

# **Unveiling the Role of Gut Bacteria in Drug Transformation: Insights from Parkinson's Treatment**

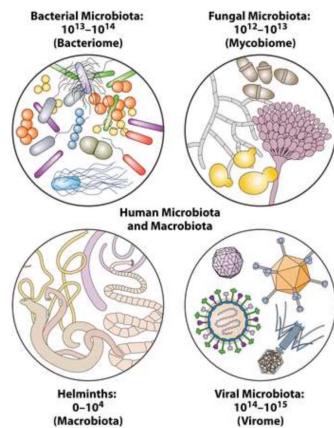
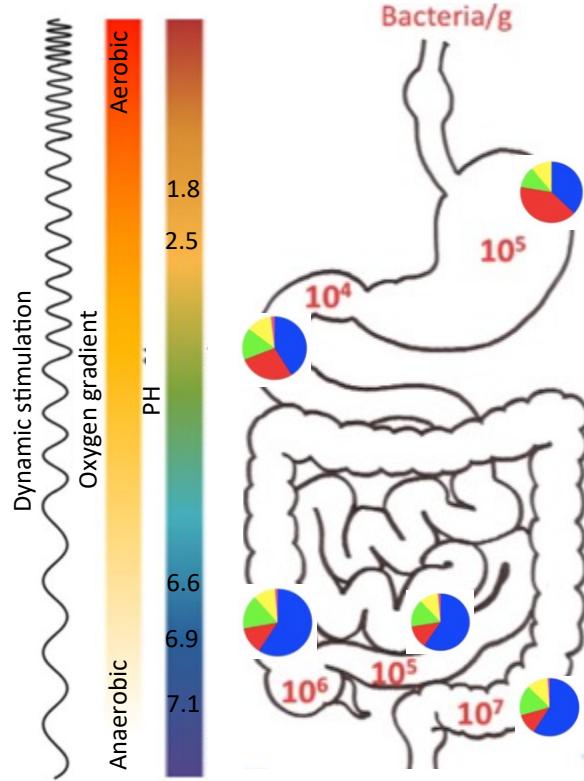


**Sahar El Aidy**

Host-Microbe Interactions group (HMI),  
Groningen Biomolecular Sciences and Biotechnology Institute  
University of Groningen

37<sup>th</sup> NIBI meeting  
Egmond aan Zee  
10/11/2023

# The Human Microbiota



# Why is it important to know the human microbiota?

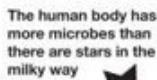
## Microbiome

### IN NUMBERS

**100 Trillion**

symbiotic microbes live in and on every person and make up the human microbiota.

The human body has more microbes than there are stars in the milky way

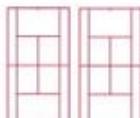


**95%**

of our microbiota is located in the GI tract

**150:1**

The genes in your microbiome outnumber the genes in our genome by about 150 to one



The surface area of the GI tract is the same size as 2 tennis courts

You have  
**1.3X**  
more microbes than human cells

**>10,000**

Number of different microbial species that researchers have identified living in and on the human body



The gut microbiota can weigh up to 2kg



Interfacing Food & Medicine

The microbiome is more medically accessible and manipulable than the human genome

**90%**

It is thought that 90% of disease can be linked in some way back to the gut and health of the microbiome

**5:1**

Viruses:Bacteria  
in the gut microbiota



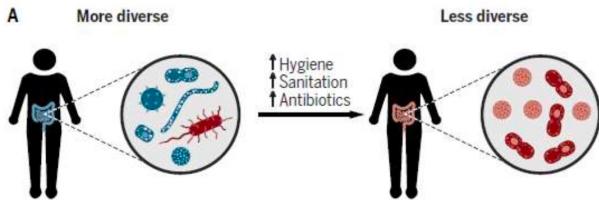
**2.5** The number of times your body's microbes would circle the earth if positioned end to end



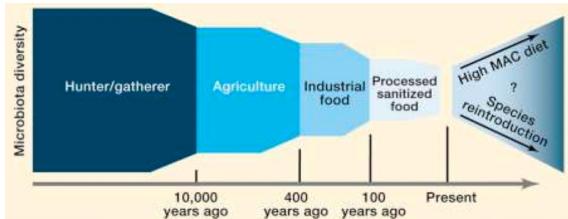
Each individual has a unique gut **microbiota**, as personal as a fingerprint



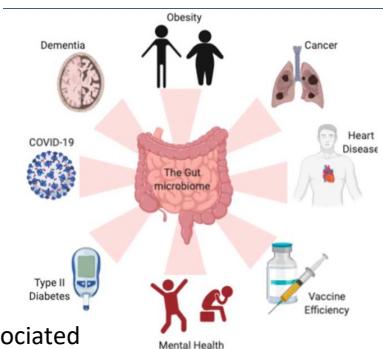
## Changes in the life-style, endangered microbiota and appearance of chronic diseases



Gut microbial diversity has been reduced to 1/3 over the past decades

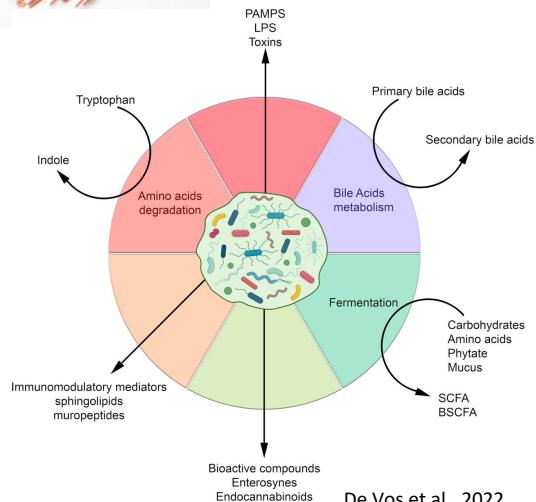


## Dramatic changes in the diet during human evolution



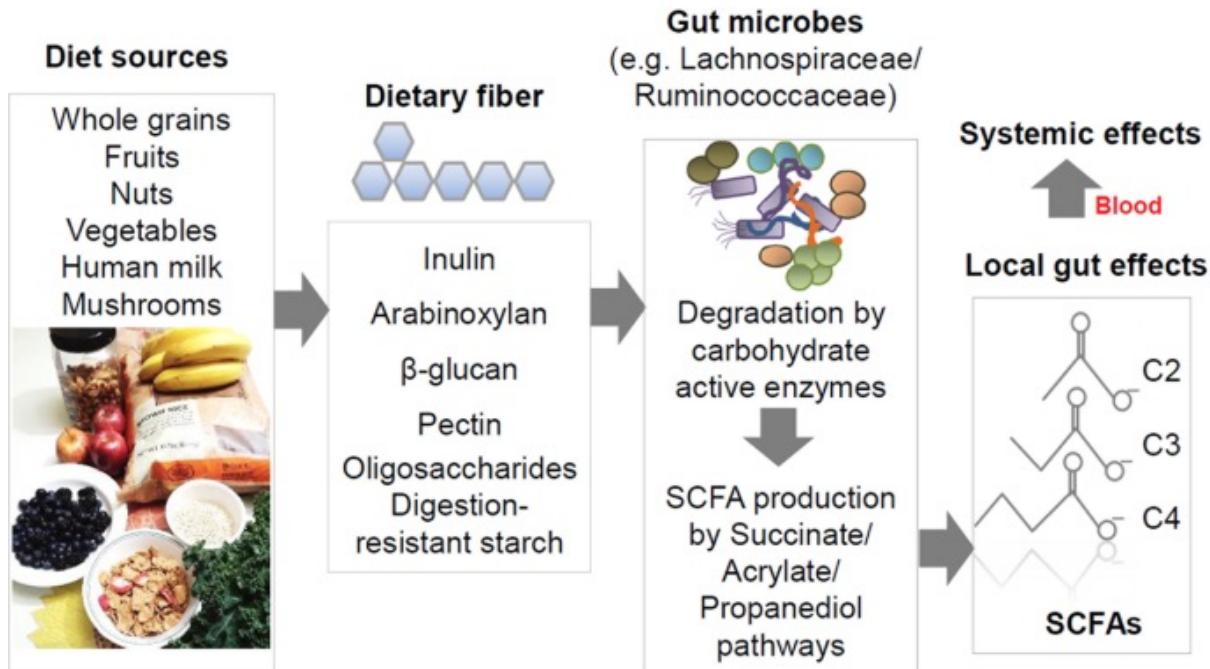
Alteration in the gut microbiota has been associated with intestinal and extra-intestinal diseases

# Gut bacteria influence the nutritional content of our food in ways that are not understood

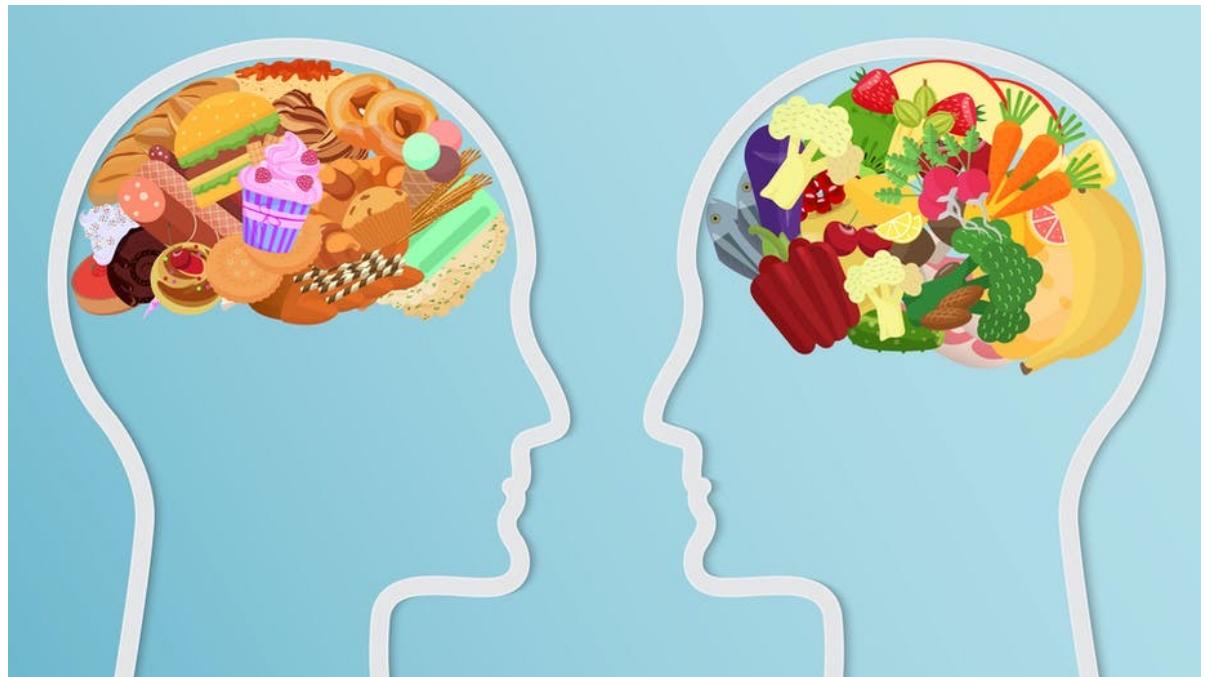


De Vos et al., 2022

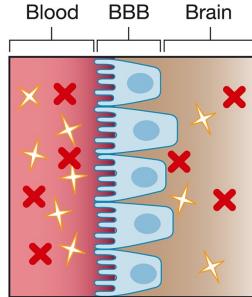
# How to feed your gut microbiota?



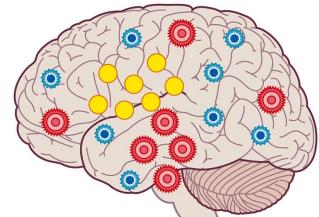
Your gut microbes play a key part in food craving,  
influencing your brain ?!



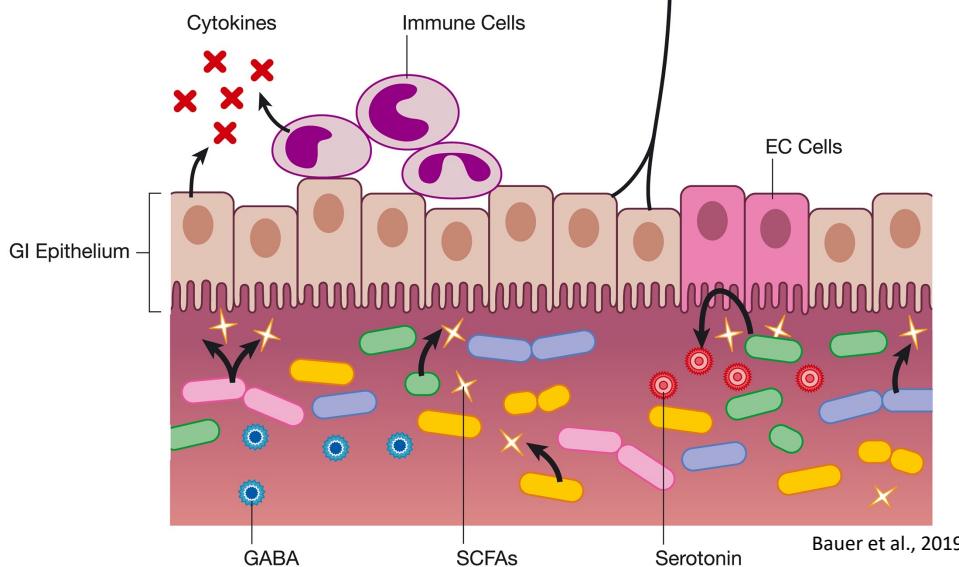
# That Gut Feeling !



★ SCFAs  
✗ Cytokines

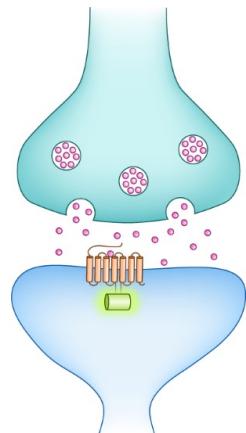
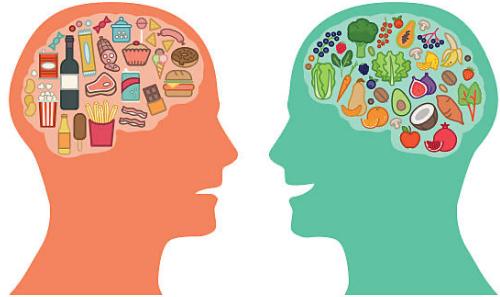
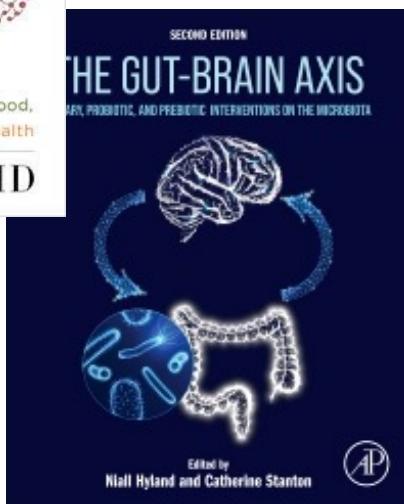
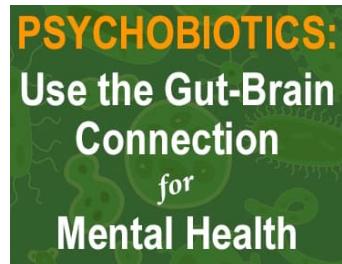
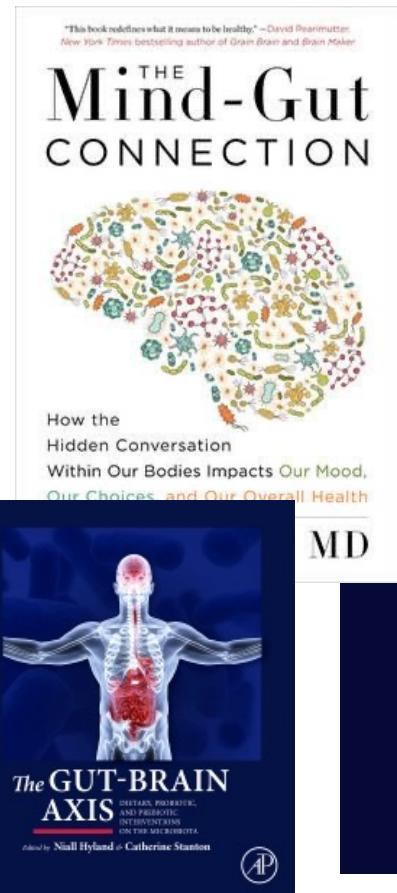


● BDNF  
● Serotonin  
● GABA

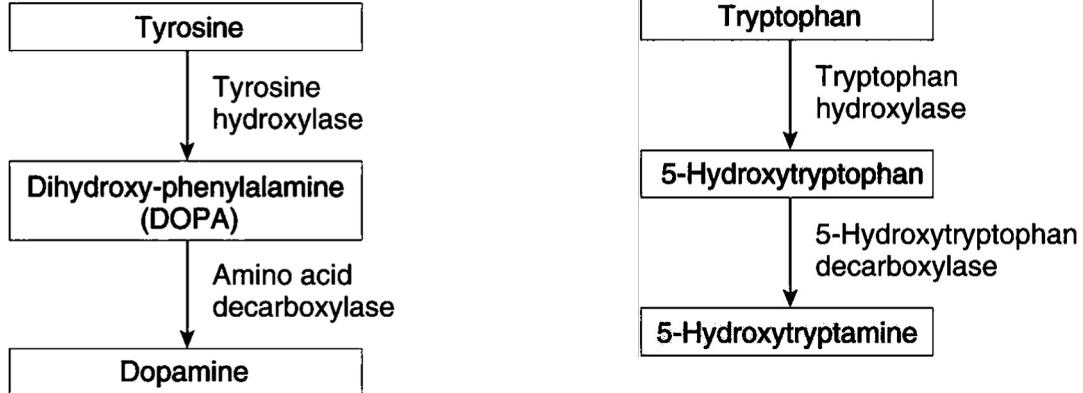


Bauer et al., 2019

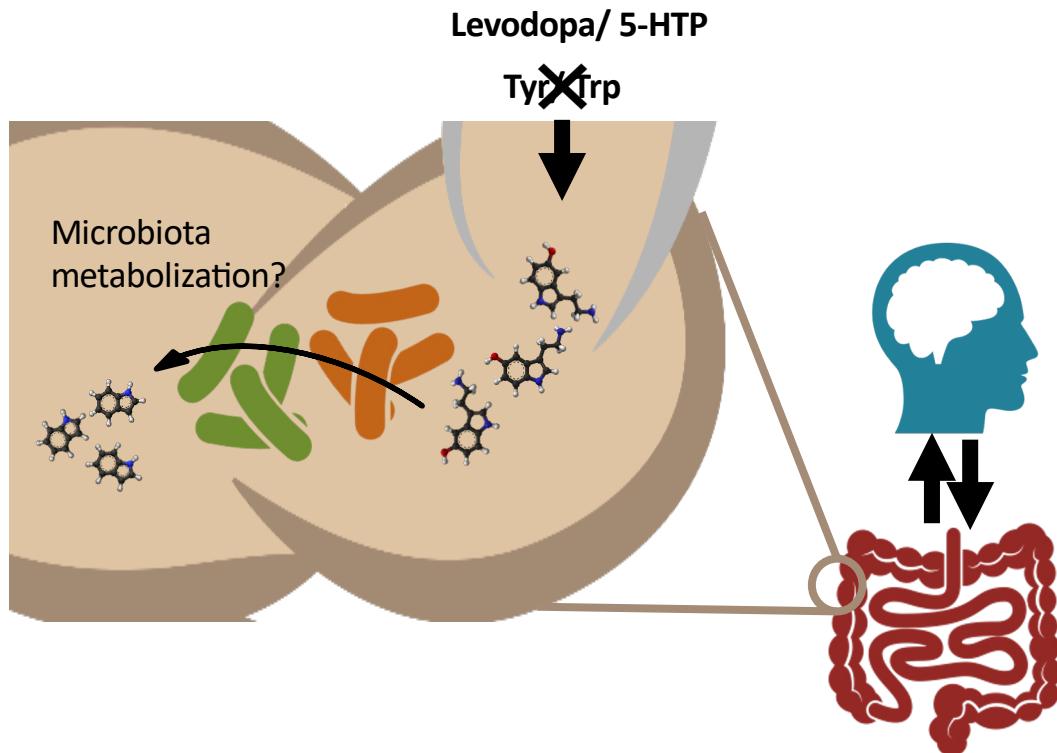
# The Microbiota–Gut–Brain Axis: Hype or Revolution?



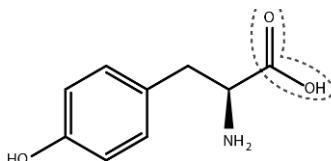
# Gut Bacteria and Neurotransmitters: Verifying Production Claims



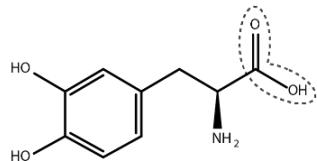
# Host-Microbiome Metabolic Interactions



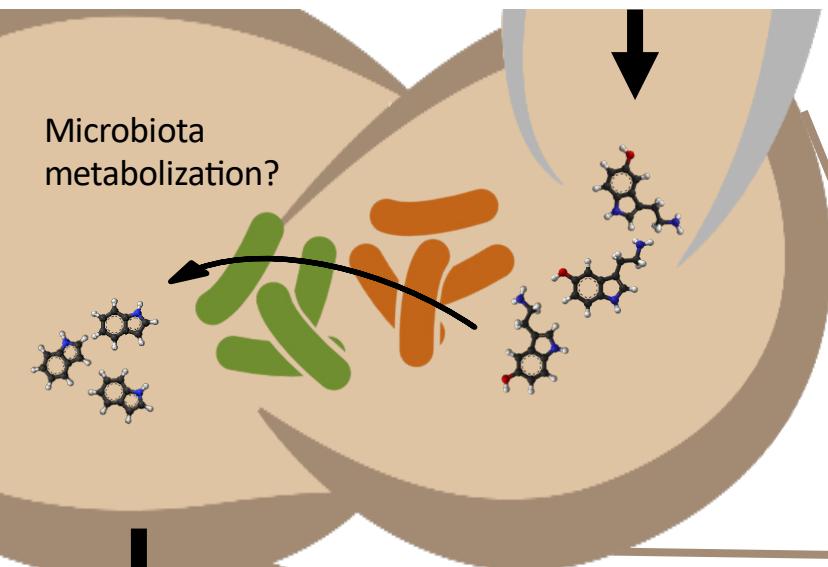
# Host-Microbiome Metabolic Interactions



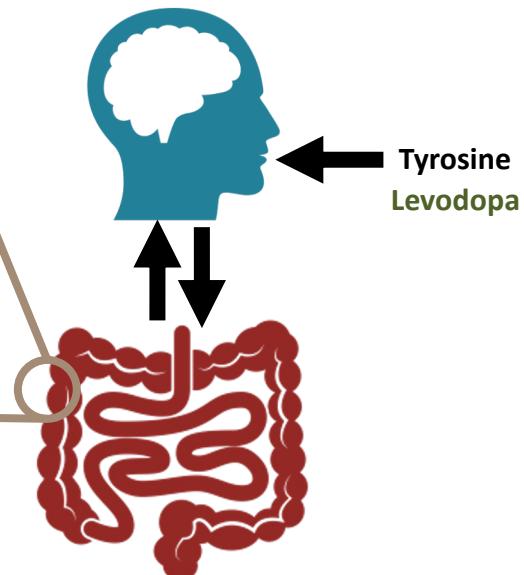
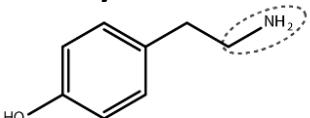
Tyrosine



Levodopa

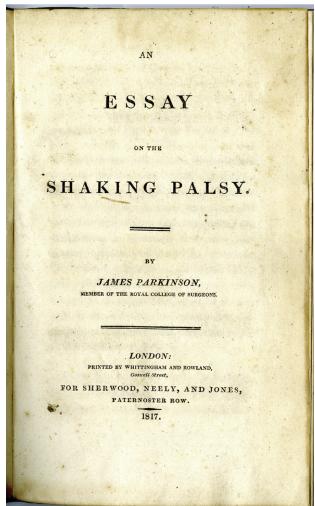


Tyramine



Tyrosine  
Levodopa

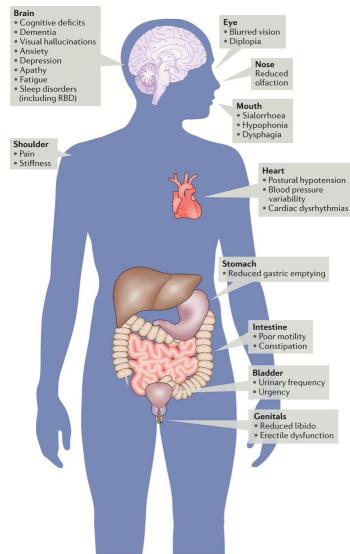
# Parkinson's Disease



"Shaking palsy", 1817.



Motor symptoms  
Brain-to-Body

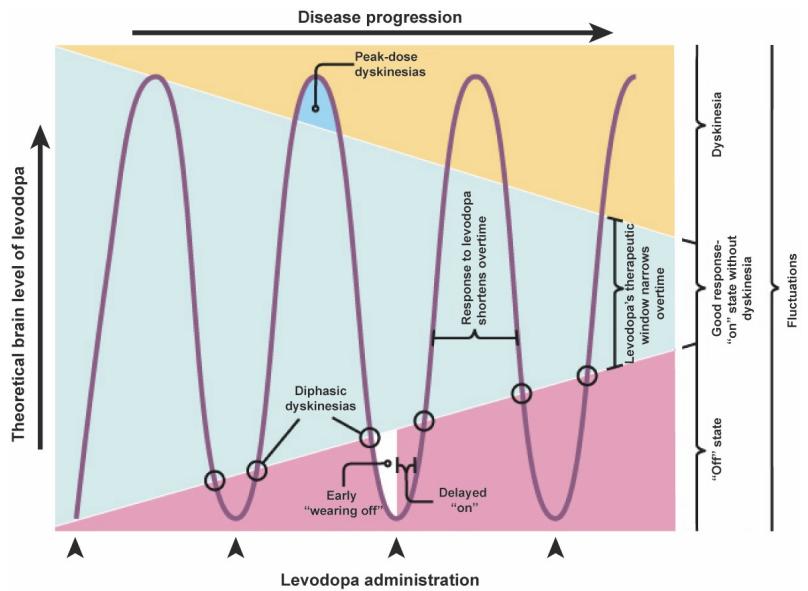


Nature Reviews | Neuroscience

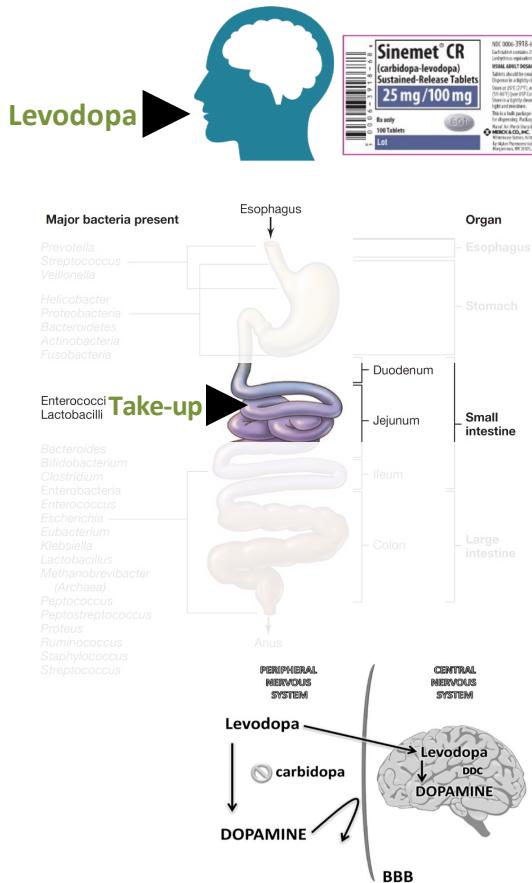
Non-motor symptoms  
Body-to-Brain

# Parkinson's Disease Treatment

## Treatment

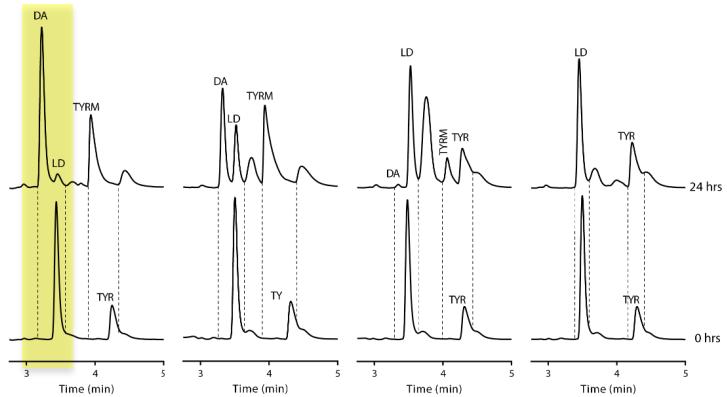


## Therapeutic window of levodopa

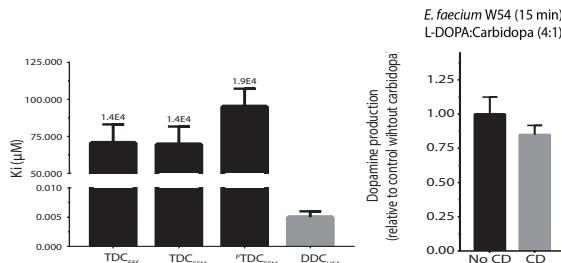
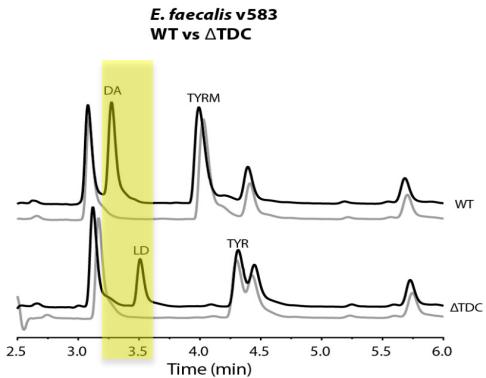


Madigan, M. T., et al.(2010). *Brock Biology of Microorganisms* 13th edition Benjamin Cummings.

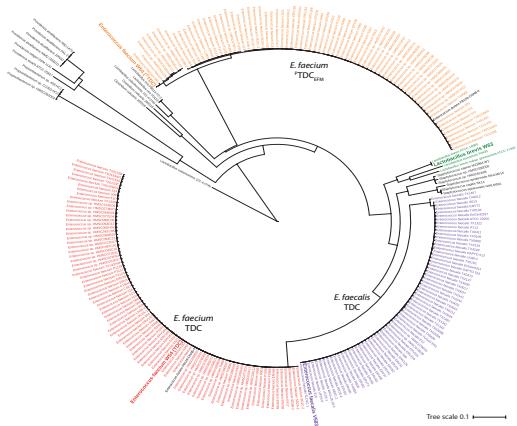
## Levodopa Conversion-I: Decarboxylation by Small Intestinal Bacteria



## Tyrosine and L-DOPA decarboxylation



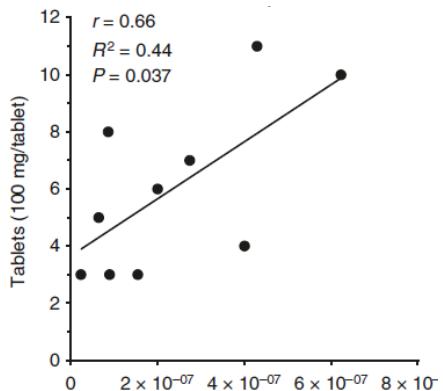
Bacilli are 1<sup>ry</sup> class harboring *tdc* genes  
in the human gut



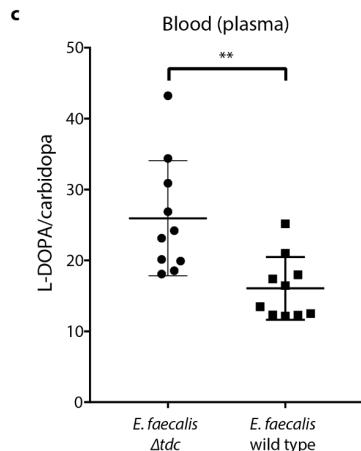
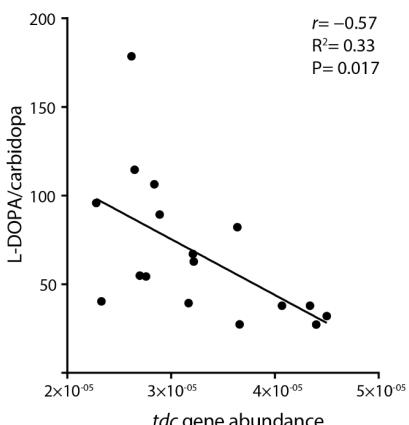
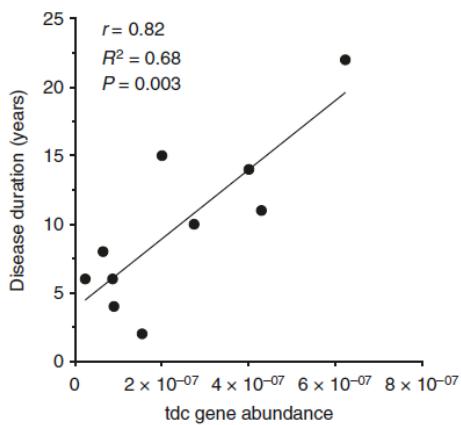
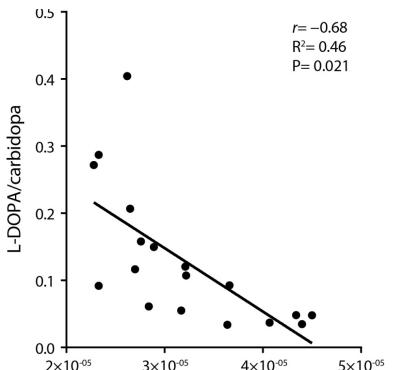
# Parkinson's Disease Patients Vary in Dosage Regimen Requirement

## *Possible Impact of Small Intestinal Microbiota?*

*Fecal samples*



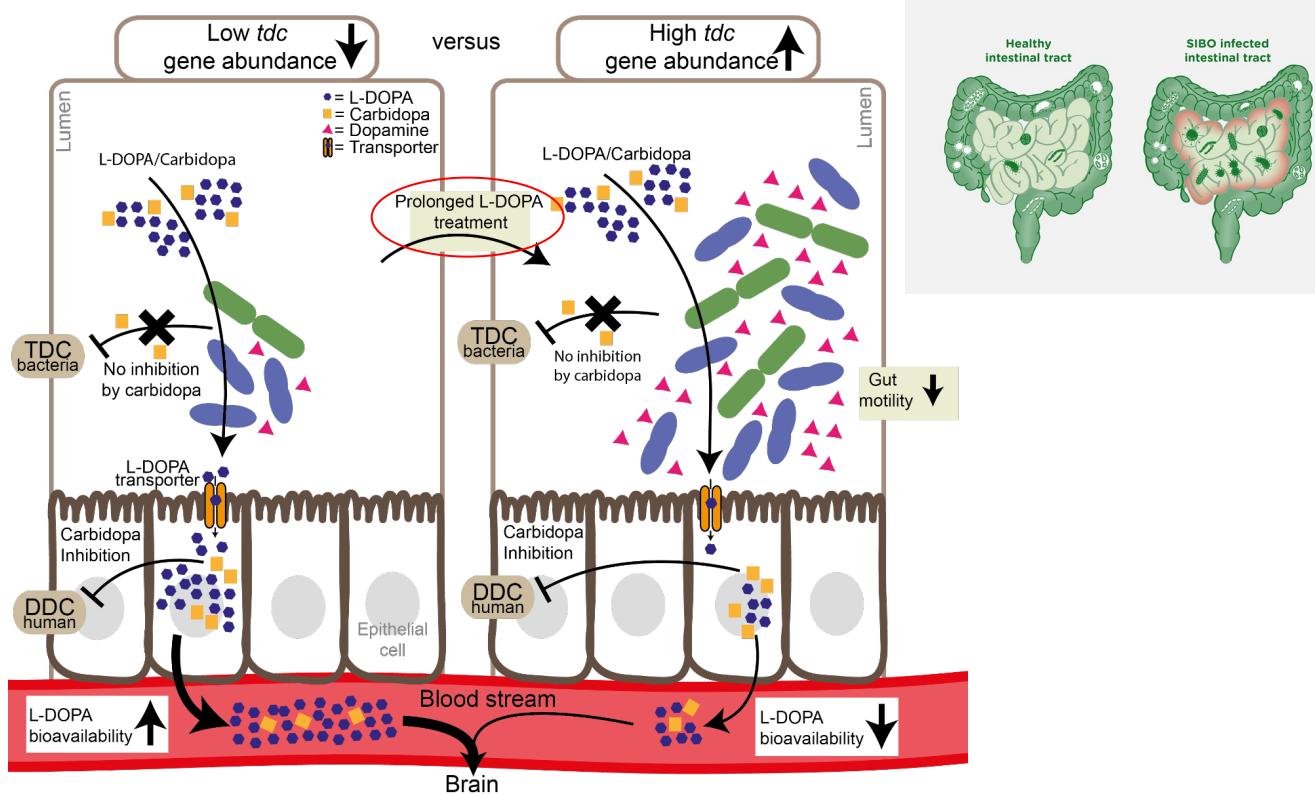
*In vivo using WTG rats*



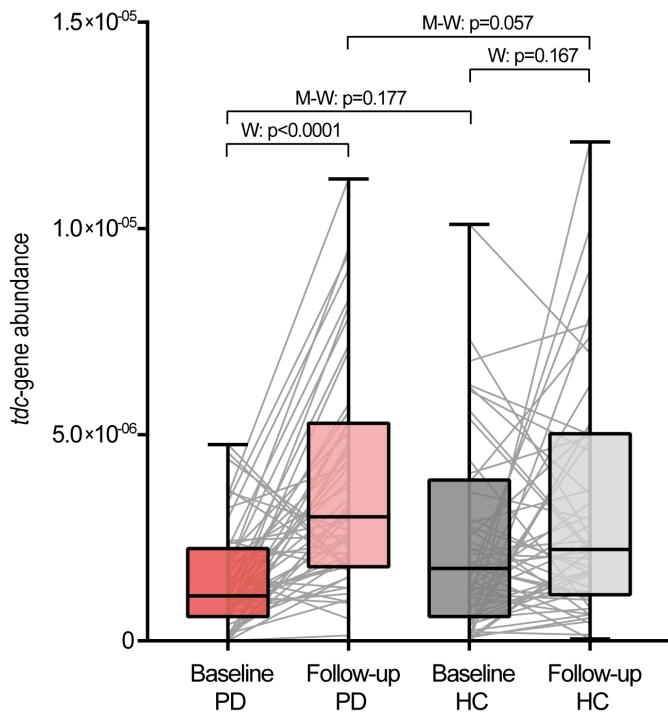
blood (plasma)  
L-DOPA  
tdc-gene



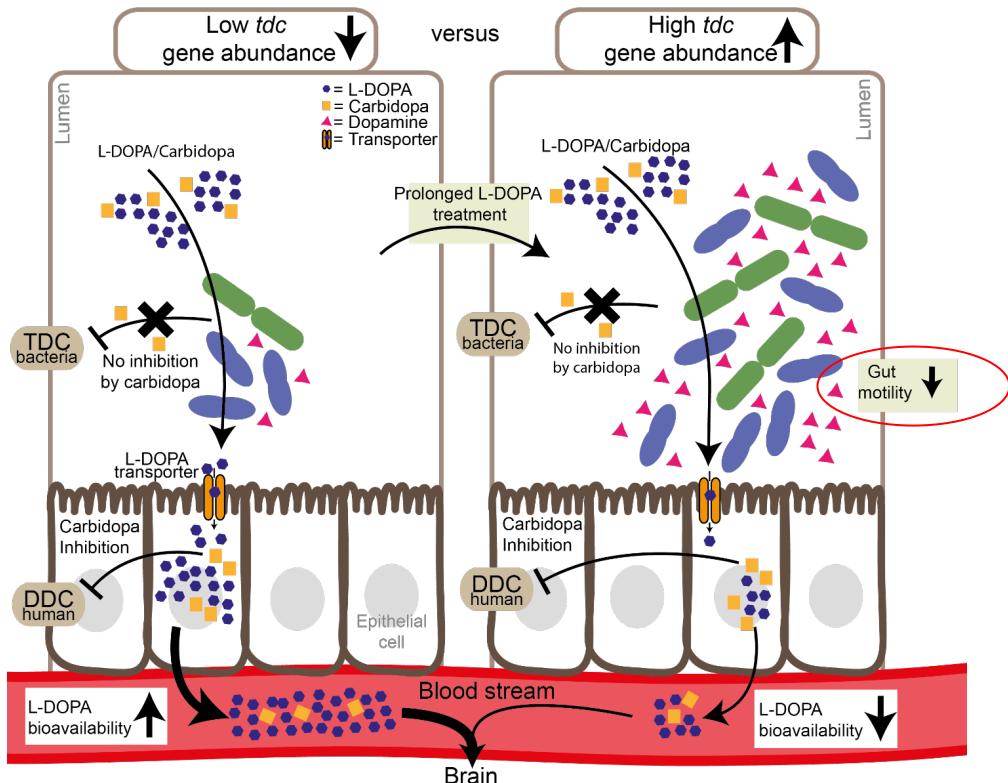
# Small Intestinal Microbiota: A Key Factor in Levodopa Treatment for Parkinson's Disease



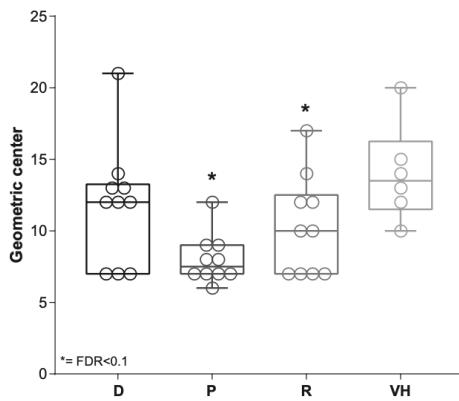
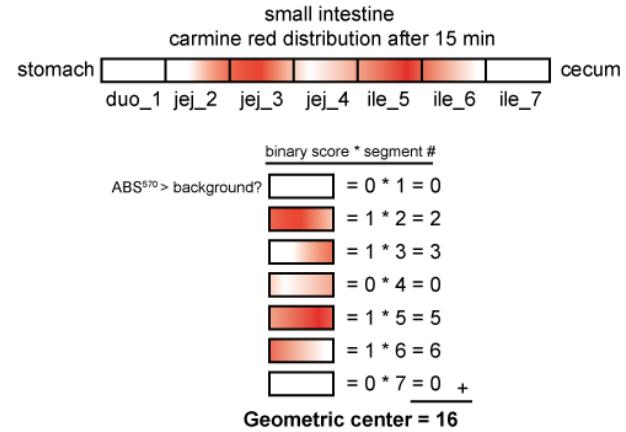
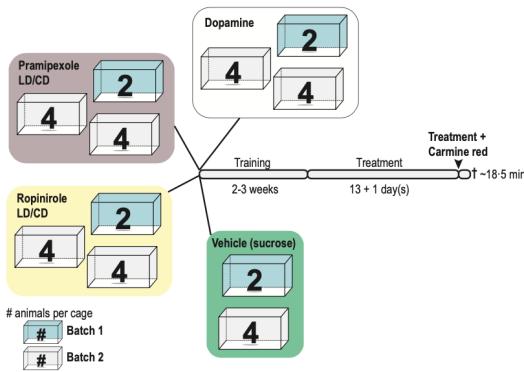
# *Tdc*-Gene Abundance Increases Over Time in Parkinson's Disease Patients



# Small Intestinal Microbiota: A Key Factor in Levodopa Treatment for Parkinson's Disease



# Parkinson's Disease Medication Alters Small Intestinal Motility in Healthy Rats



# Small Intestine Bacterial Overgrowth in the Healthy Rats Treated with Parkinson's Disease Medication

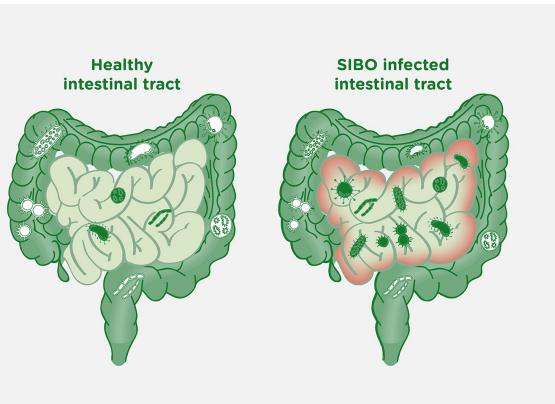
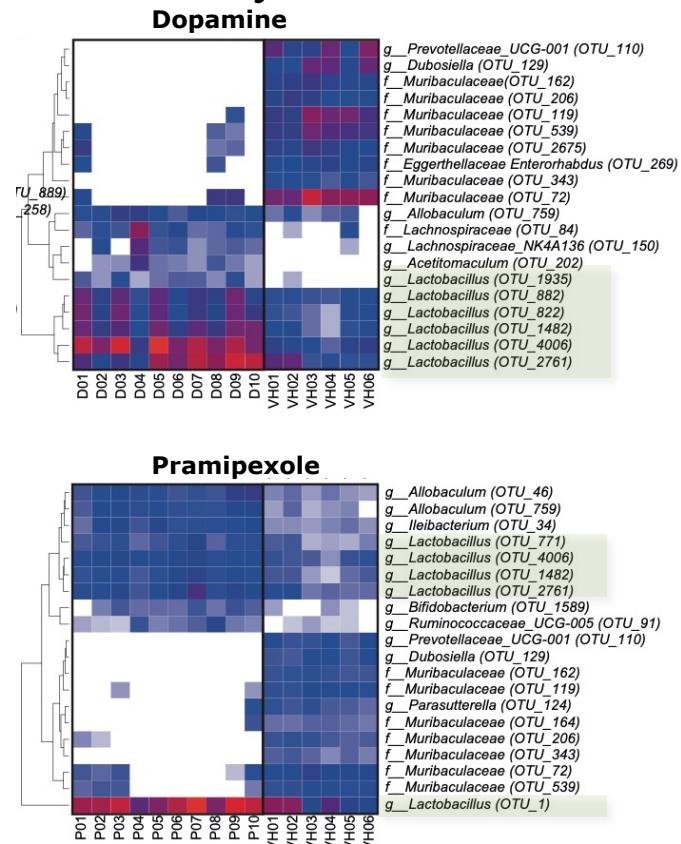
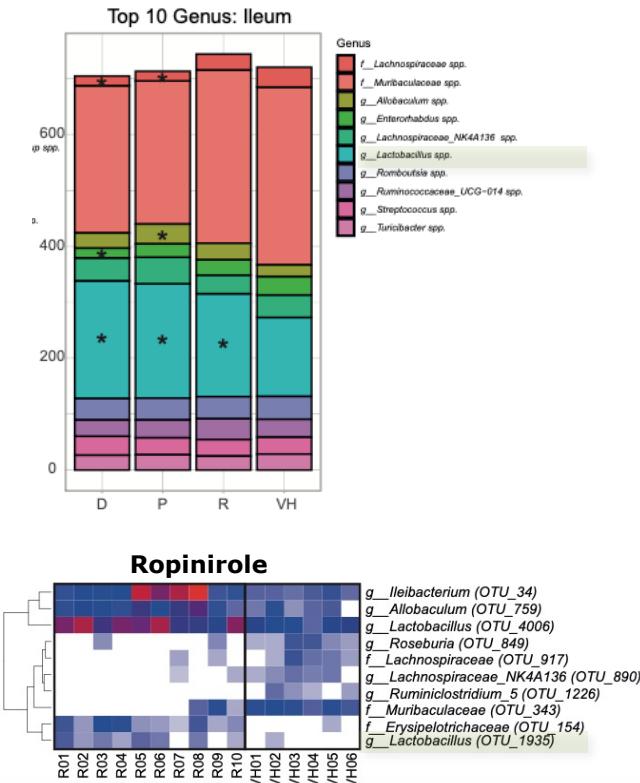


Table 1 - Bacterial counts from rat small intestine

	Aerobic (CFU/mL, median (IQR))		Anaerobic (CFU/mL, median (IQR))	
	Jejunum		Ileum	
	Jejunum	Ileum	Jejunum	Ileum
D	1.7E+7 (3.1E+6 – 1.5E+6)	3.6E+7 (2.5E+7 – 4.2E+6)	4.2E+7 (1.6E+7 – 2.3E+6)	5.9E+7 (4.1E+7 – 1.4E+7)
P	2.4E+7 (1.5E+7 – 2.2E+6)	5.6E+7 (2.5E+7 – 1.4E+7)	6.2E+7 (3.8E+7 – 4.6E+6)	3.4E+8 (6.8E+7 – 2.1E+7)†
R	1.0E+7 (4.6E+6 – 1.3E+6)	1.8E+8 (7.5E+7 – 3.6E+7)*	2.7E+7 (1.0E+7 – 3.9E+6)	2.8E+8 (1.2E+8 – 4.4E+7)*
VII	3.5E+7 (9.5E+6 – 2.6E+6)	2.4E+7 (2.1E+7 – 7.0E+6)	6.9E+7 (2.8E+7 – 3.8E+6)	7.0E+7 (4.8E+7 – 3.4E+7)

# Dopamine Agonists Increase *Lactobacillus* abundance in the Small Intestine of Healthy Rats



# Microbiota imbalance in Parkinson's disease Patients

**Comparing 13 different studies:**

- 54% (7/13) of the studies report an **increase** of *Lactobacillaceae* or *Lactobacillus*

Which are associated with increase in tyramine (or downstream metabolites) and important as they could potentially contribute to decarboxylation of levodopa.

# *Lactobacillus* taxa Linked to Lower Levodopa Levels in Blood samples of Healthy Rats

OTUs from *Lactobacillus* genus

OTU\_168

OTU\_4

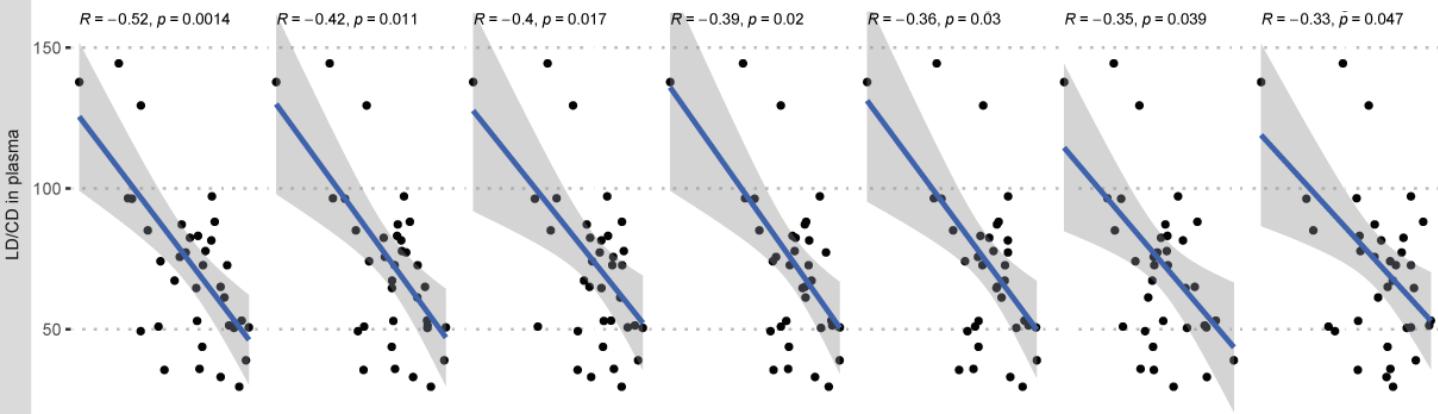
OTU\_174

OTU\_822

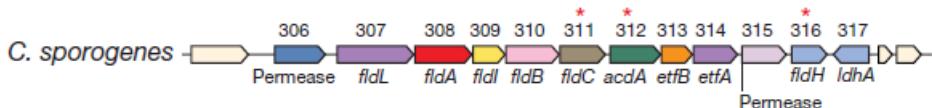
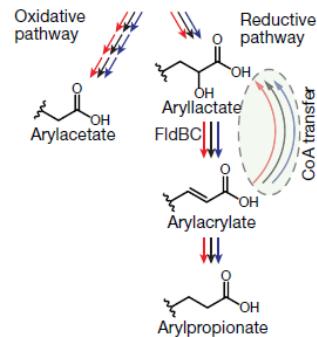
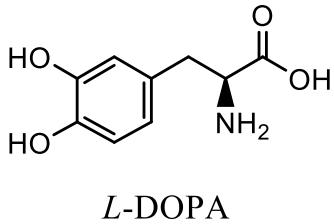
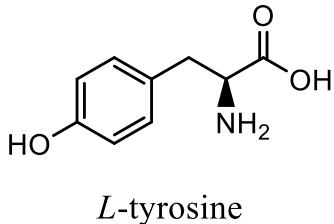
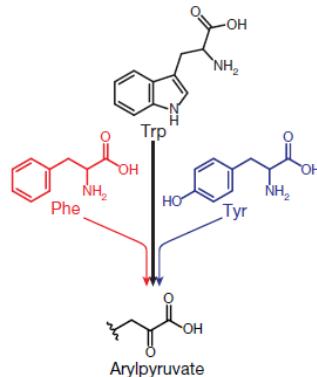
OTU\_882

OTU\_4006

OTU\_1482

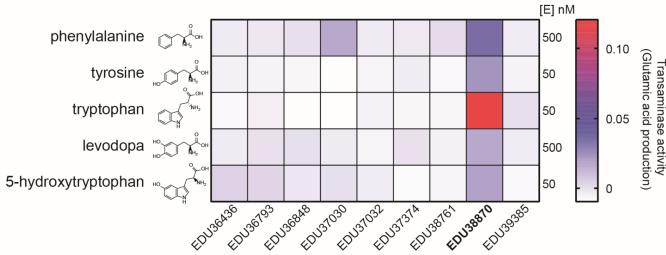
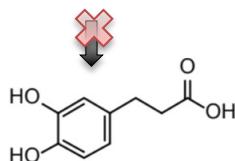
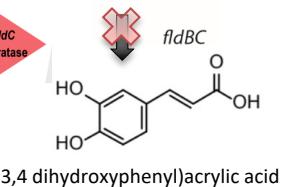
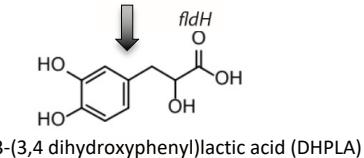
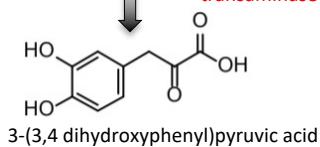
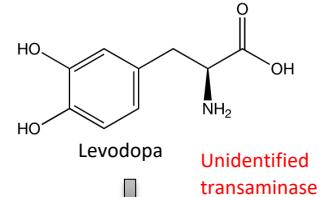


# When Gut Bacteria Encounter Unabsorbed Levodopa Residues...



Anaerobic aromatic amino acid deaminase pathway in *C. sporogenes*

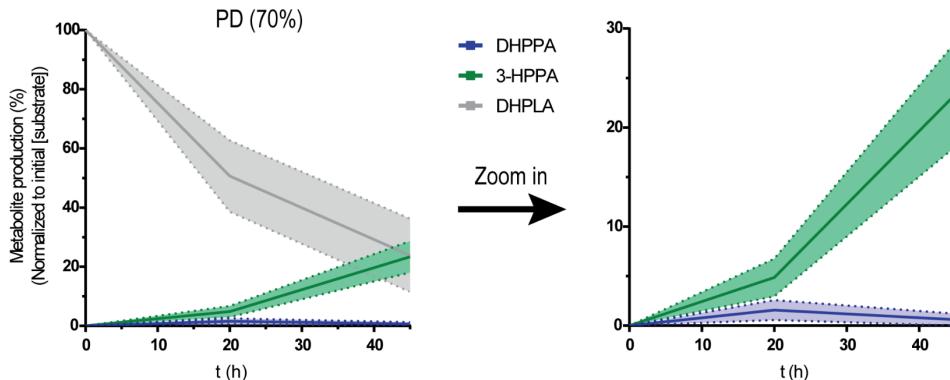
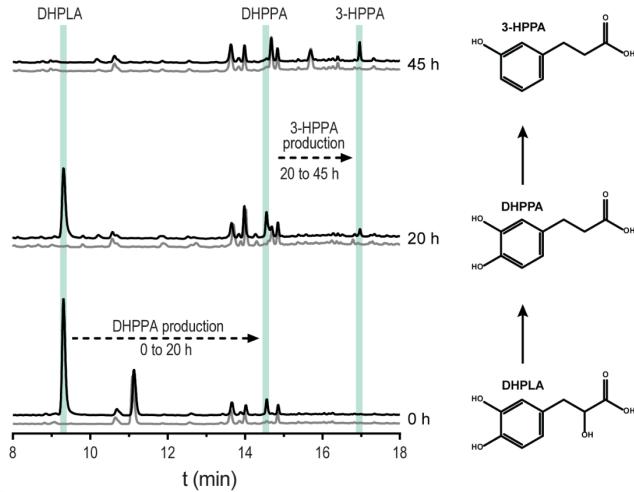
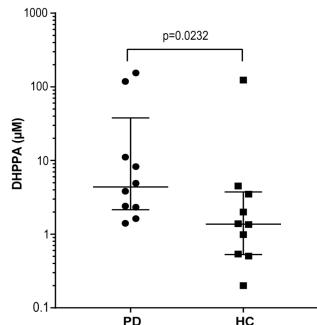
# Levodopa Conversion-II: deamination by Colonic Bacteria



*C. sporogenes* class II aromatic aminotransferases

Uncovering of the first step  
in anaerobic deamination:  
AAA transaminase

# Higher levels of levodopa deamination products in Parkinson's Disease patients



# Implications of Levodopa deamination Metabolites on Parkinson's Disease Patients

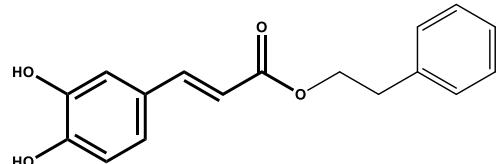
**Table 1.** Prevalence of gastrointestinal symptoms in patients with Parkinson's disease affected by SIBO versus those without SIBO

	SIBO positive, % (n = 26)	SIBO negative, % (n = 22)	OR (CI)
Abdominal discomfort	30.8	27.3	ns
Bloating	69.2	31.8	2.07 (1.42–16.40)
Flatulence	65.4	36.4	1.74 (1.01–10.83)
Constipation	73.1	81.8	ns
Diarrhea	19.2	9.1	ns

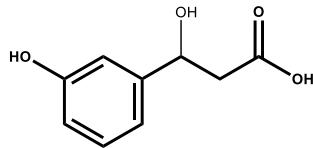
Gabrielli et al. *Movement Disorders*, Vol. 26, No. 5, 2011

## Test the effect on gut transit time in animal models

Affected gut contractility in rat intestine  
Aviello et al. *Eur J Pharmacol*. 2010



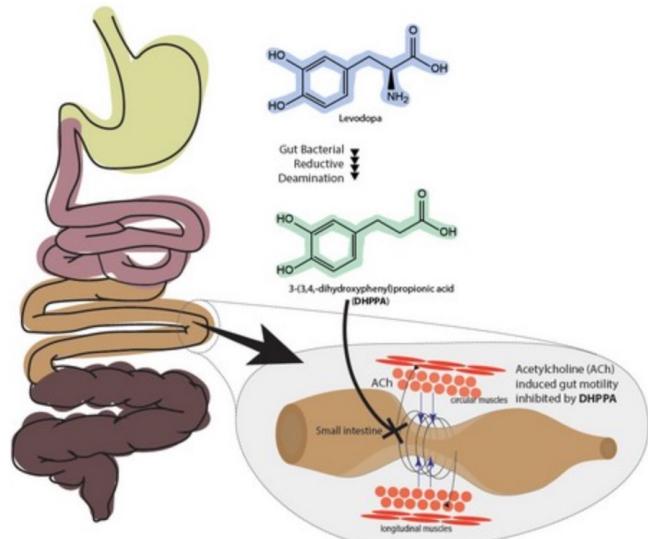
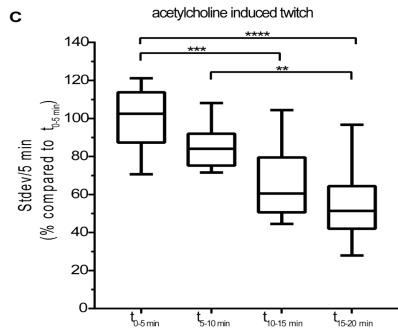
phenethyl (E)-3-(3,4-dihydroxyphenyl)acrylate



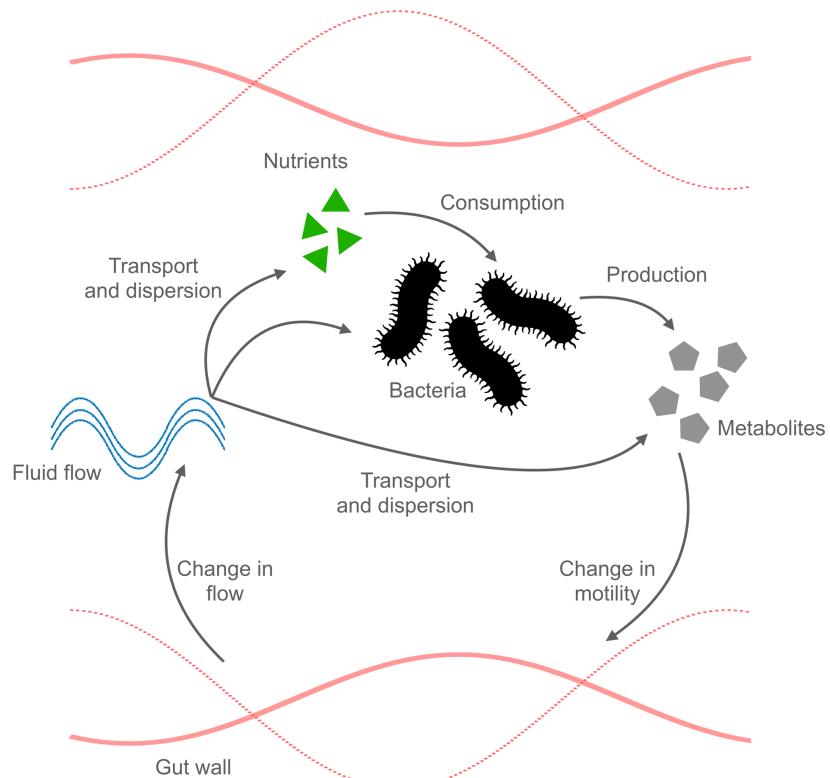
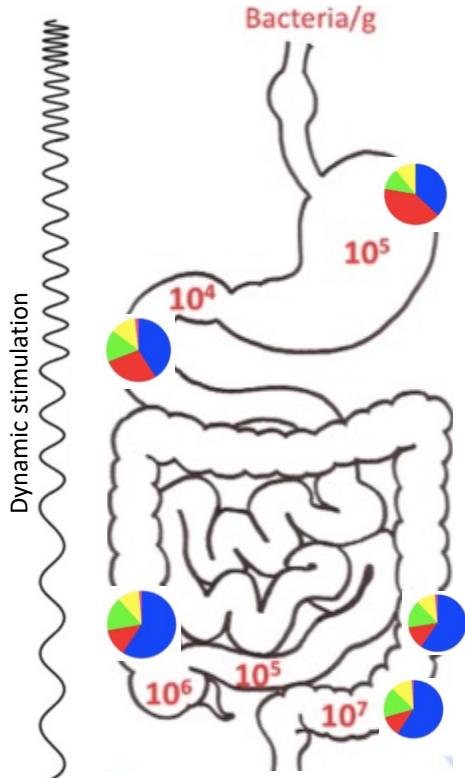
3-hydroxy-3-(3-hydroxyphenyl)propanoic acid

Negatively associated with gut transit time  
Roager et al. *Nat Microbiol*. 2016

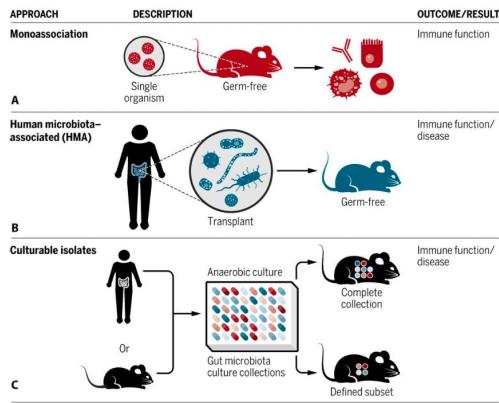
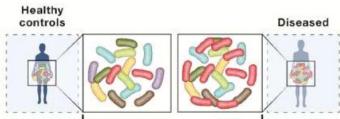
# Unabsorbed Resides of Levodopa & Delayed Intestine Transit Time



# Gut microbiota-motility inter-regulation



# From Bench to Bedside



Observation in independent cohorts

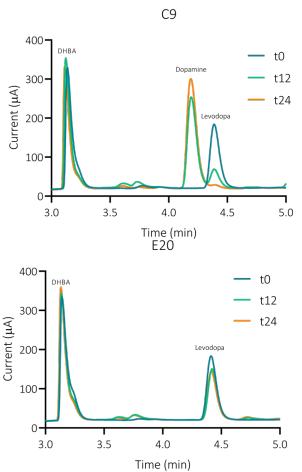
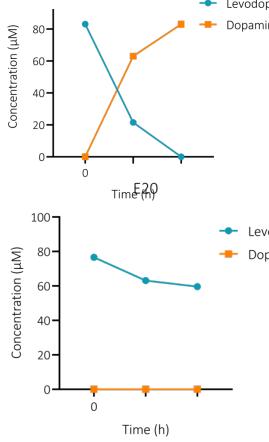
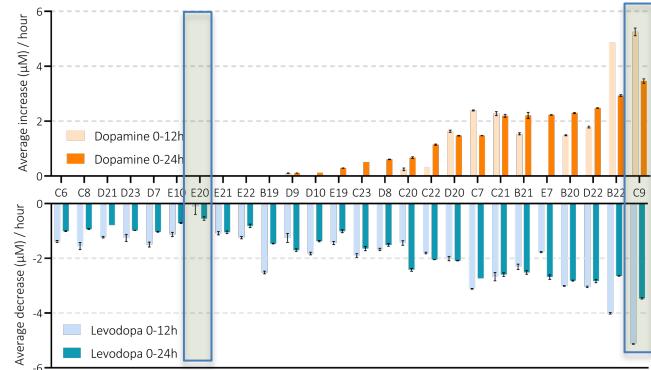
Explore mode of action

- Test TDC activity in longitudinal *de novo* cohort (>600 PD patients)
- Design of anti-microbials targeting TDC-harboring bacteria

# TDC Activity as a Stratification Tool to Enhance Medication Response in Parkinson's Disease Patients



- Test TDC activity in longitudinal *de novo* cohort (>600 PD patients)
- Target TDC-harboring bacteria

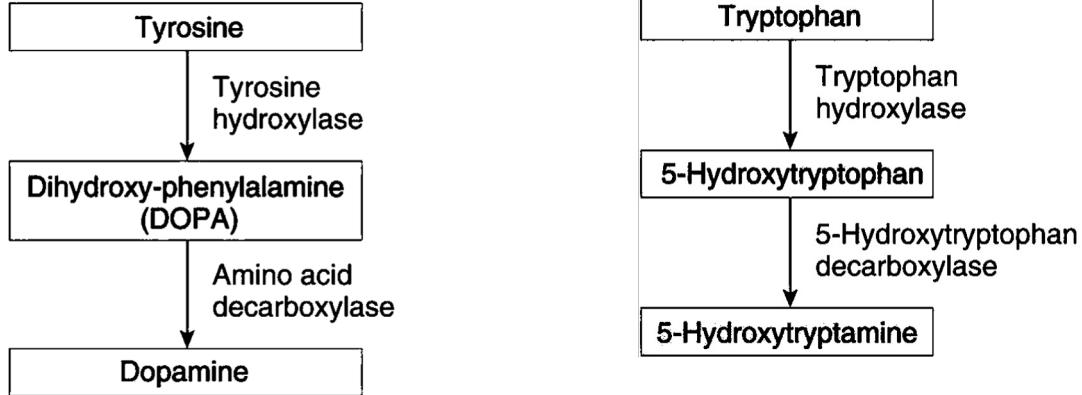


# Summary

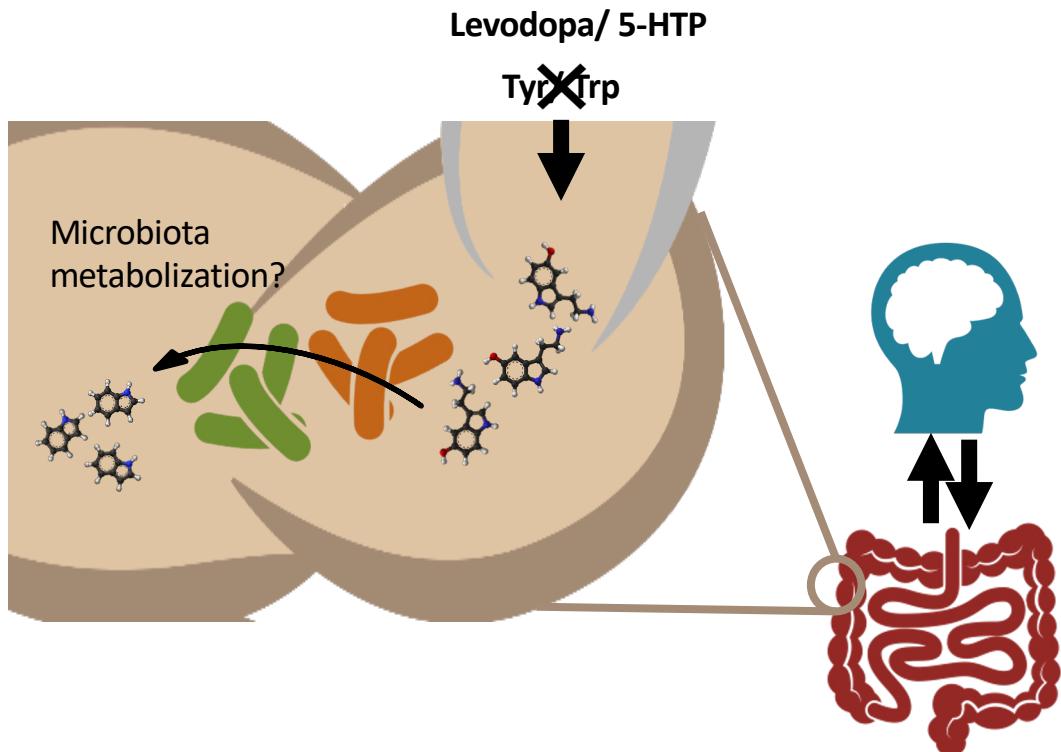
- The small intestinal microbiota, despite its low number of resident bacteria, high flow rate, and short transit time, has the potential to impact drug bioavailability.
- The primary PD medications could potentially alter the composition of the microbiota and generate a state of SIBO by affecting small intestinal motility, the primary site of drug absorption.
- The unabsorbed residues of levodopa can be metabolized by colonic bacteria into different compounds that can influence intestinal motility.

**The site of absorption in the gut plays a crucial role in the gut bacteria-driven chemical transformation of drugs**

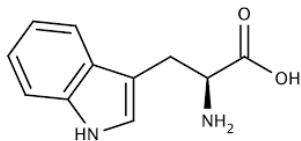
# Gut Bacteria and Neurotransmitters: Verifying Production Claims



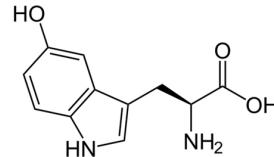
# Host-Microbiome Metabolic Interactions



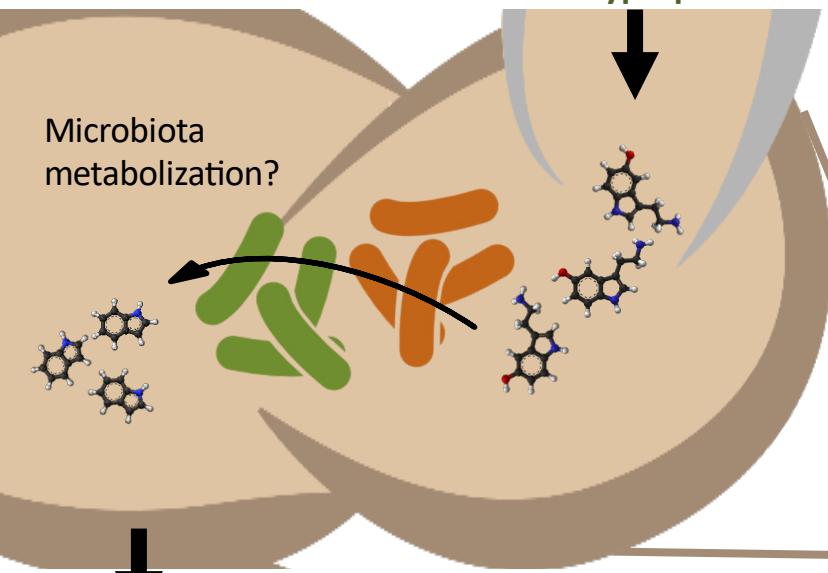
# Host-Microbiome Metabolic Interactions



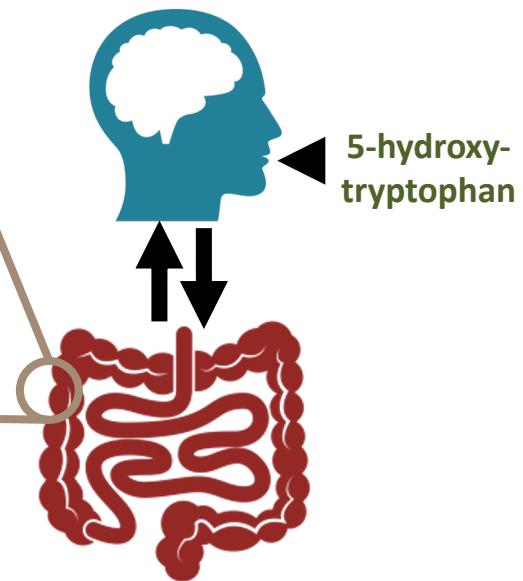
Tryptophan



5-hydroxy-tryptophan



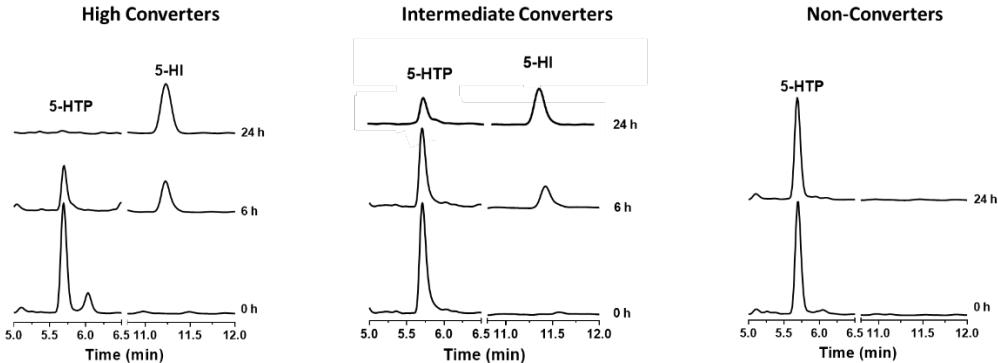
Indole



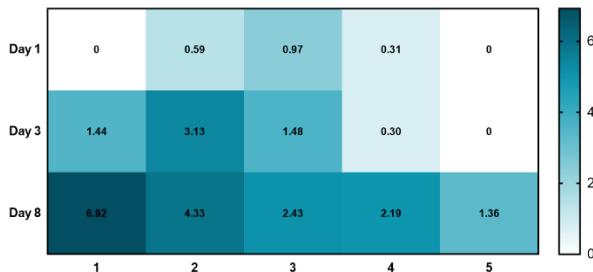
# 5-Hydroxytryptophan



# Gut microbiota converts 5-hydroxytryptophan to 5-hydroxyindole

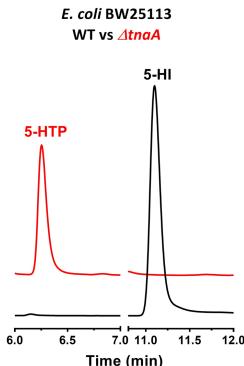
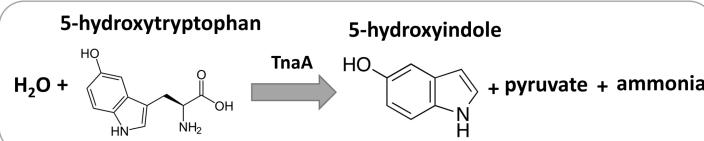
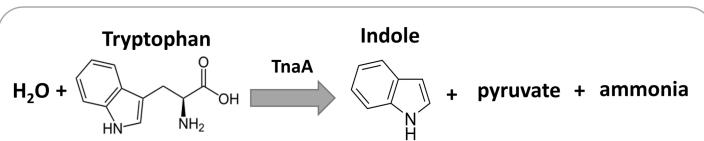


5-HI concentration in fecal samples  
(fold change/normalized to Day 0)



**Human administration of 5-HTP**

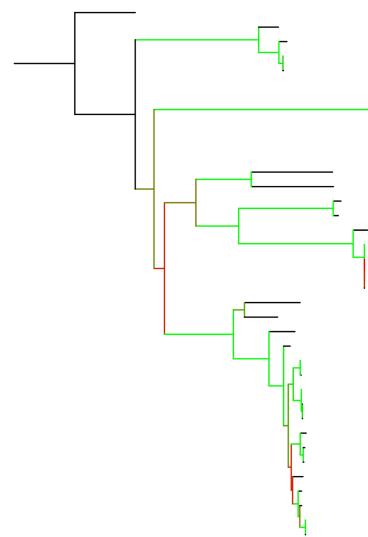
# Bacterial tryptophanase is responsible for the conversion of 5-HTP



Tree scale: 0.1 ←→

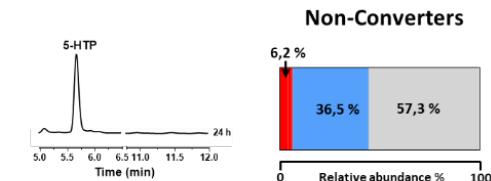
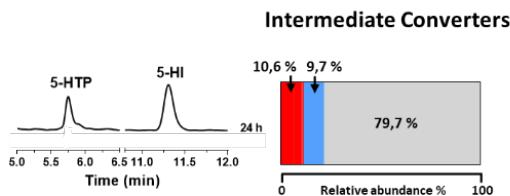
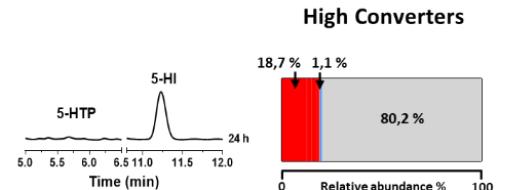
bootstrap

- 14
- 35.5
- 57
- 78.5
- 100

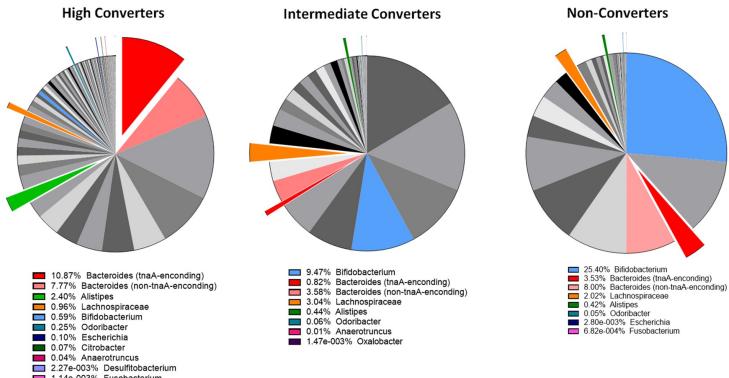


Anaerotruncus colihominis  
Clostridiales bacterium  
Fusobacterium varium  
Fusobacterium ulcerans  
Fusobacterium ulcerans  
Anaerotruncus colihominis  
Lachnospiraceae bacterium  
Anaerococcus hydrogenalis  
**Fusobacterium nucleatum**  
**Fusobacterium gondiiformans**  
**Fusobacterium gondiiformans**  
**Fusobacterium varium**  
Protonibacterium sp.  
Providencia rustigianii  
Providencia stuartii  
Edwardsiella tarda  
Escherichia coli  
Escherichia coli  
Escherichia coli  
**Alistipes shahii**  
Odoribacter laneus  
Alistipes putredinis  
Bacteroides salyersiae  
Bacteroides sp.  
**Bacteroides thetaiaomicron**  
Bacteroides xyloisolvans  
Bacteroides xyloisolvans  
Bacteroides xyloisolvans  
Bacteroides oleicinplicans  
Bacteroides intestinalis  
Bacteroides cellulolyticus  
Bacteroides uniformis  
Bacteroides stercoris  
Bacteroides clarus  
Bacteroides eggerthii  
Bacteroides eggerthii

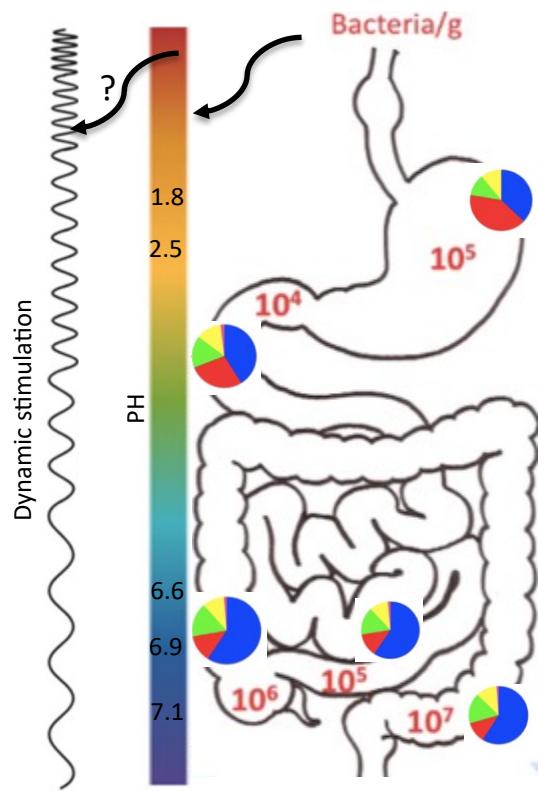
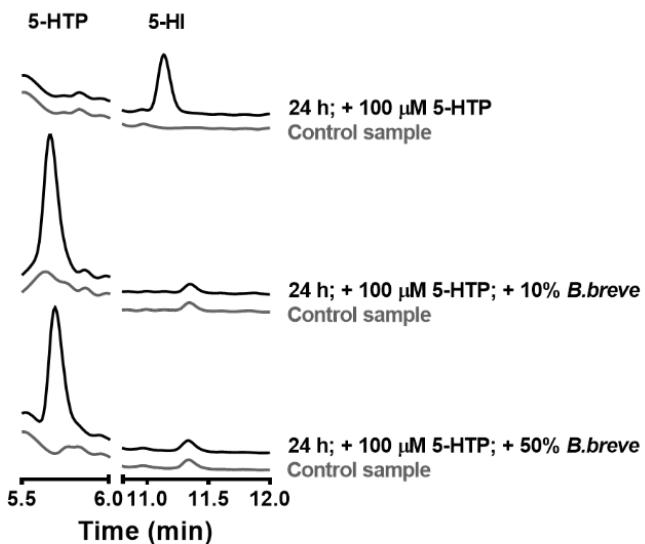
# Bacterial production of 5-hydroxyindole is dependent on microbiota composition



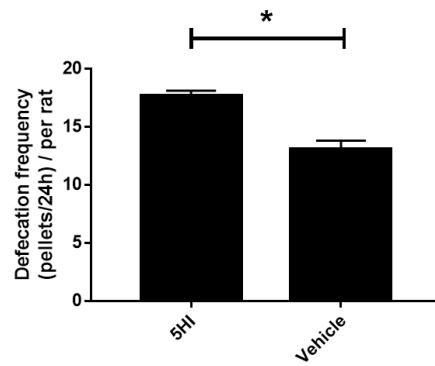
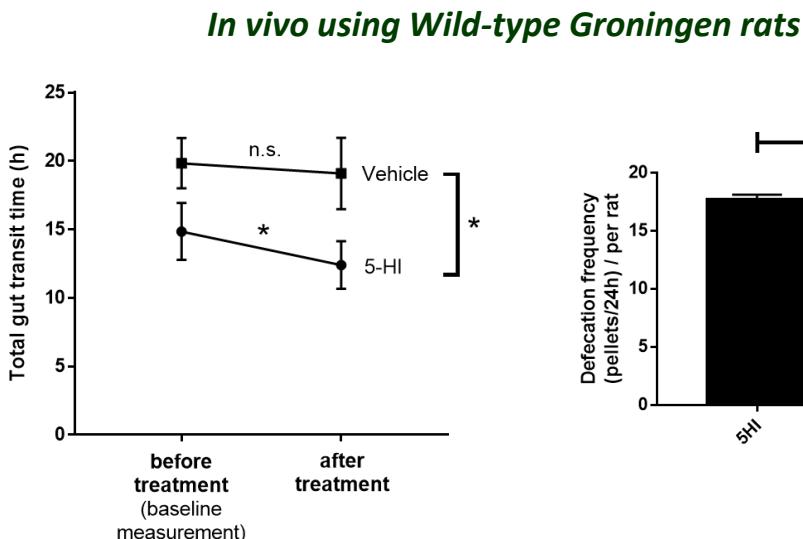
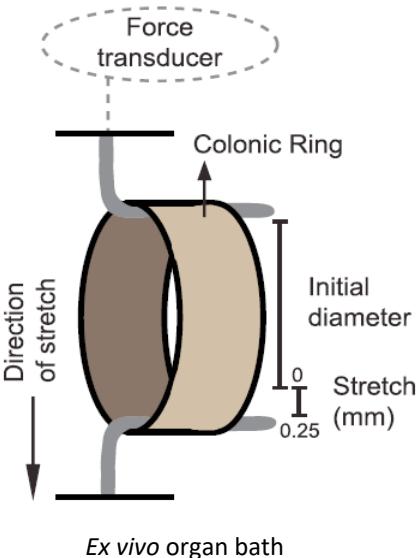
■ tnaA-encoding  
 ■ Bifidobacteria  
 ■ Other non-tnaA encoding



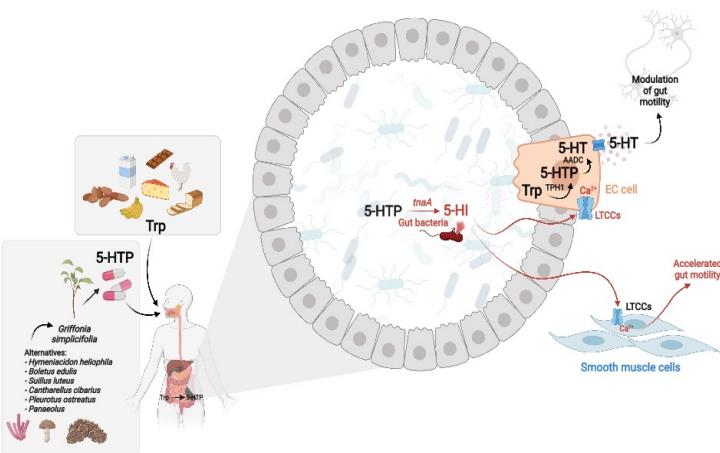
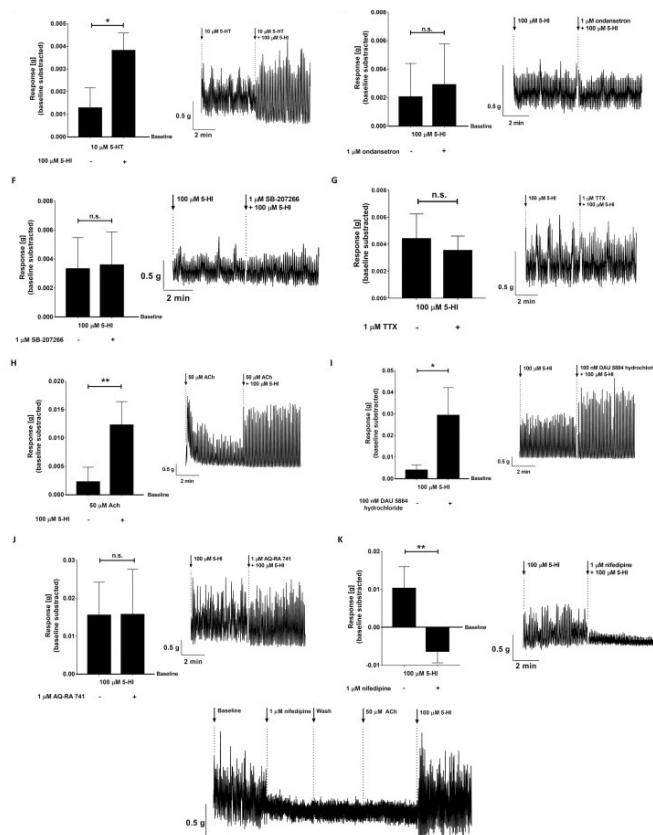
# Reduction in pH results in a complete inhibition of the production of 5-hydroxyindole



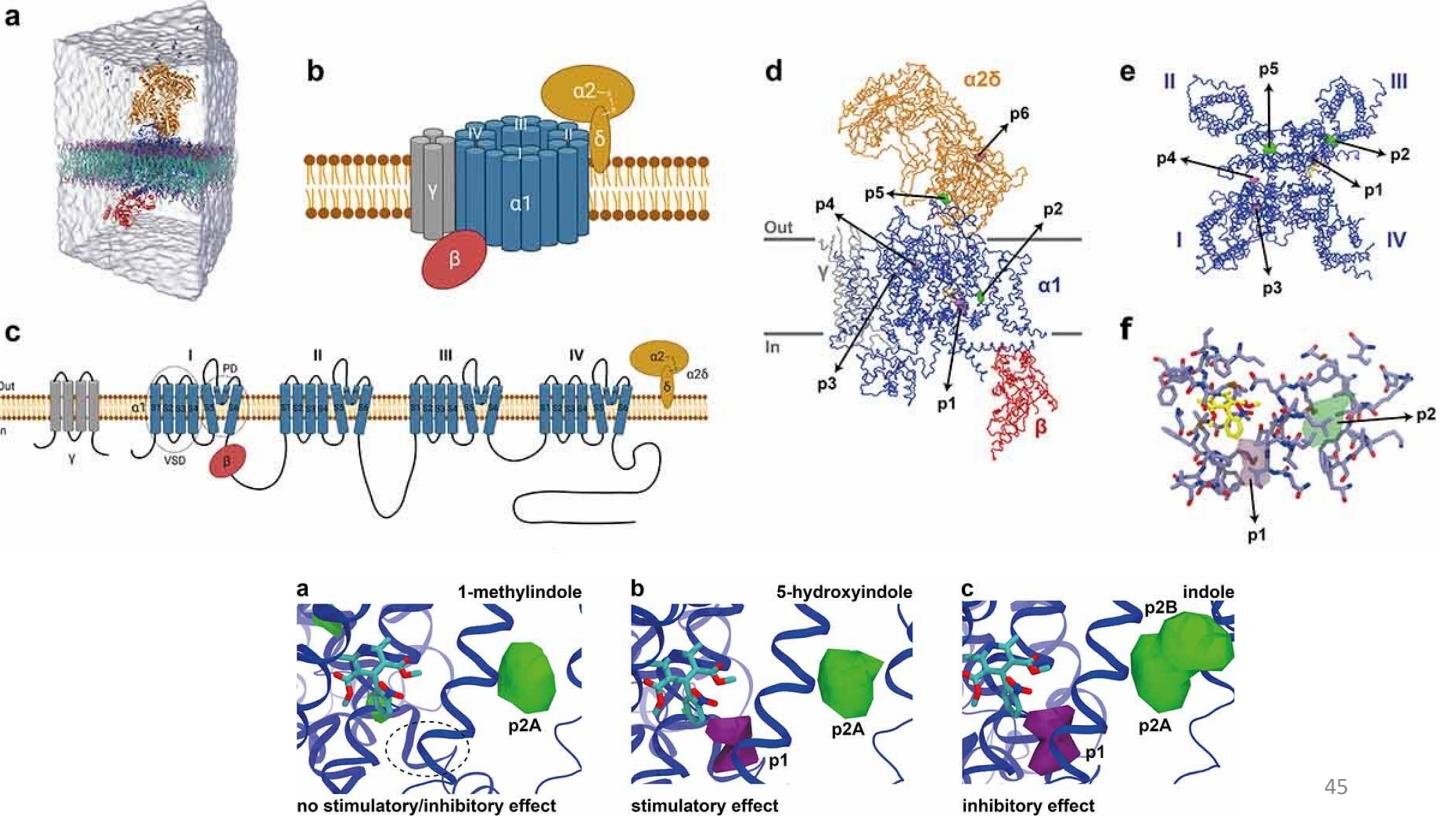
# 5-hydroxyindole is a potent stimulator of gut contractility *in vivo*



# L-Type Voltage-Gated Calcium Channels Mediate the Gut Motility-Stimulating Effects of 5-Hydroxyindole



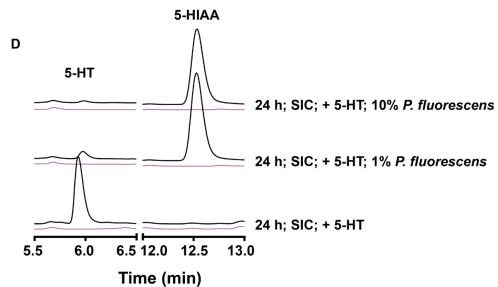
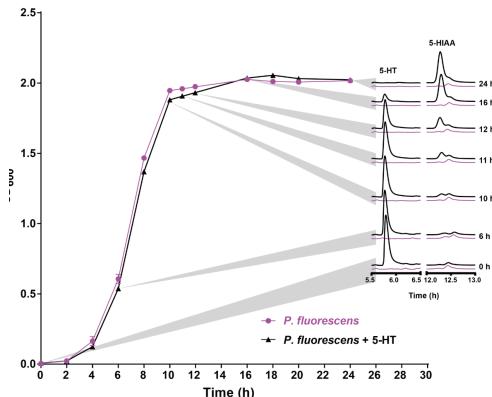
# 5-Hydroxyindole Confirmed to Bind to $\alpha 1$ Subunit of L-Type Calcium Channels



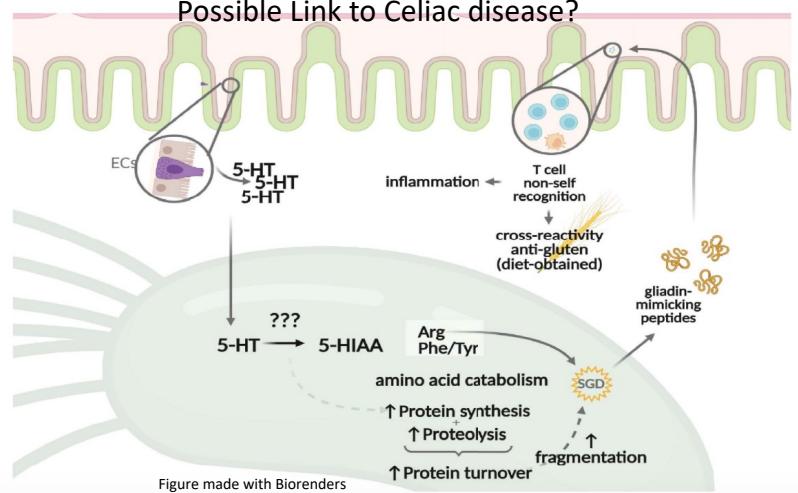
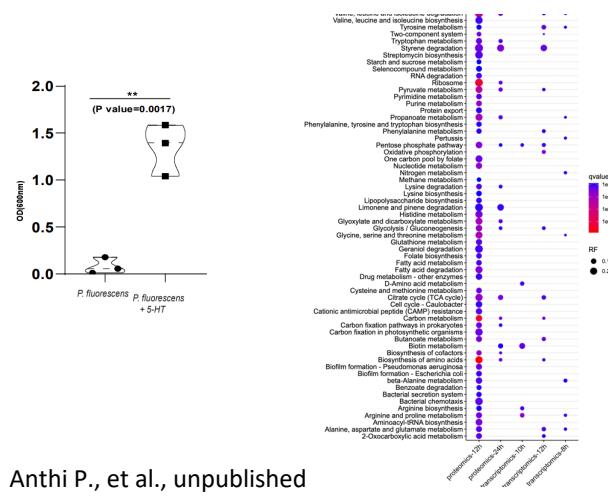
# Summary

- Gut bacterial metabolic product; 5-hydroxyindole, plays an important role in inducing gut contractility, a comorbidity of various diseases as shown by *in vivo, ex vivo* experiments
- 5-hydroxyindole functions through the activation of L-type voltage dependent  $\text{Ca}^{2+}$  channels.
- 5-hydroxyindole may prove as a therapeutic targeted at modulating LVCCs function. So far, only 3 synthetic compounds are known to work as LVCCs agonists, none of which is approved clinically.

# 5-HT Conversion by Intestinal Bacteria

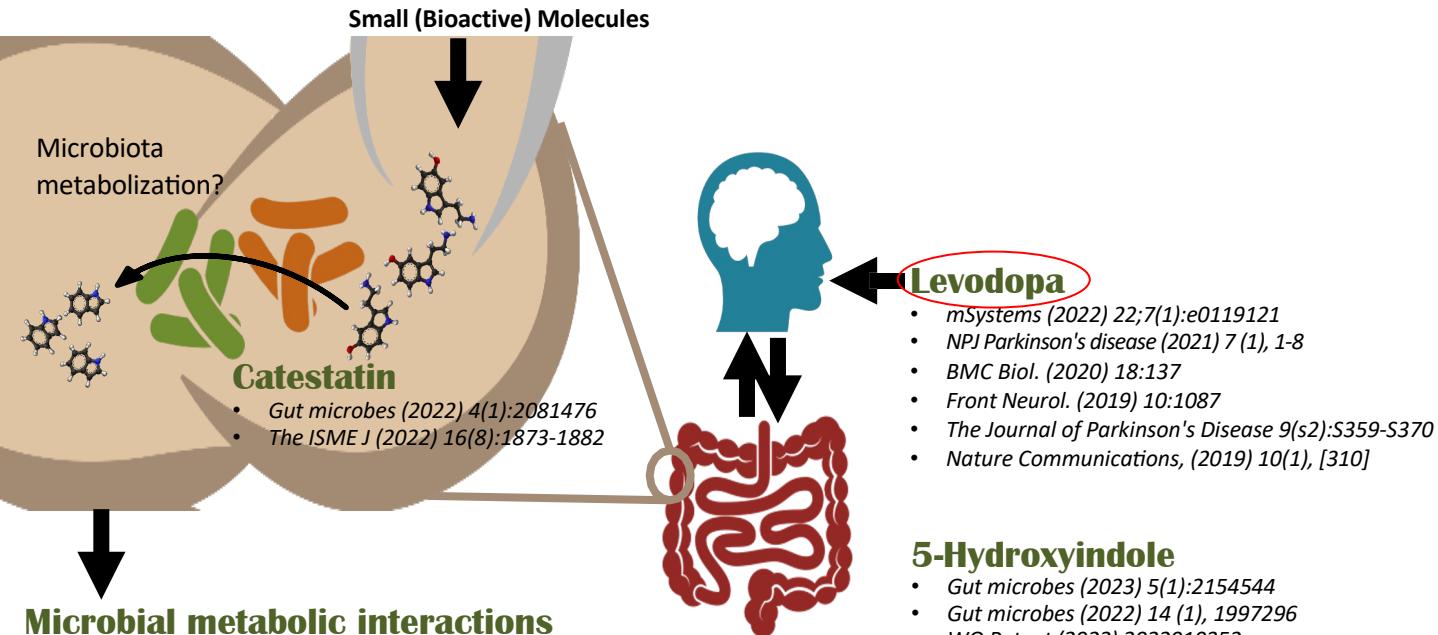


## Serotonin Degradation by *P. fluorescens*; Possible Link to Celiac disease?



# Beyond the Liver: Gut Microbiota and Drug Processing

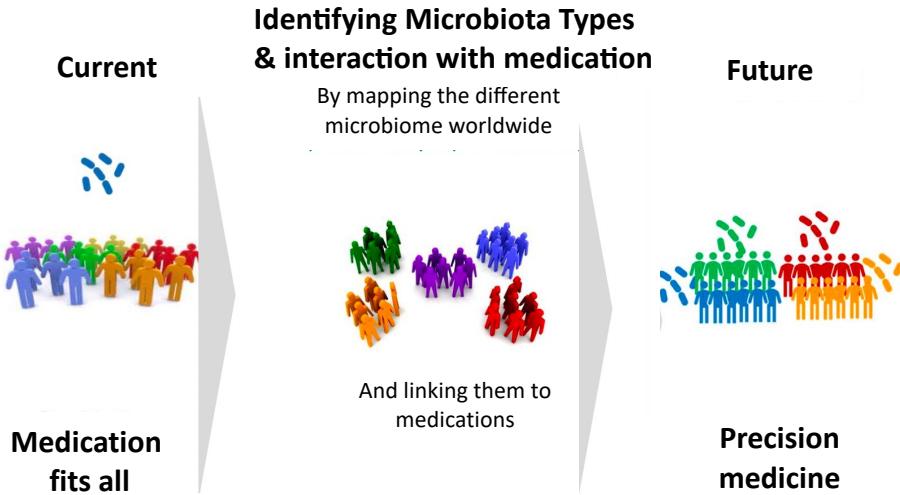
Examples from the Lab



## Microbial metabolic interactions

- *Microbiome* (2021) 9:16
- *bioRxiv*, 2023.03. 29.5346792
- *bioRxiv*, 2023.01. 29.525861

# Towards Precision medicine





## HMI

**Sebastiaan van Kessel**

Nektaria Liakouli

Mink Siders

Anthi Psoma

Panagiotis Kelefiotis-Stratidakis

Markus Schwalbe

Alex K. Frye

Maria Castejon

Hiltje R. de Jong

Simon L. Winkel

Amber Bullock

Ahmed Osama El-Gendy

## The Netherlands

Gertjan van Dijk, GELIFES, UG

Sieger A. Nelemans, GELIFES, UG

Hjalmar Permentier, GRIP, UG

Sander S. van Leeuwen, UMCG

Iris Sommer, UMCG

Marcel Verbeek, Radboud UMC

Bas Bloem, Radboud UMC

# Acknowledgments

## Europe

**Filip Schepersjans, Helsinki University Hospital, Finland**

Kristin Verbeke, Katholieke Universiteit, Leuven, Belgium

Karen Alim, Technical University of Munich, Germany

Paulo Telles de Souza, CNRS, University of Lyon, France

Constantinos Neochoritis, University of Crete, Greece

Angelo Corti, Universita Vita-Salute San Raffaele, Italy

## USA

**Ali Keshavarzian, RUSH University, Chicago**

Jonas Cremer, Stanford University, Stanford

Stefania Senger, Harvard Medical School, Boston

Kara Gross Margolis, Colombia University, New York

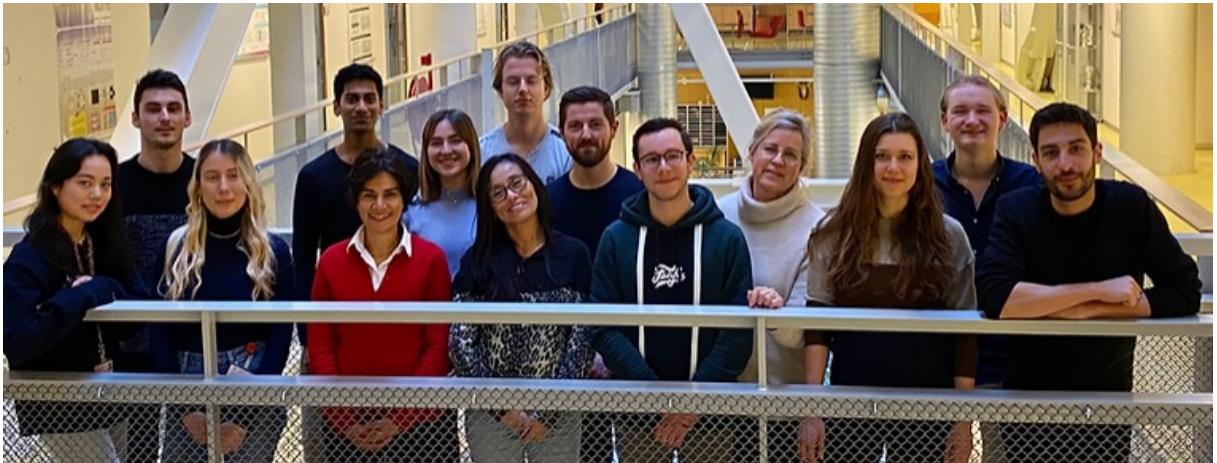
Sushil Mahata, UCSD, San Diego



rijksuniversiteit  
groningen

SELFRIDGES GROUP  
FOUNDATION

# HMI Group

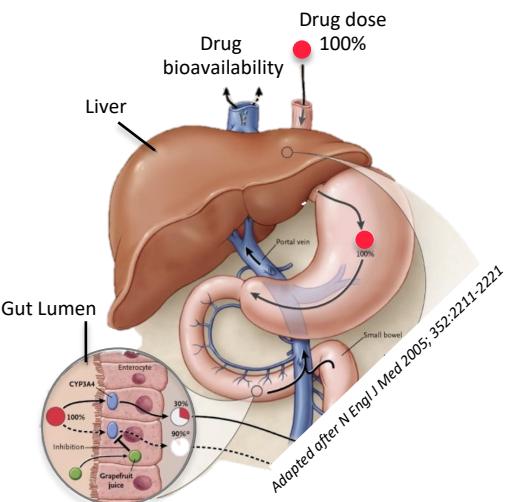
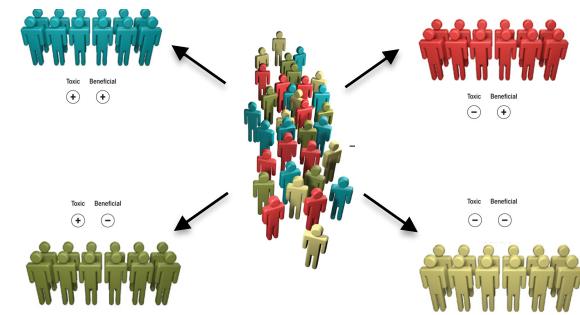


*sahar.elaidy@rug.nl*

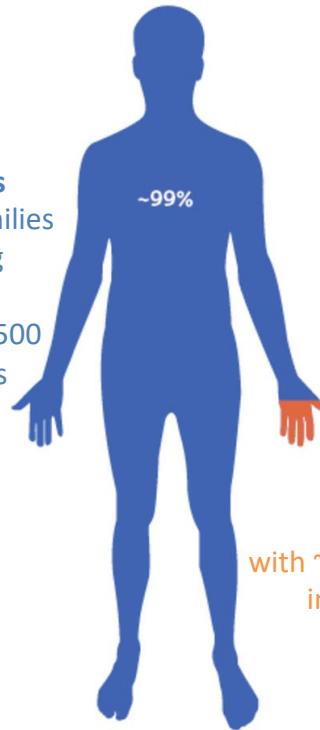


*www.elaidylab.com*

# Microbial metabolic-host interactions



**~2,000,000**  
Microbial genes  
with (?) protein families  
involved in drug  
metabolism  
derived from 200-500  
bacterial species



**~23,000**  
Human genes  
with ~30 protein families  
involved in drug  
metabolism

First-Pass Metabolism after  
oral administration of  
a drug

➤ Why would the microbiota harbor genes to metabolize drugs??

<https://www.amnh.org/explore/science-topics/>