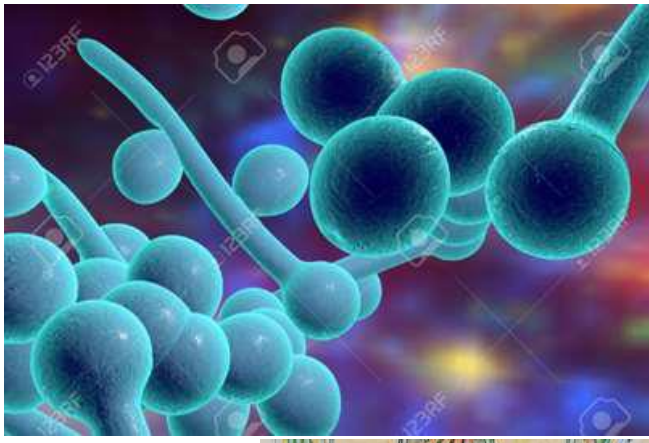
- The mycobiome (the resident fungal community and their genome), is a key component of the human microbiome
- Within a microbiome, there are interactions between and within species or genera among fungi and bacteria
- Alterations within the mycobiota are associated with different diseases
- The mycobiota might directly or indirectly interact with the host immune system
- Interactions between the mycobiota and host immune system can lead to exacerbation of gastrointestinal diseases such as IBD

Curr Gastroenterol Rep (2015) 17: 16
Curr Gastroenterol Rep (2015) 17: 16
DOI 10.1007/s11894-015-0436-2

Small Intestinal Fungal Overgrowth

Askin Erdogan · Satish S. C. Rao

SIFO



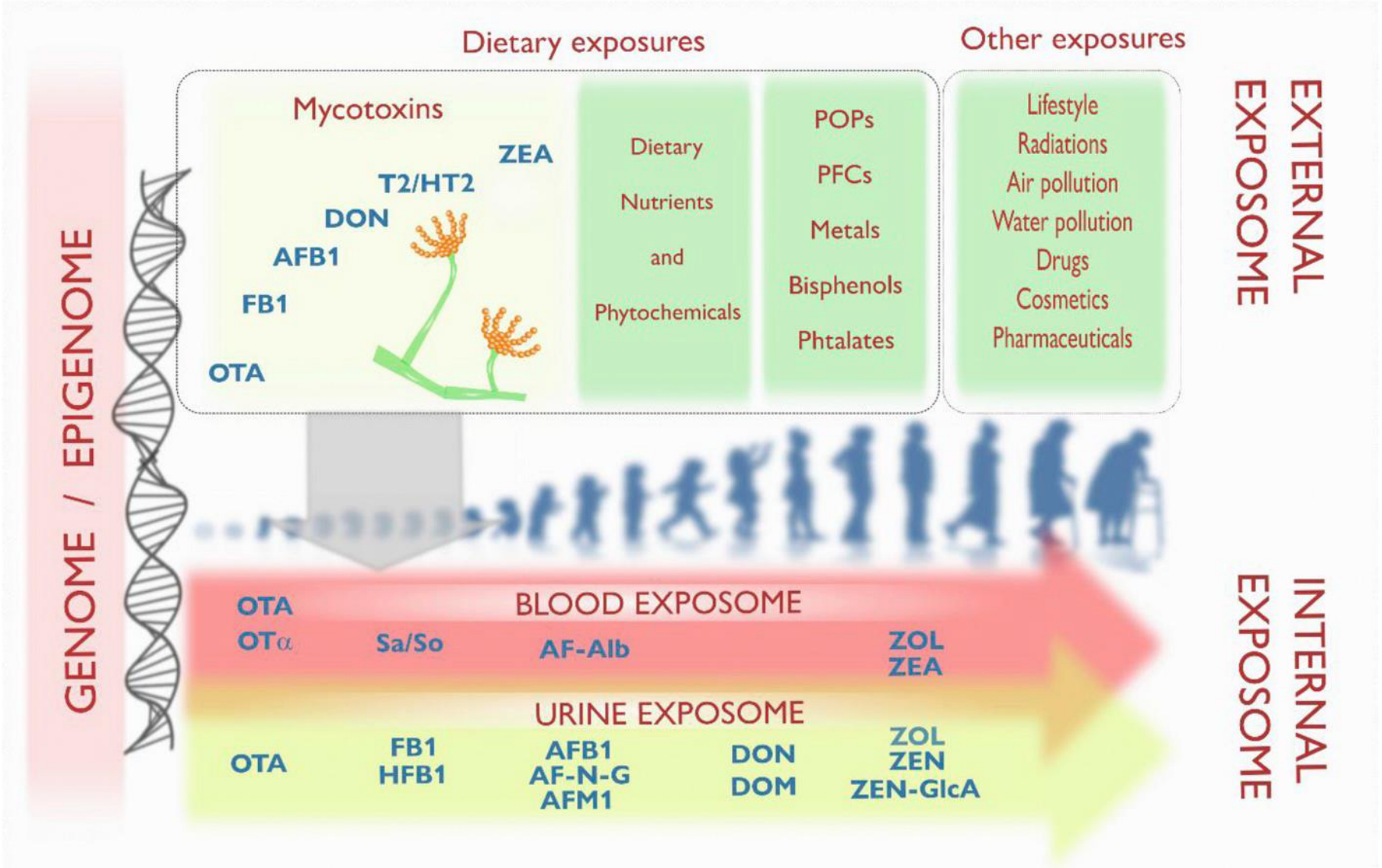
26 % (24/94) and 25.3 % (38/150) of a series of patients with **unexplained GI symptoms had SIFO**
- symptoms observed in these patients were **belching, bloating, indigestion, nausea, diarrhea, and gas**
- small intestinal dysmotility and use of proton pump inhibitors are possible underlying mechanism(s)
- a **2–3-week course of antifungal therapy is recommended and may be effective in improving** symptoms, but evidence for eradication is lacking

Food Chem Toxicol. 2018 Sep 21. pii: S0278-6915(18)30685-9. doi: 10.1016/j.fct.2018.09.039. [Epub ahead of print]

The role of mycotoxins in the human exposome: Application of mycotoxin biomarkers in exposome-health studies.

Marín S[1], Cano-Sancho G[2], Sanchis V[3], Ramos AJ[3].

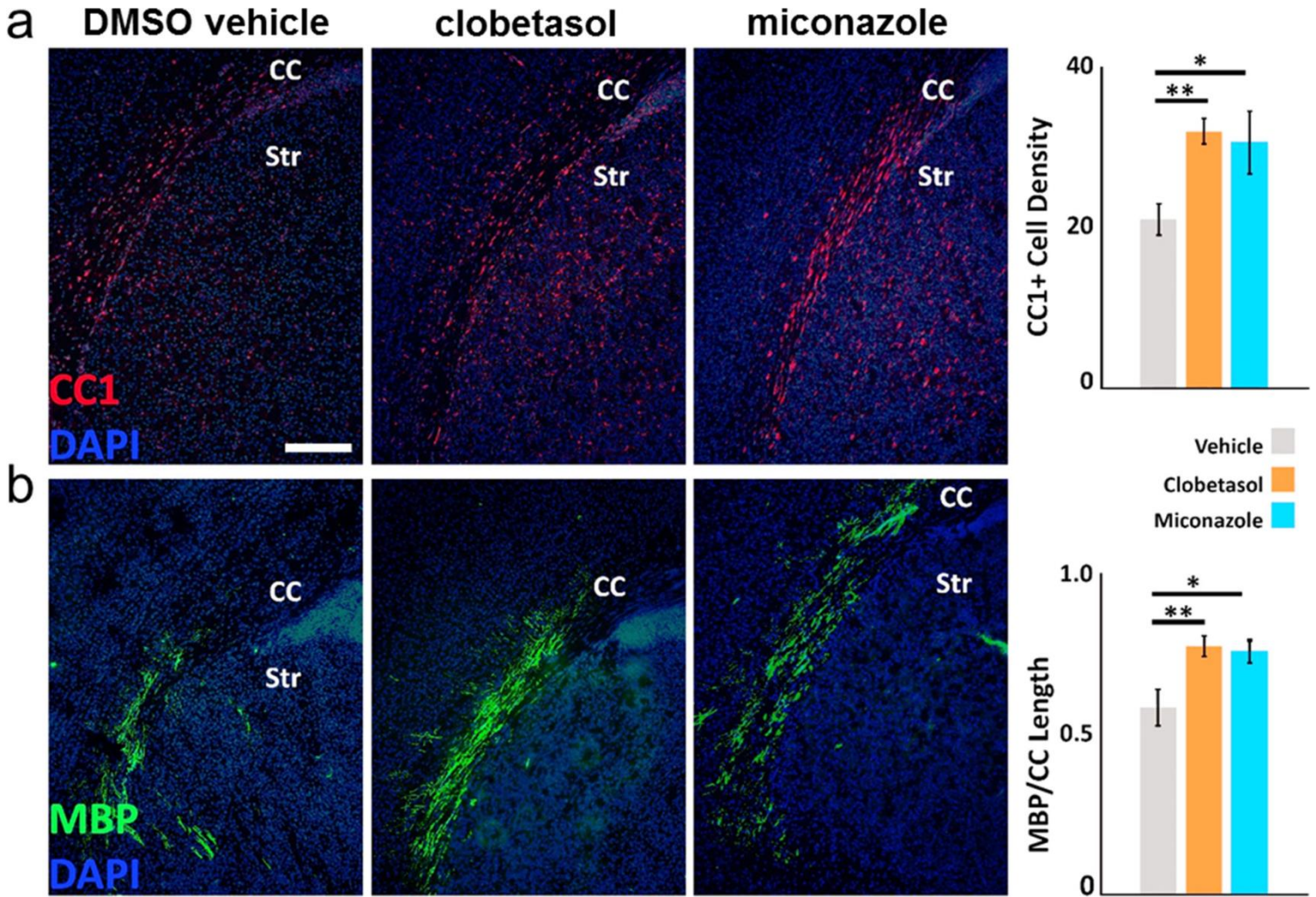
Fungal metabolites of clinical and diagnostic interest



Nature. 2015 June 11; 522(7555): 216–220. doi:10.1038/nature14335.

Drug-based modulation of endogenous stem cells promotes functional remyelination in vivo

Fadi J. Najm[1], Mayur Madhavan[1], Anita Zaremba[2], Elizabeth Shick[1], Robert T. Karl[1], Daniel C. Factor[1], Tyler E. Miller[1,3,4], Zachary S. Nevin[1], Christopher Kantor[2], Alex Sargent[2],



Influence of diet on gut fungi

- *Candida* abundance was positively correlated with recent consumption of carbohydrates and negatively correlated with total saturated fatty acids (1)
- Recent consumption of short chain fatty acids drove down the abundance of *Aspergillus* (1)
- A decrease in *Candida* and *Penicillium* related to almond and pistachio consumption (2)

1. Hoffmann C, et al. PLoS One 2013

2. Ukhanova M, et al. Br J Nutr 2014; 111:2146-52

Influence of diet on gut fungi

Most common taxa in vegetarian and conventional diet samples

Genus	Vegetarian	Conventional
Fusarium	14 (88%)	2 (3%)
Candida	10 (63%)	58 (84%)
Malassezia	13 (81%)	8 (12%)
Penicillium	12 (75%)	1 (1%)
Aspergillus	11 (68%)	4 (6%)
Geotrichum	ND	32 (46%)
Pichia	1 (6%)	11 (16%)
Cladosporium	4 (25%)	11 (16%)

Hallen-Adams HE, et al. Fungal Ecol 2015; 15:9-17
Suhr MJ, et al. Lett Appl Microbiol 2016; 62:209-15

AMERICAN SOCIETY FOR MICROBIOLOGY | mSphere®

RESEARCH ARTICLE
Host-Microbe Biology

High-Fat Diet Changes Fungal Microbiomes and Interkingdom Relationships in the Murine Gut

Timothy Heisel,[a] Emmanuel Montassier,[b] Abigail Johnson,[c] Gabriel Al-Ghalith,[d] Yi-Wei Lin,[e] Li-Na Wei,[e] Dan Knights,[c,f] Cheryl A. Gale[a]

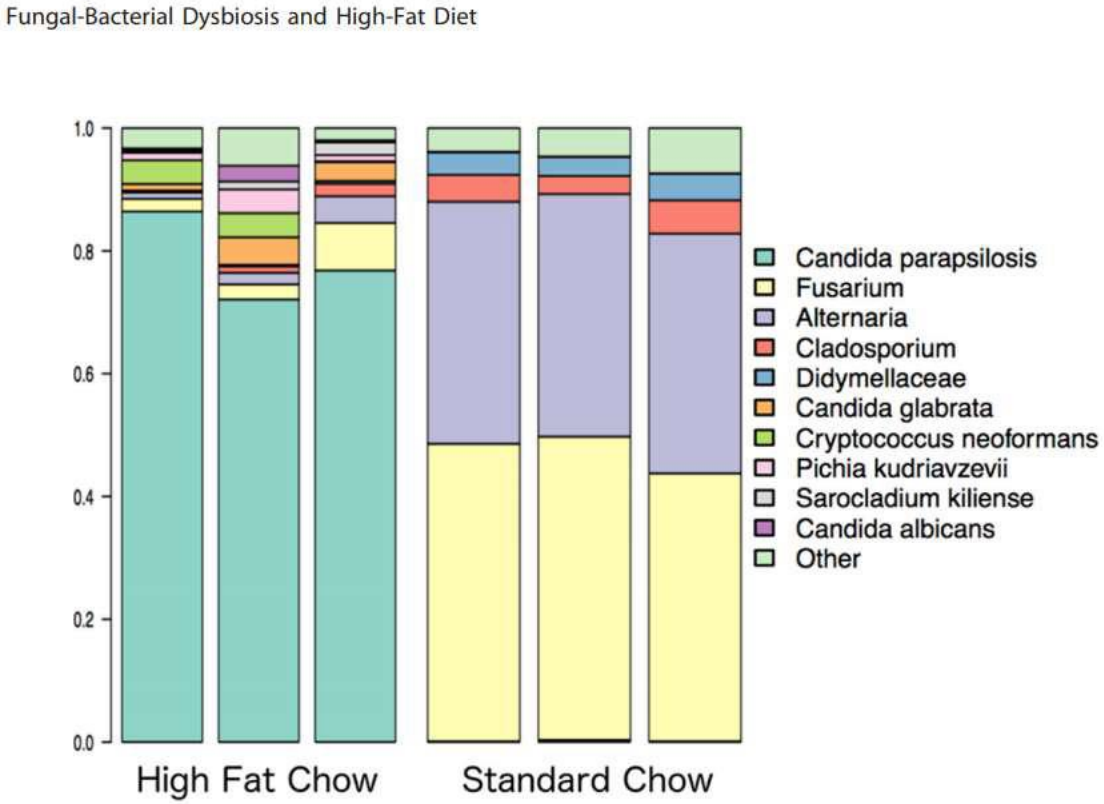
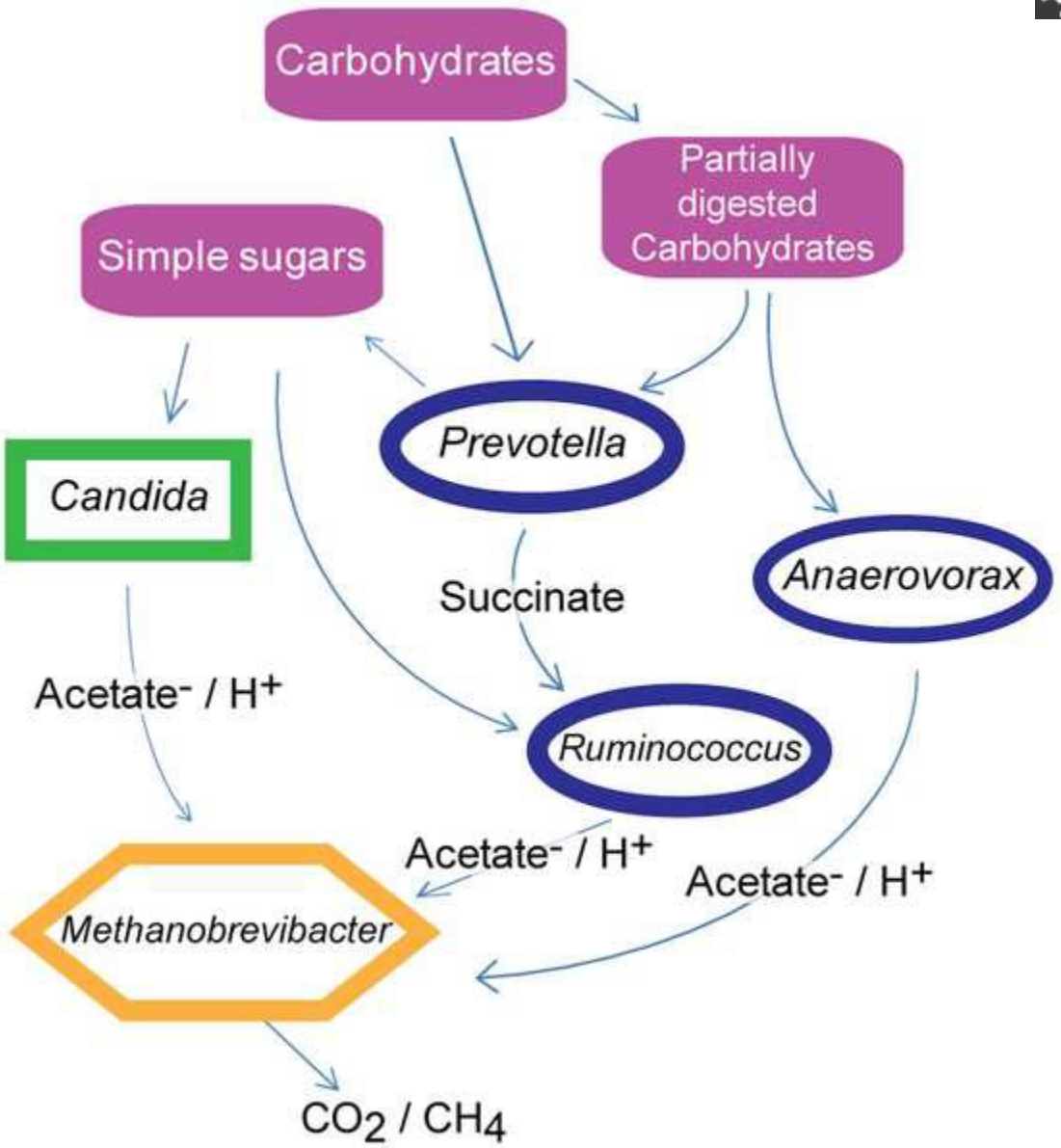


FIG 4 Relative abundance plots of fungal taxa for mouse chows. Each chow was sequenced three individual times (DNA was isolated from different pieces of chow for each sequencing run), and results for each chow were pooled after sequencing. Fungi were identified to the species level, as described in Materials and Methods.

Figure 6. Possible syntrophic relationships in the human gut consistent with data reported in this study.

Hoffmann C, et al. PLOS ONE 2013; 8(6): e66019



Saccharomyces boulardii

Ο Henri Boulard απομόνωσε *μύκητα* από τα φρούτα lychee και mangosteen το 1923 που ονομάσθηκε *Saccharomyces boulardii* , νέο είδος του *γένους Saccharomyces* , με προβιοτικές ιδιότητες

Απουσία γαλακτόζης και σχηματισμού σπορίων συγκριτικά με *S. cerevisiae* (*Sc*)

SCIENTIFIC REPORTS

OPEN

Complete genome sequence and comparative genomics of the probiotic yeast *Saccharomyces*

Received
Accepted
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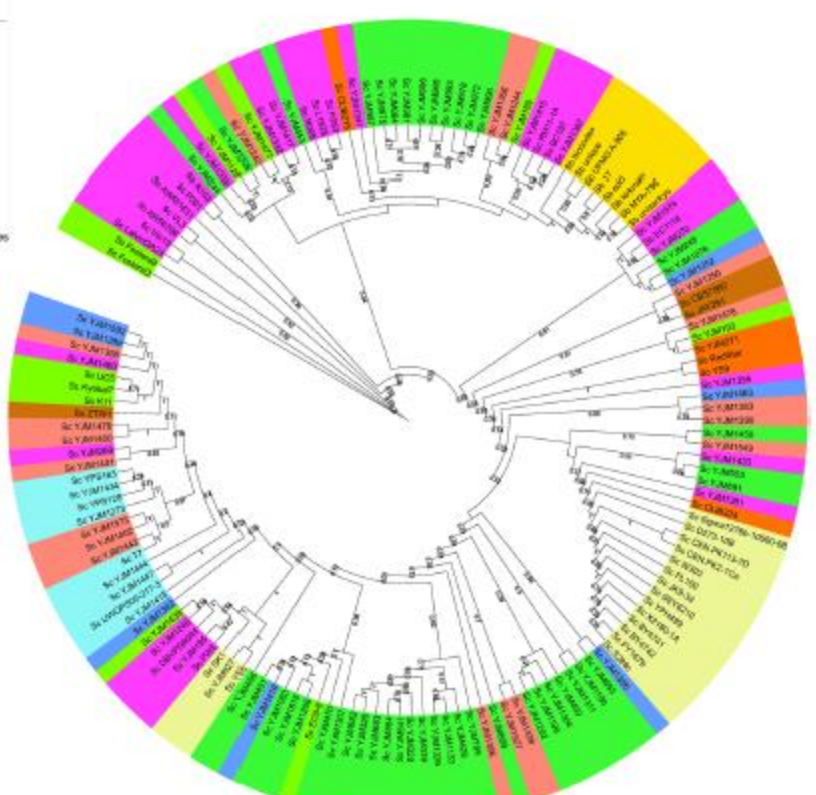

& Srikrishna Subramanian

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PLoS one

Capric Acid Secreted by *S. boulardii* Inhibits *C. albicans* Filamentous Growth, Adhesion and Biofilm Formation

Anna Murzyn[1], Anna Krasowska[1], Piotr Stefanowicz[2], Dorota Dziadkowiec[1], Marcin Łukaszewicz[1,3]*

1 Faculty of Biotechnology, University of Wrocław, Wrocław, Poland, **2** Faculty of Chemistry, University of Wrocław, Wrocław, Poland, **3** Faculty of Chemistry, Wrocław University of Technology, Wrocław, Poland

Abstract

Candidiasis are life-threatening systemic fungal diseases, especially of gastro intestinal track, skin and mucous membranes lining various body cavities like the nostrils, the mouth, the lips, the eyelids, the ears or the genital area. Due to increasing resistance of candidiasis to existing drugs, it is very important to look for new strategies helping the treatment of such fungal diseases. One promising strategy is the use of the probiotic microorganisms, which when administered in adequate amounts confer a health benefit. Such a probiotic microorganism is yeast *Saccharomyces boulardii*, a close relative of baker yeast. *Saccharomyces boulardii* cells and their extract affect the virulence factors of the important human fungal pathogen *C. albicans*, its hyphae formation, adhesion and biofilm development. Extract prepared from *S. boulardii* culture filtrate was fractionated and GC-MS analysis showed that the active fraction contained, apart from 2-phenylethanol, caproic, caprylic and capric acid whose presence was confirmed by ESI-MS analysis. Biological activity was tested on *C. albicans* using extract and pure identified compounds. Our study demonstrated that this probiotic yeast secretes into the medium active compounds reducing candidal virulence factors. The chief compound inhibiting filamentous *C. albicans* growth comparably to *S. boulardii* extract was capric acid, which is thus responsible for inhibition of hyphae formation. It also reduced candidal adhesion and biofilm formation, though three times less than the extract, which thus contains other factors suppressing *C. albicans* adherence. The expression profile of selected genes associated with *C. albicans* virulence by real-time PCR showed a reduced expression of *HWP1*, *INO1* and *CSH1* genes in *C. albicans* cells treated with capric acid and *S. boulardii* extract. Hence capric acid secreted by *S. boulardii* is responsible for inhibition of *C. albicans* filamentation and partially also adhesion and biofilm formation.

Zorić et al. BMC Complementary and Alternative Medicine (2017) 17:268
DOI 10.1186/s12906-017-1773-5

BMC Complementary and Alternative Medicine

RESEARCH ARTICLE Open Access

Membrane of *Candida albicans* as a target of berberine

Received: 28 August 2019 | Revised: 2 September 2019 | Accepted: 3 September 2019

DOI: 10.1111/myc.12999

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mycoses Diagnosis, Therapy and Prophylaxis of Fungal Diseases

WILEY

REVIEW ARTICLE

A European ECMM-ESCMID survey on goals and practices for mycobiota characterisation using next-generation sequencing

Jean-Pierre Gangneux[1] | Hélène Guegan[1] | Louise-Eva Vandenborght[2] | Sylvie Buffet-Bataillon[1] | Raphael Enaud[2] | Laurence Delhaes[2]

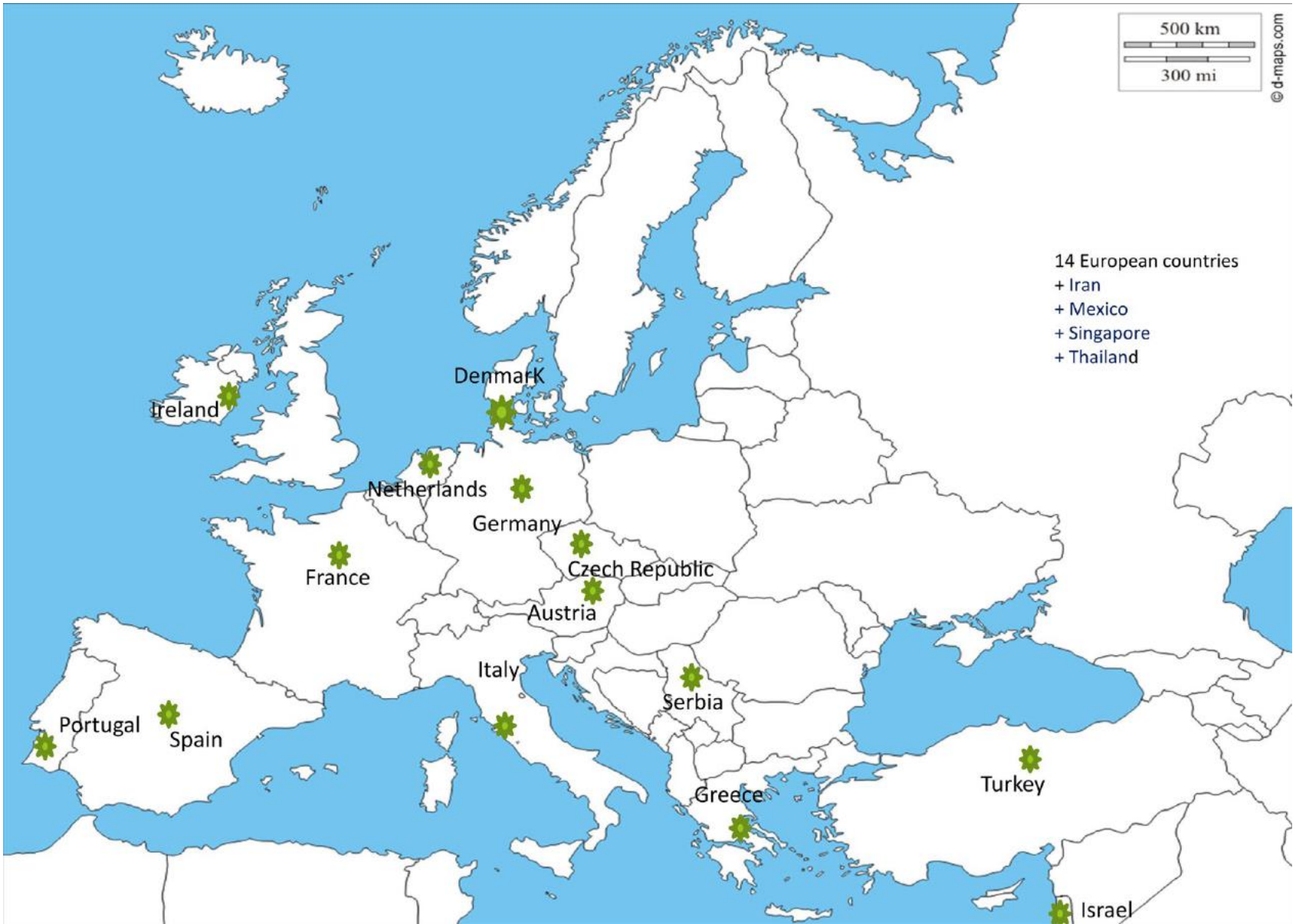
for the ECMM-ESCMID NGS study group

Twenty-six questionnaires from**18** countries were received. The use of NGS to characterise the mycobiota was not in routine for most of the laboratories (N = 23, 82%) and the main reason of using NGS was primary to understand the pathophysiology of a dysbiosis (N = 20), to contribute to a diagnosis (N = 16) or to implement a therapeutic strategy (N = 12).

Other reported reasons were to evaluate the exposome (environmental studies) (N = 10) or to investigate epidemics (N = 8).

No consensus has emerged for the choice of the targets with 18S, ITS1 and ITS2 used alternatively among the laboratories.

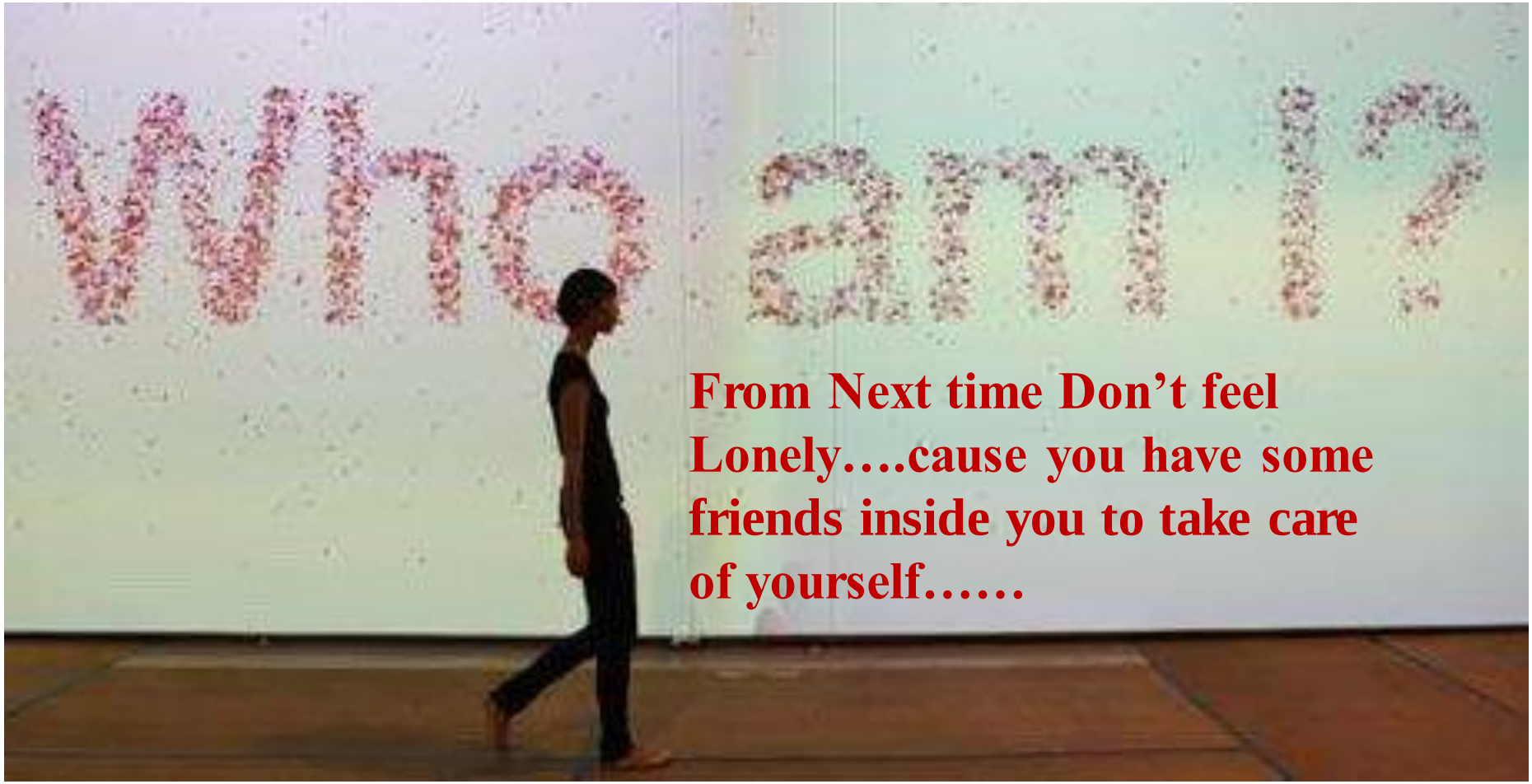
Map of the 14 European countries that participated in the ECMM-ESCMID survey



Questions	Answers (%)
Goals of using NGS to study the mycobiota	Understand the pathophysiology of a dysbiosis: 71% Contribute to a diagnosis: 57% Implement a therapeutic strategy: 43% Evaluate the exposome (environmental studies): 36% Investigate epidemics: 33%
Mycobiota sites studied or planned to be studied	Lower respiratory tract: 54% Digestive tract: 39% Upper respiratory tract: 36% Environmental samples: 25% Oral cavity: 11% Skin: 3%
Samples used for NGS processing	Sputum: 50% Stool: 43% Broncho-alveolar lavage: 39% Environment samples: 21% Oral wash: 11% Skin 3%

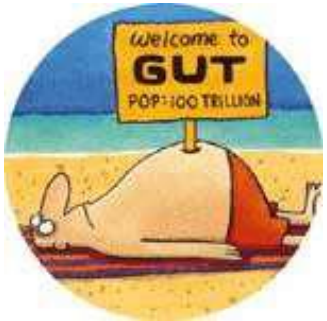
Results of the survey on goals and practices for mycobiota characterisation using next-generation sequencing in European laboratories (N = 27 laboratories in 18 countries)

Lung diseases to be studied by NGS	Cystic fibrosis: 50% Lung transplantation: 32% COPD: 29% Asthma: 29% Pneumonia: 29%
Digestive tract diseases to be studied by NGS	Crohn disease: 18% Pseudomembranous colitis: 14% Chronic ulcerative colitis: 11% Other (<10%): rheumatoid polyarthritis, diabetes mellitus, AIDS...
Target used	18s rRNA: 40% ITS1: 40% ITS2: 40% Shotgun approach: 18% 28s rRNA: 0%


From Next time Don't feel
Lonely….cause you have some
friends inside you to take care
of yourself……

Unanswered questions about GI Mycobioma

- What are fungi doing in a healthy host, and would their absence be detrimental?
- Are species interchangeable, is there any effect in replacing *C. albicans* with *C. tropicalis* or *C. parapsilosis* in an individual host?
- Do species, or strains of the same species, compete and, if so, are there predictable outcomes?
- Stability of the gut mycobiome?
- Are there geographical differences in mycobiome?
- Differences based on diet, age, gender or other demographic factors?
- Which groups of fungi are likely to be of importance to the host and the overall microbiome?
- How do we best categorize the diverse members of gastrointestinal mycobiota in order to separate true residents from transient passersby?



Σας ευχαριστώ! !!!!!!!!!!!!!