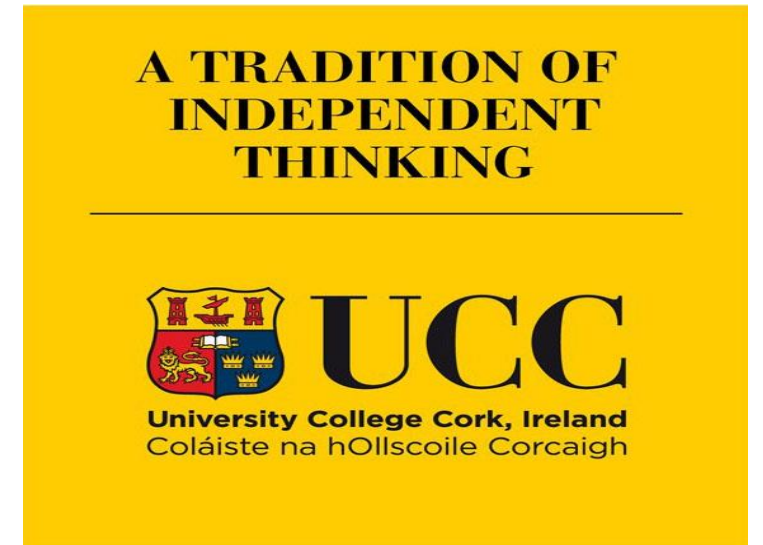




Gut Microbiome and drug interactions: Biopharmaceutical and oral bioavailability considerations

Dr Brendan Griffin



The Gut Microbiome

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

1.3X
You have more microbes than human cells

>10,000
Number of different microbial species that researchers have identified living in and on the human body

2kg
The gut microbiota can weigh up to 2kg



Interfacing Food & Medicine

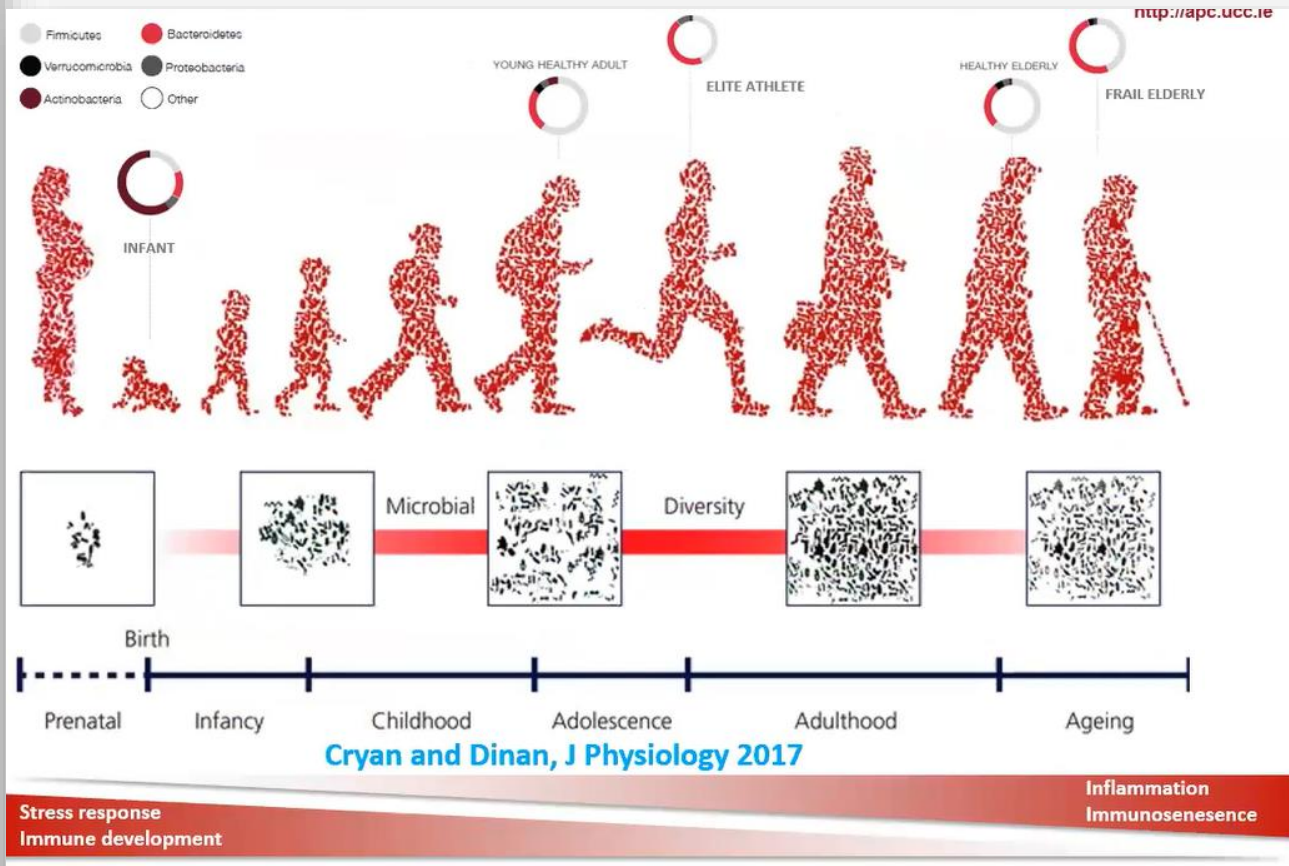
The microbiome is more medically accessible and manipulable than the human genome

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

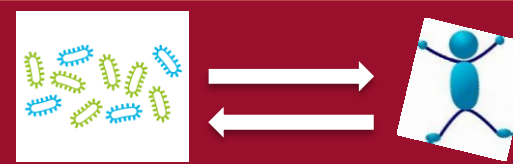
5:1
Viruses:Bacteria in the gut microbiota

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



Gut Microbiota – host interactions



Cell Host Microbe. 2008 June 12; 3(6): 417–427. doi:10.1016/j.chom.2008.05.001.

Metagenomic Approaches for Defining the Pathogenesis of Inflammatory Bowel Diseases

Daniel A. Peterson^{1,*}, Dan
¹Center for Genome Science
USA



²Department of Molecular, Cellular and Developmental Biology, University of Colorado, Boulder, CO, 80309 USA
Article | OPEN | Published: 04 December 2012

Symptomatic atherosclerosis is associated with an altered gut metagenome

Fredrik H. Karlsson, Frida Fåk, Intawat Nookaew, Valentina Tremaroli, Björn Fagerberg, Dina

REPORT

Predicting and Manipulating Cardiac Drug Inactivation by the Human Gut Bacterium *Eggerthella lenta*

Henry J. Haiser¹, David B. Gootenberg¹, Kelly Chatman¹, Gopal Sirasani², Emily P. Balskus², Peter J. Turnbaugh^{1,*}

OPEN

Citation: *Transl Psychiatry* (2013) 3, e309; doi:10.1038/tp.2013.83

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www.nature.com/tp

ORIGINAL ARTICLE

Antipsychotics and the gut microbiome: olanzapine-induced metabolic dysfunction is attenuated by antibiotic administration in the rat

KJ Davey^{1,2}, PD Cotter^{1,3}, O O'Sullivan^{1,3}, F Crispie³, TG Dinan^{1,4}, JF Cryan^{1,5} and SM O'Mahony^{1,5}

Psychiatric Research 82 (2016) 109–118

available at ScienceDirect

Psychiatric Research

www.elsevier.com/locate/psychires

Altered gut microbiota induces

Shelley A. Patterson^{a,c}, Sahar El Aidy^{a,d},
Benjamin Scott^a, Gerard Moloney^a,
Paul Ross^c, Catherine Stanton^c,
John A. Cryan^{a,b,*}

University of

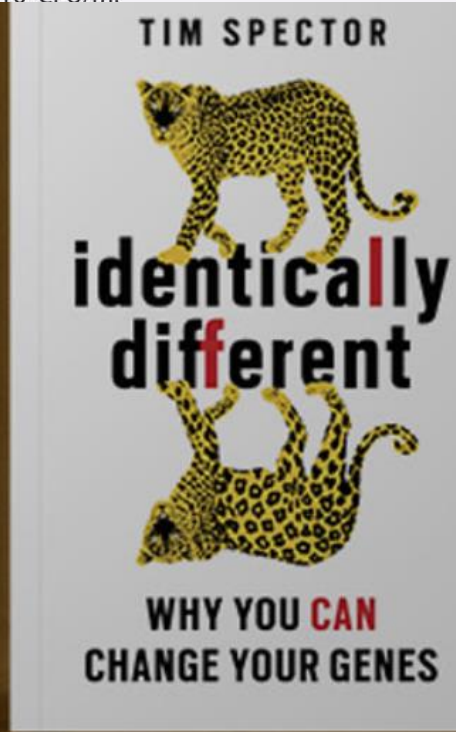
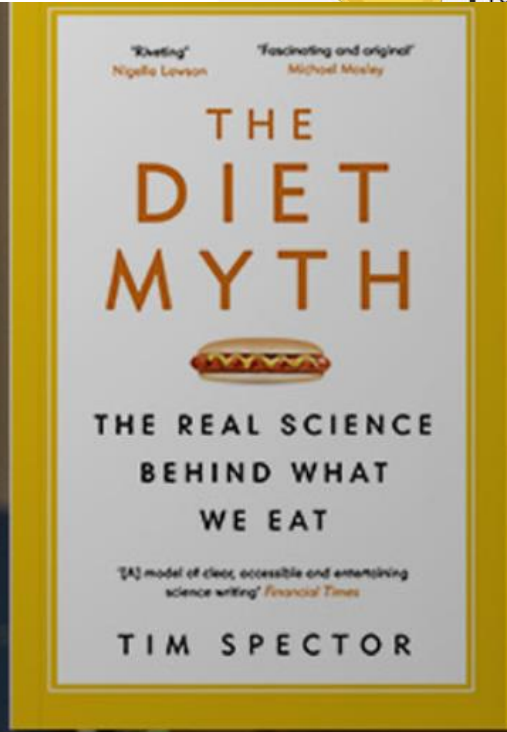
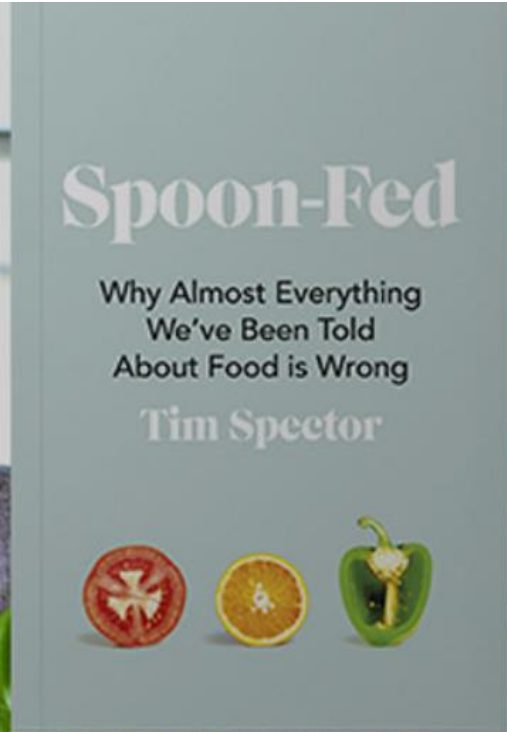
Leiden, The Netherlands

et al. 2018



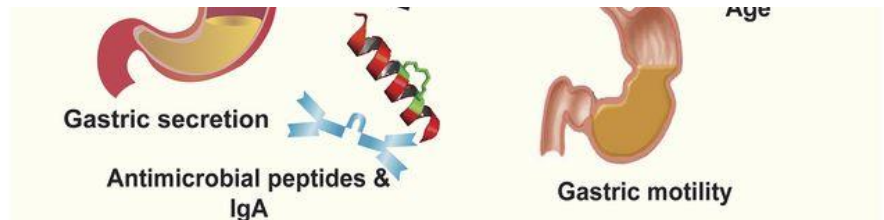
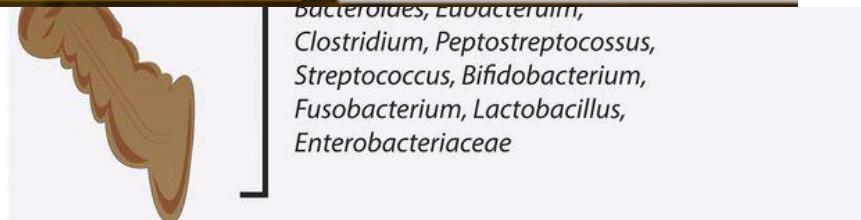
Factors defining the Gut Microbiome

- Characteristics of



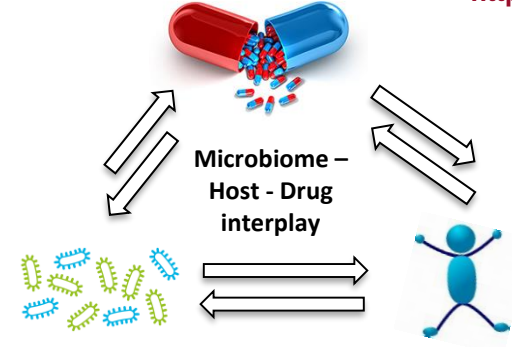
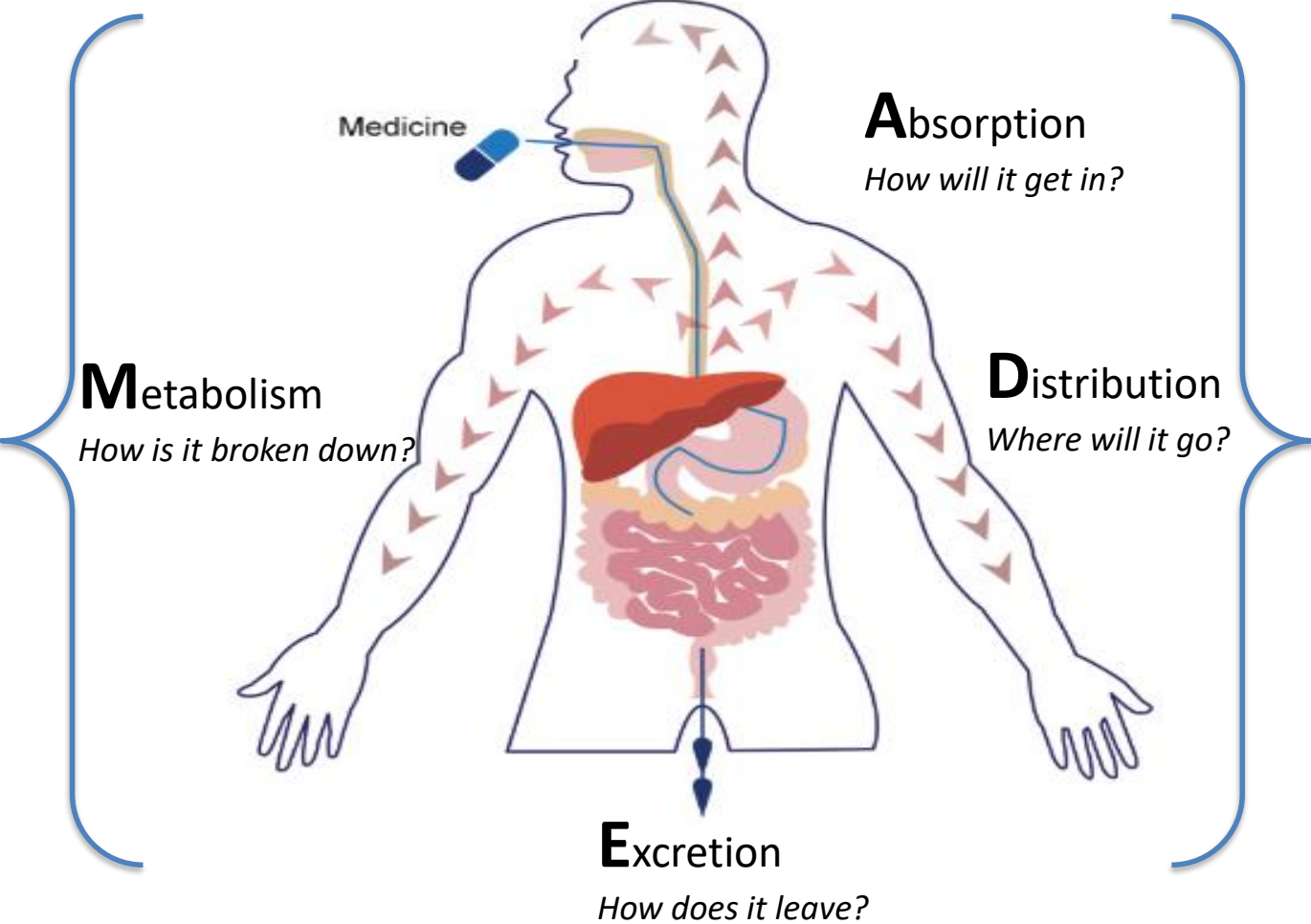
Tim Spector lost 1,300 species of gut microbes when he switched to a fast-food diet for 10 days (Tim Spector)

- Drugs can modify Gut Microbiome



“what the HOST does to the drug”

PK= ADME



Gut Microbiome?

DRUG-MICROBIOTA INTERACTIONS

Antibacterial effects e.g. sertraline



British Journal of
Pharmacology

British Journal of Pharmacology (2018) 175 4415–4429 4415

Themed Section: When Pharmacology Meets the Microbiome: New Targets for Therapeutics?

REVIEW ARTICLE

Drug–gut microbiota interactions: implications for neuropharmacology

Correspondence Gerard Clarke, APC Microbiome Ireland, University College Cork, Cork, Ireland. E-mail: g.clarke@ucc.ie

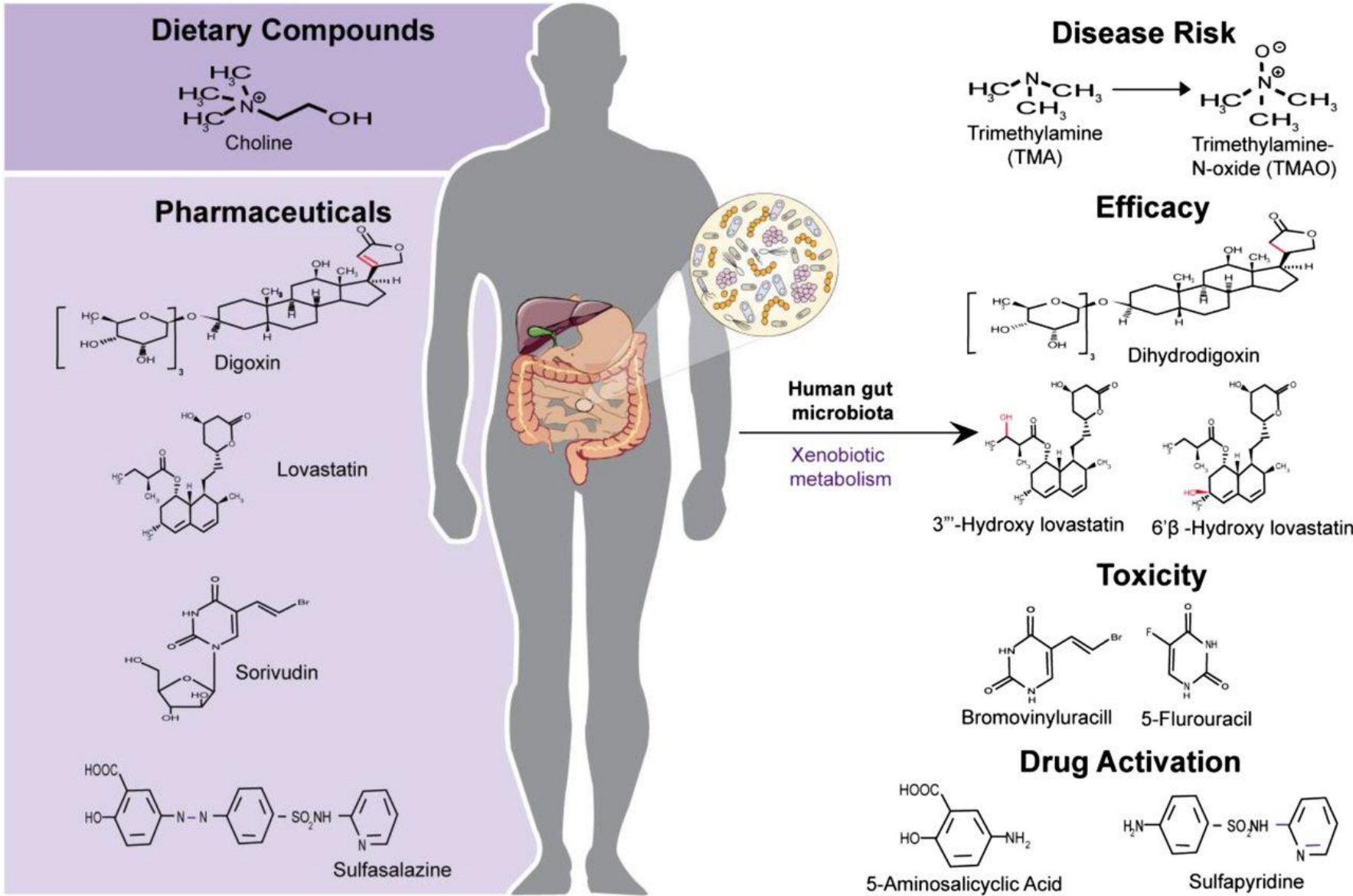
Received 23 November 2017; **Revised** 4 April 2018; **Accepted** 17 April 2018

Jacinta Walsh^{1,4}, Brendan T Griffin^{2,4}, Gerard Clarke^{3,4} and Niall P Hyland^{1,4,5} 

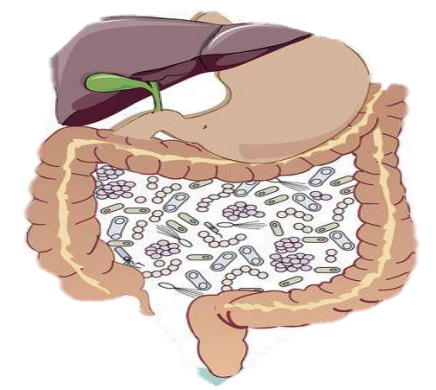
Metabolism by bacterial enzymes e.g. sulfasalazine

MICROBIOTA-DRUG INTERACTIONS

Clinically relevant microbiome-mediated drug metabolism



Gut Microbiota – Drug metabolic Interactions



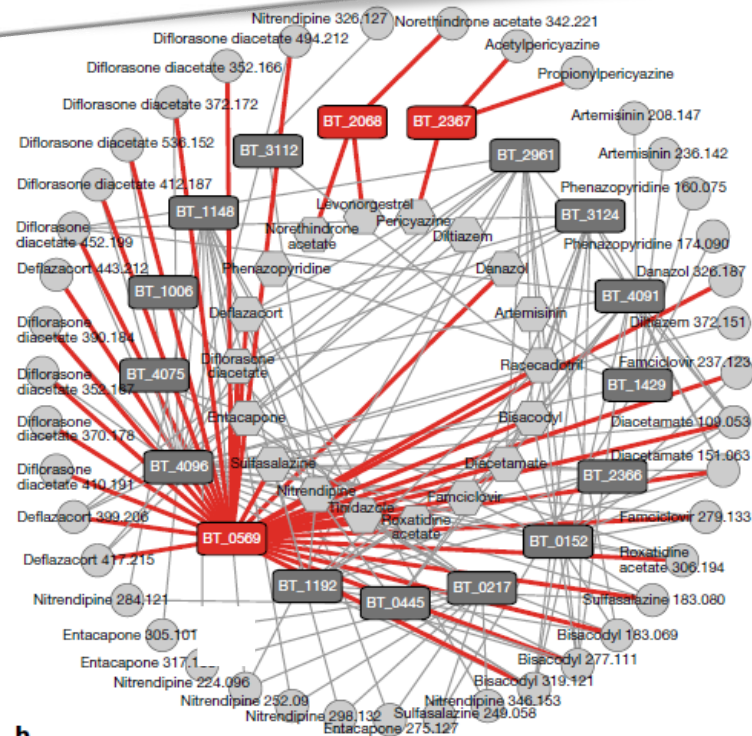
Gut microbiome-mediated drug metabolism

ARTICLE

<https://doi.org/10.1038/s41586-019-1291-3>

Mapping human microbiome drug metabolism by gut bacteria and their genes

Michael Zimmermann^{1,2}, Maria Zimmermann-Kogadeeva^{1,2}, Rebekka Wegmann^{1,2} & Andrew L. Goodman^{1*}



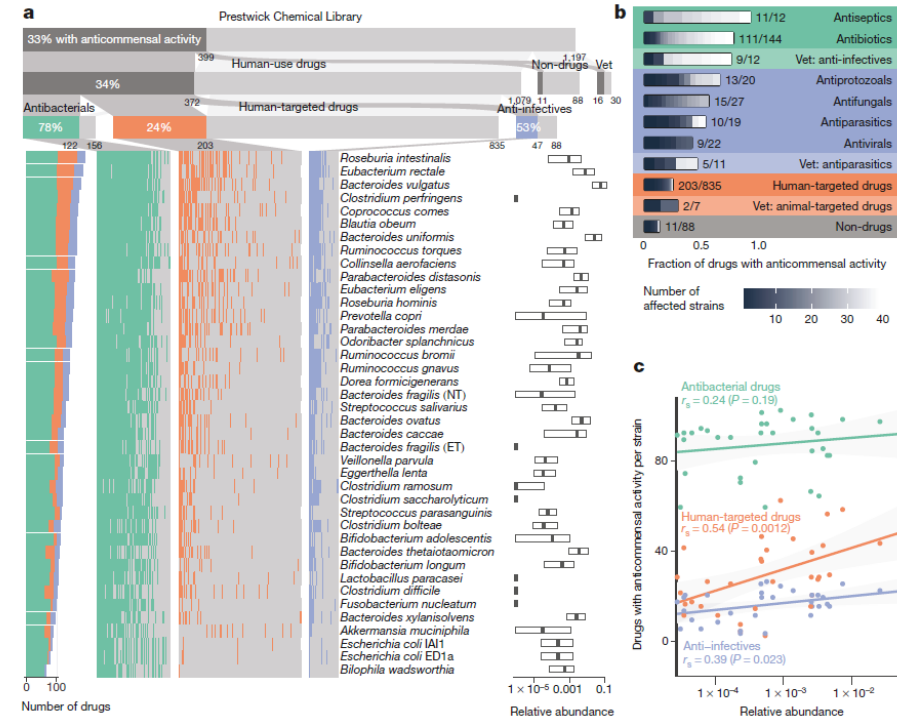
Of 271 orally administered drugs, 66% were susceptible to gut bacteria mediated metabolism

ARTICLE

doi:10.1038/nature25979

Extensive impact of non-antibiotic drugs on human gut bacteria

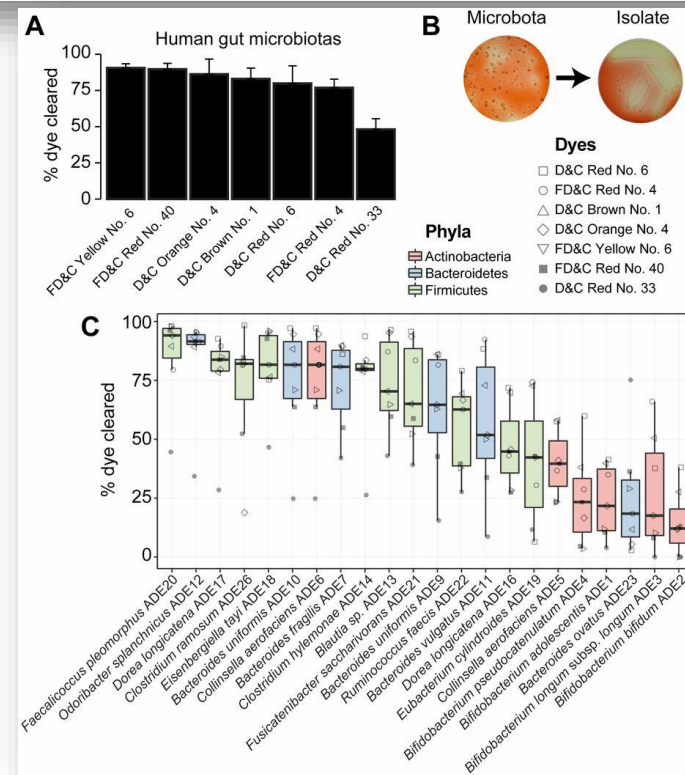
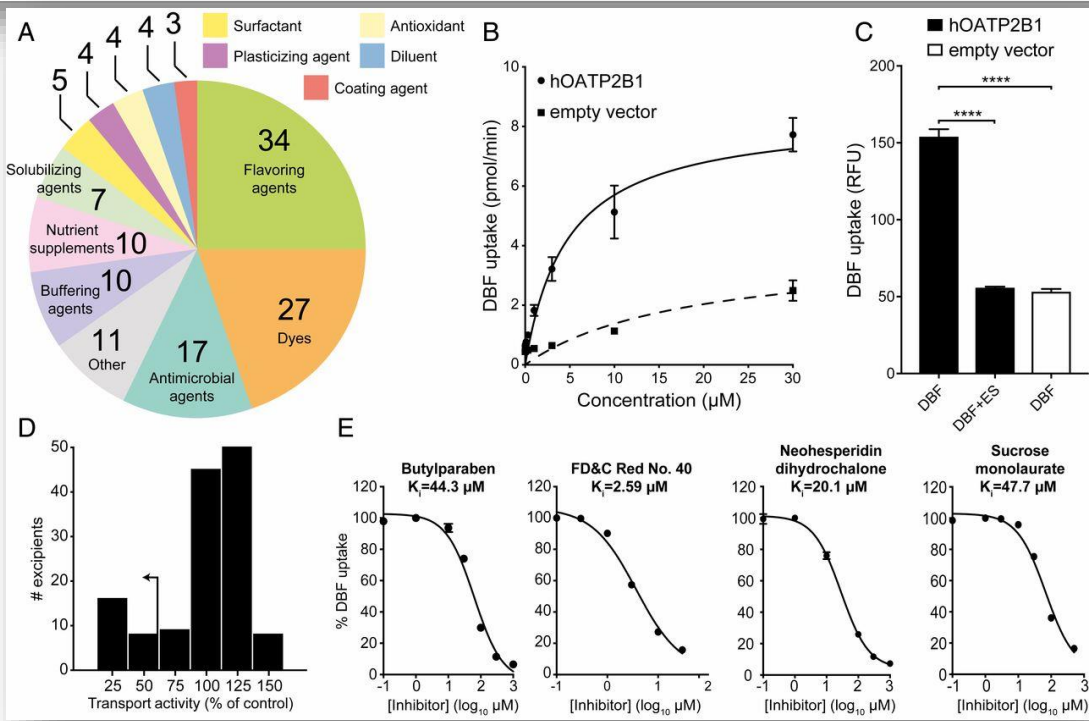
Lisa Maier^{1*}, Mihaela Pruteanu^{1†*}, Michael Kuhn^{2*}, Georg Zeller², Anja Telzerow¹, Exene Erin Anderson¹, Ana Rita Brochado¹, Keith Conrad Fernandez¹, Hitomi Dose¹, Hirotada Mori¹, Kiran Raosaheb Patil², Peer Bork^{2,4,5,6} & Athanasios Typas^{1,2}



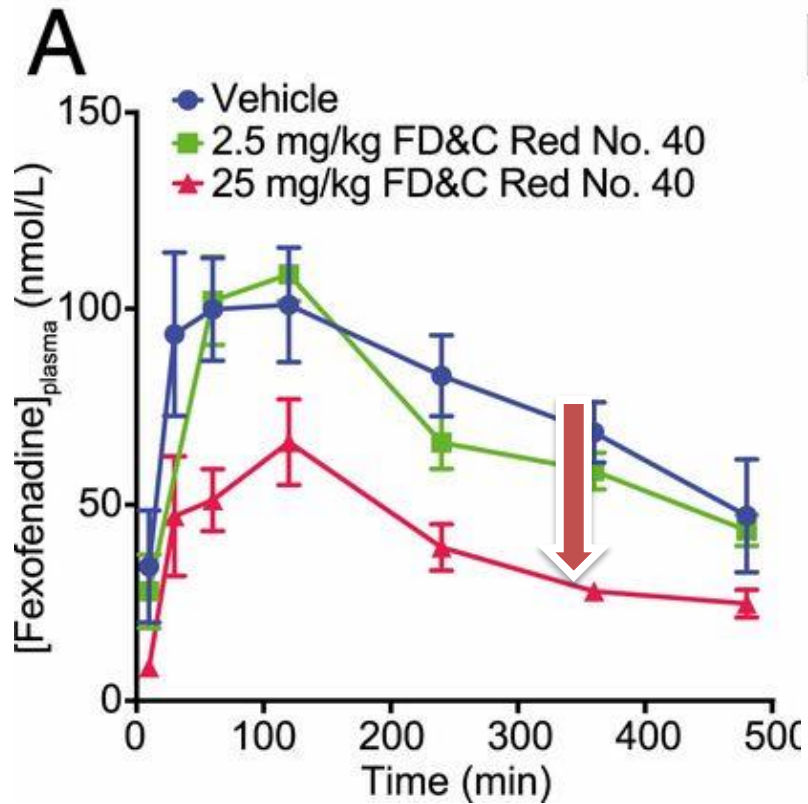
Of more than 1,000 drugs screened, 24% of the drugs with human targets negatively impact growth of gut microbiome growth

Bacterial metabolism rescues the inhibition of intestinal drug absorption by food and drug additives

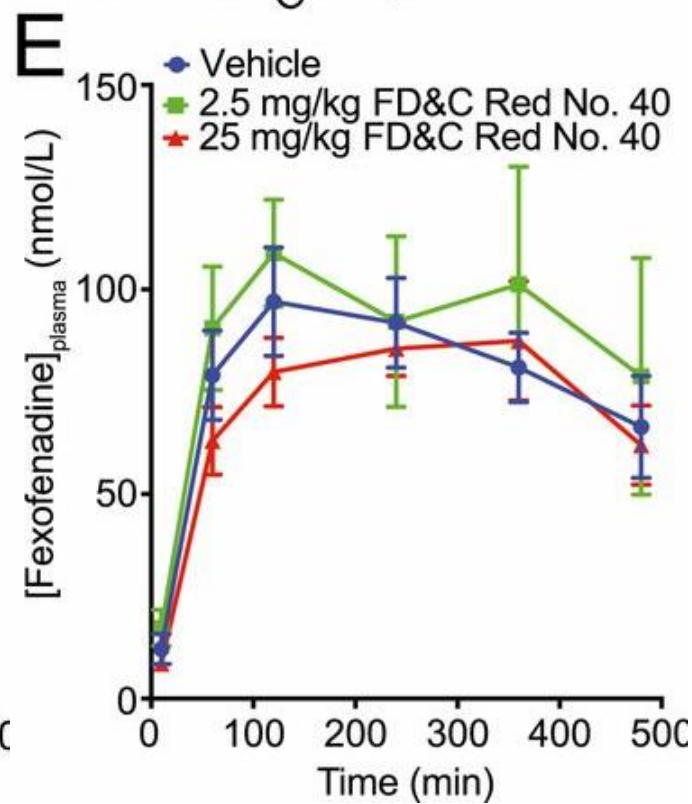
Ling Zou^{a,1} , Peter Spanogiannopoulos^{b,1} , Lindsey M. Pieper^b, Huan-Chieh Chien^a, Wenlong Cai^c, Natalia Khuri^d , Joshua Pottel^{e,f} , Bianca Vora^a, Zhanglin Ni^g, Eleftheria Tsakalozou^g, Wenjun Zhang^{c,h} , Brian K. Shoichet^{e,f}, Kathleen M. Giacomini^{a,2} , and Peter J. Turnbaugh^{b,h,2} 



Microbiome metabolism – impact on excipients effect



High dose Red azo dye reduces fexofenadine bioavailability – saturation of gut bacterial azoreductase activity



No impact in Germ free mice

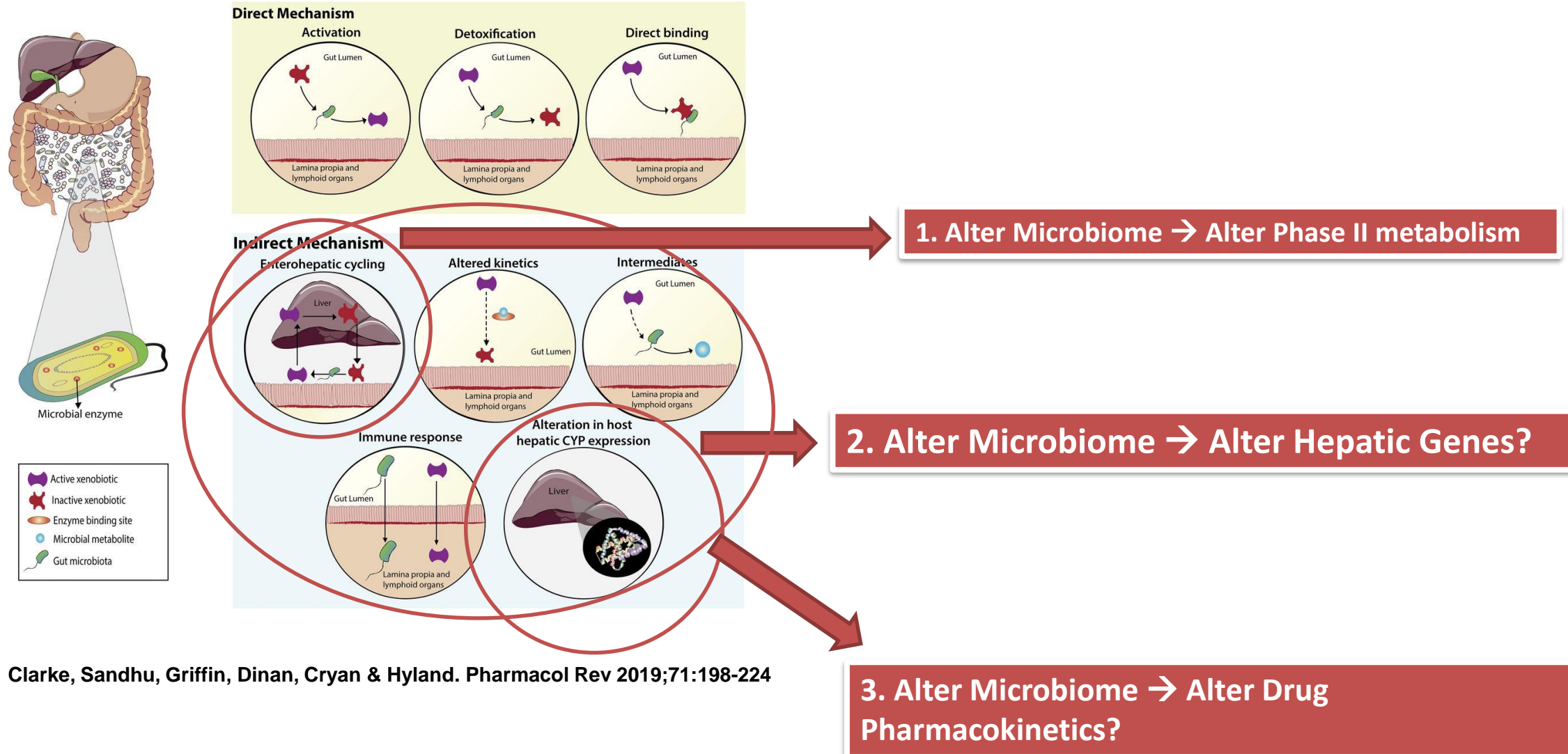


Significance

Food and drug products are supplemented with small molecules called excipients that are assumed to be inert. In this study, we screened a collection of common oral excipients and identified 24 that inhibit intestinal drug transport, including the common excipient FD&C Red No. 40, which decreased drug absorption in mice. Excipient inhibitors were enriched for azo dyes, which human gut bacteria could metabolize, producing metabolites that no longer inhibit intestinal drug transporter activity. This work demonstrates the unintended consequences of oral excipients and a beneficial role for the gut microbiome in limiting these unfavorable effects.

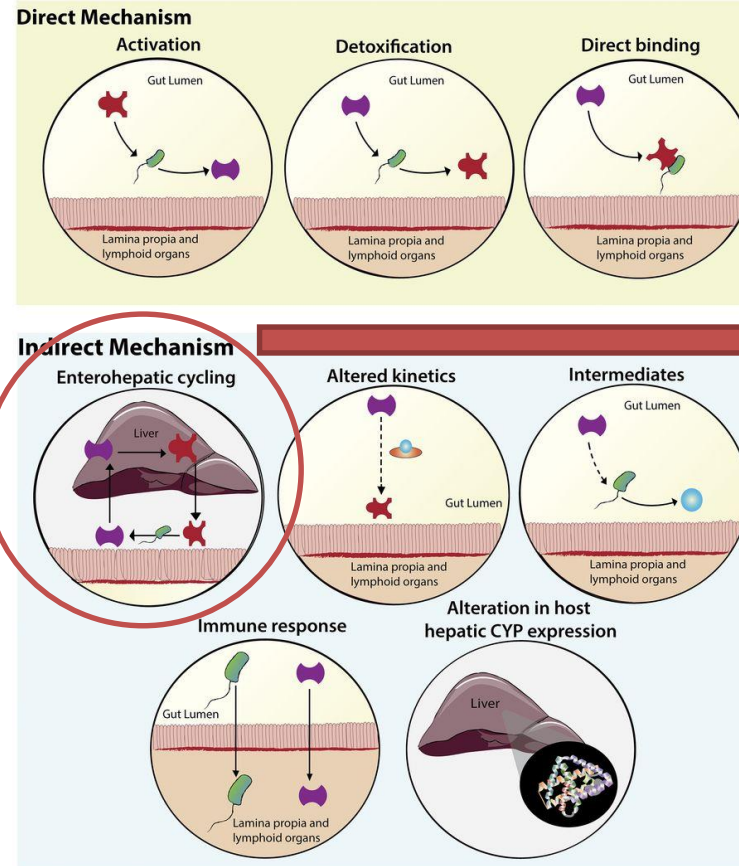
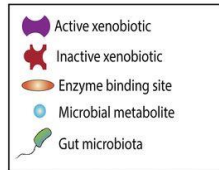
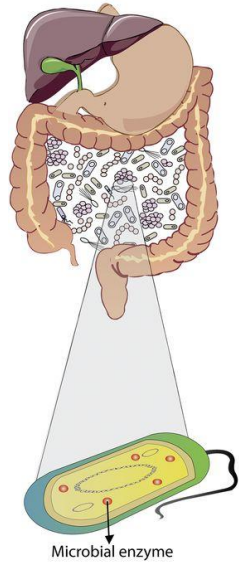
Ling Zou et al. PNAS 2020;117:27:16009-16018

Understanding Microbiome – Host - Drug interactions



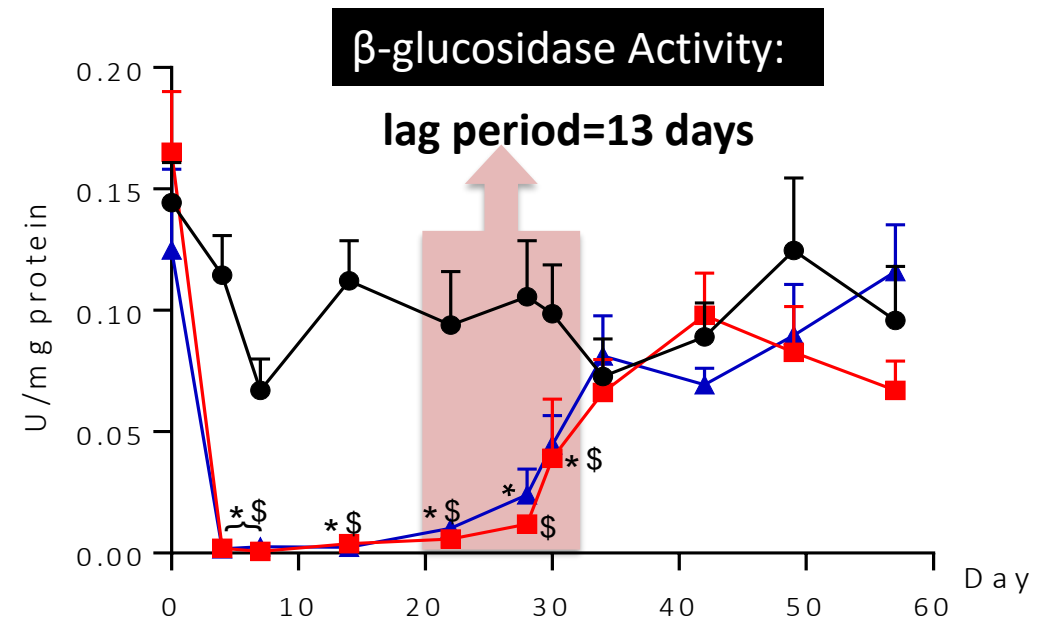
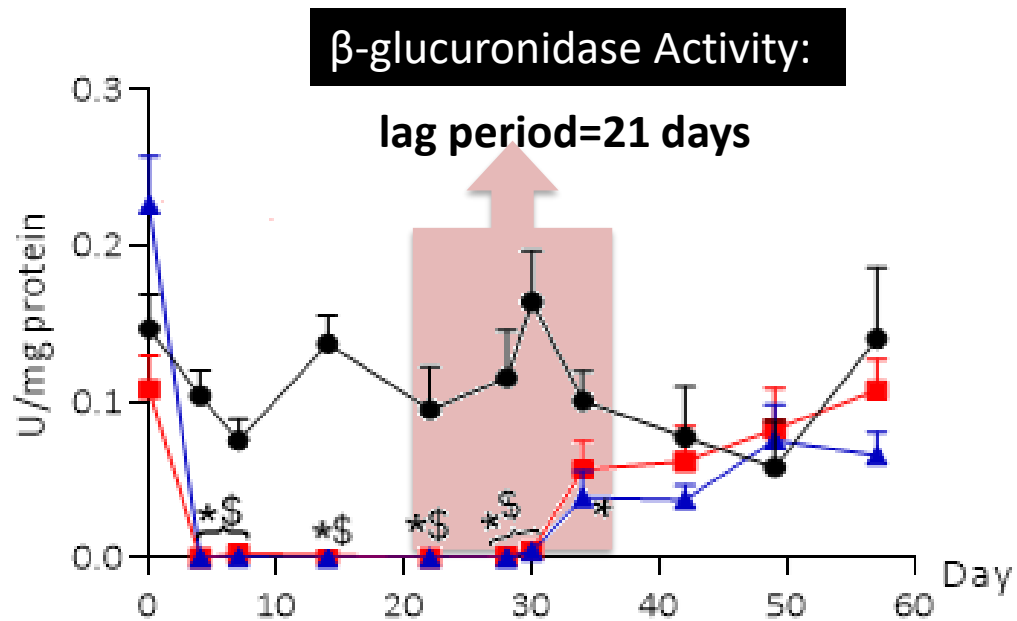
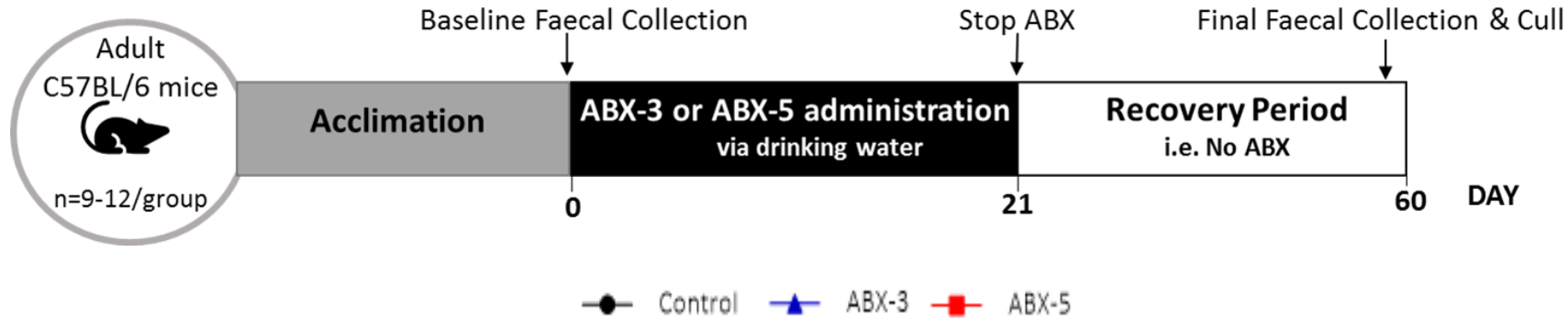
Clarke, Sandhu, Griffin, Dinan, Cryan & Hyland. Pharmacol Rev 2019;71:198-224

Microbiome – Host metabolism interplay



1. Alter Microbiome → Alter Phase II metabolism

Impact of Antibiotic Treatment on Faecal Enzymatic Activity



Walsh et al, *Gastro. Liver. Physiol.* 2020 <https://doi.org/10.1152/ajpgi.00026.2020>

***ABX-3 Cocktail:** Ampicillin & Vancomycin & Neomycin

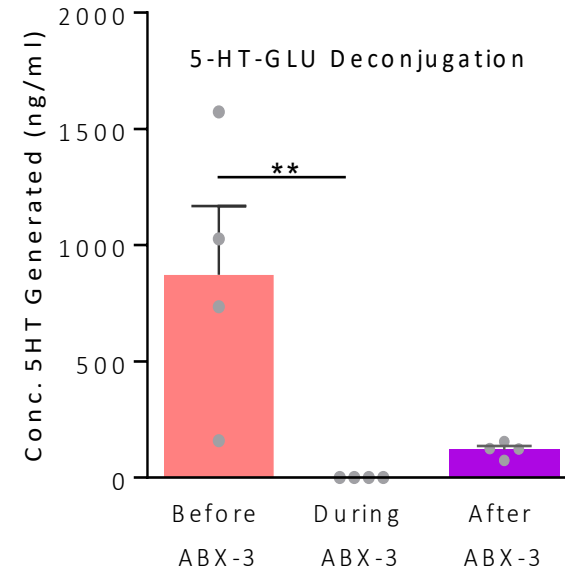
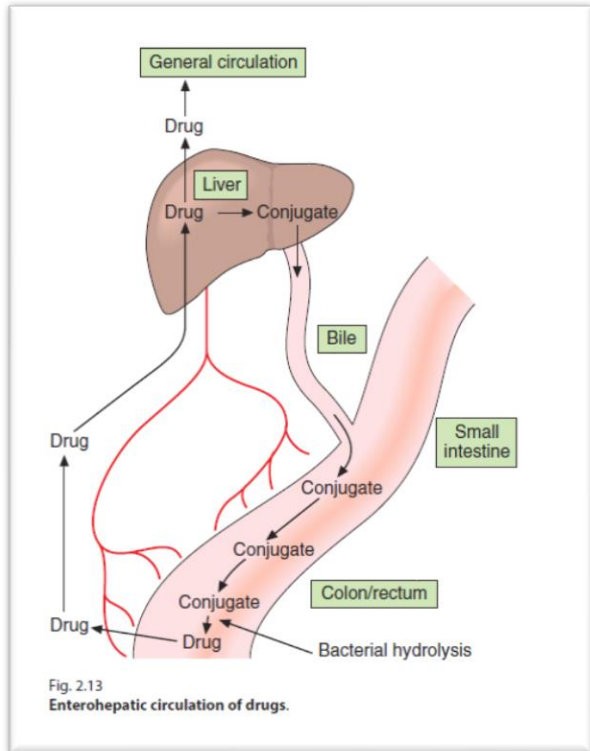
****ABX-5 Cocktail:** Ampicillin & Vancomycin & Ciprofloxacin & Imipenem & Metronidazole

* $p < 0.05$; RM-ANOVA with Fishers LSD
n=9-12/group

Implications for Phase II metabolism

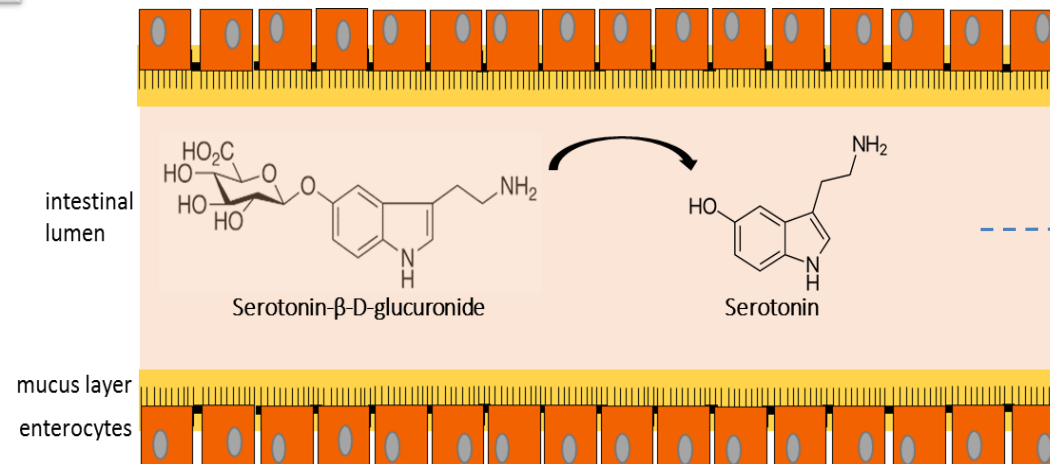
Microbiota-Derived Enzyme:	Hypothesised reaction mechanisms:	Drug (or Metabolite) Substrate:	Ref:
β-glucuronidase	Remove glucuronic acid moiety from hepatic phase 2 metabolites	Irinotecan (SN-38 glucuronide) NSAIDS, e.g. Indomethacin and Diclofenac	(Yamamoto et al., 2008, Saitta et al., 2014)
β-glucosidase	Hydrolyse the glycosidic bond of a carbohydrate moiety to release non-reducing terminal glycosyl residues	Prodrugs Herbal substances e.g. anthocyanins, genistin and naringin	(You et al., 2015)
Azoreductase	Reduction of azo or quinone bonds	Azo-containing drugs, e.g. Olsalazine (5ASA prodrug) Nitrofurantoin antibiotics Ester containing prodrugs	(Ryan, 2017)
Carboxylesterase	Hydrolyse ester, thioester, amide, or carbamate containing drugs to respective free acids Hydrolyse esters to carboxylic acids	Aspirin, Ester containing prodrugs	(Kim et al., 2016, Laizure et al., 2013, Imai and Ohura, 2010)
Nitroreductase	Reduction of the nitro group	Metronidazole Benzodiazepines	(Koch et al., 1979, Elmer and Remmel, 1984, Takeno et al., 1990)
N-acetyltransferase	Transfer of acetyl group to nitrogen or oxygen atom of primary arylamines, hydrazines and N-hydroxylated metabolites	5-aminosalicylic acid	(Deloménie et al., 2001, van Hogezaand et al., 1992)
Sulfatases	Hydrolysis of sulfate esters utilising formylglycine	Sulfate ester hepatic metabolites	(Koppel et al., 2017, Ulmer et al., 2014)

Implications of Antibiotic treatment on Phase II metabolism



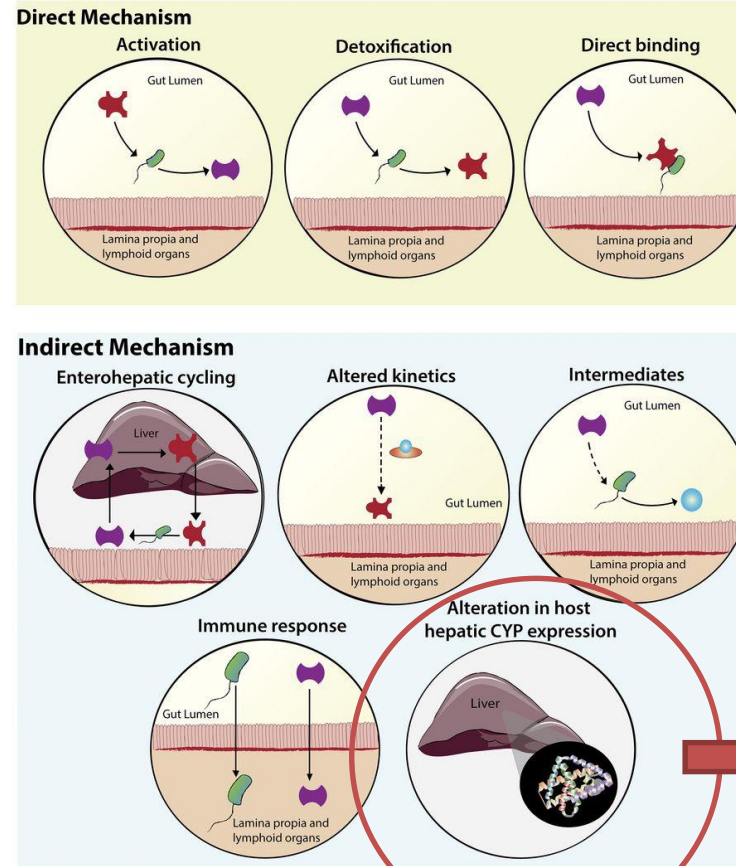
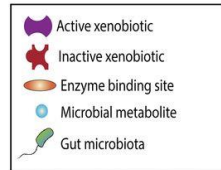
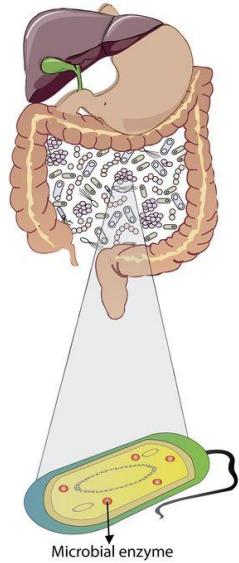
****p<0.01;**
ANOVA (RM or one-way)
n=9-12/group (enzyme)
n=4 (5-HT)

Walsh et al, *Gastro. Liver. Physiol.* 2020 <https://doi.org/10.1152/ajpgi.00026.2020>



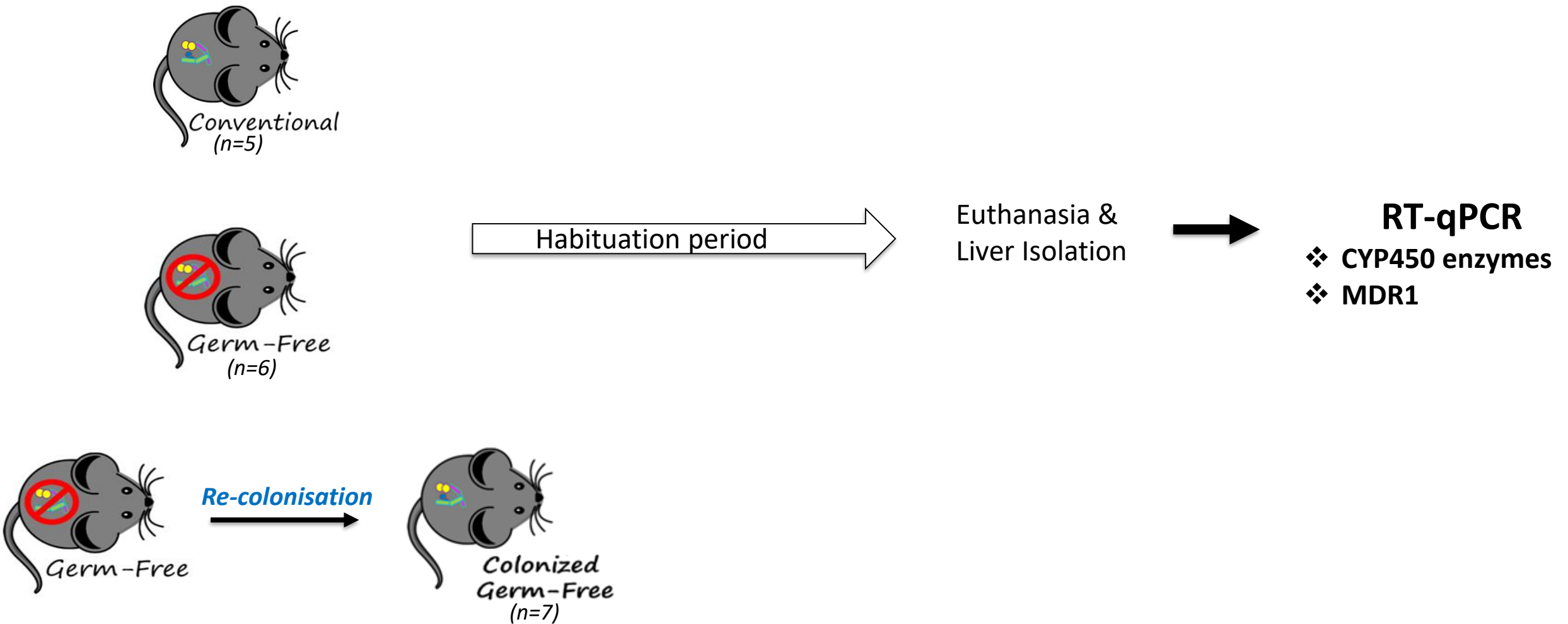
Implications for
Gut Function?

Microbiome – Host metabolism interplay

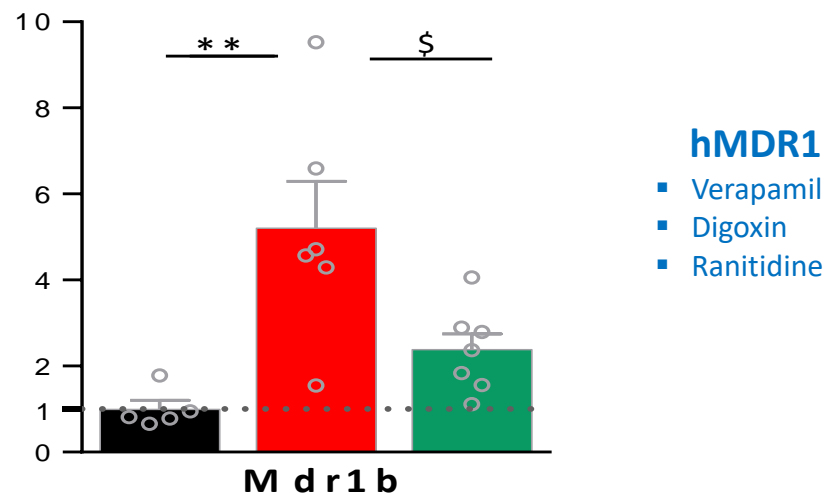
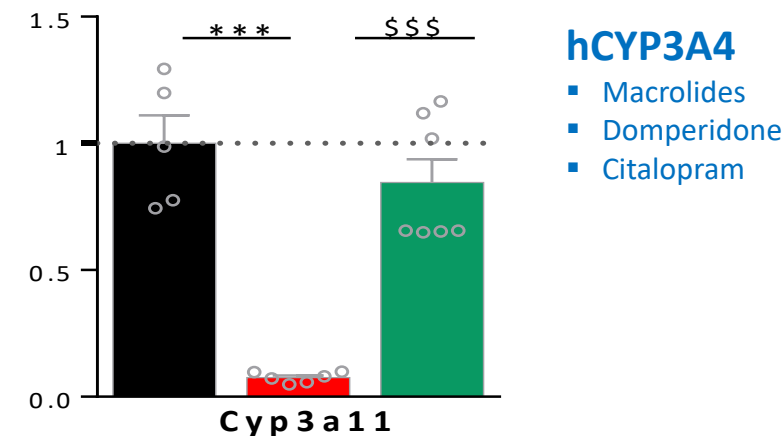
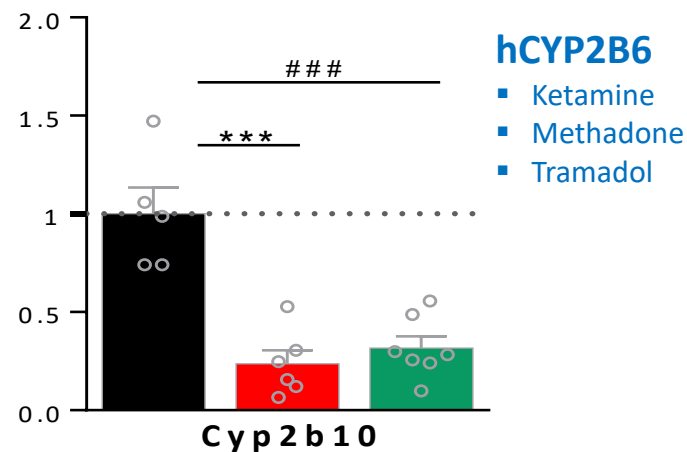
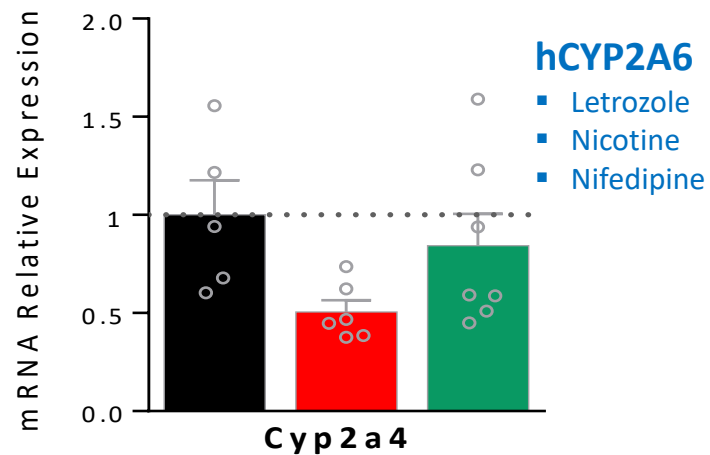


2. Alter Microbiome → Alter Hepatic Genes?

Microbial Regulation of Hepatic Drug Metabolism and Transport?



CYP/MDR Enzymes Subject to Microbial Regulation

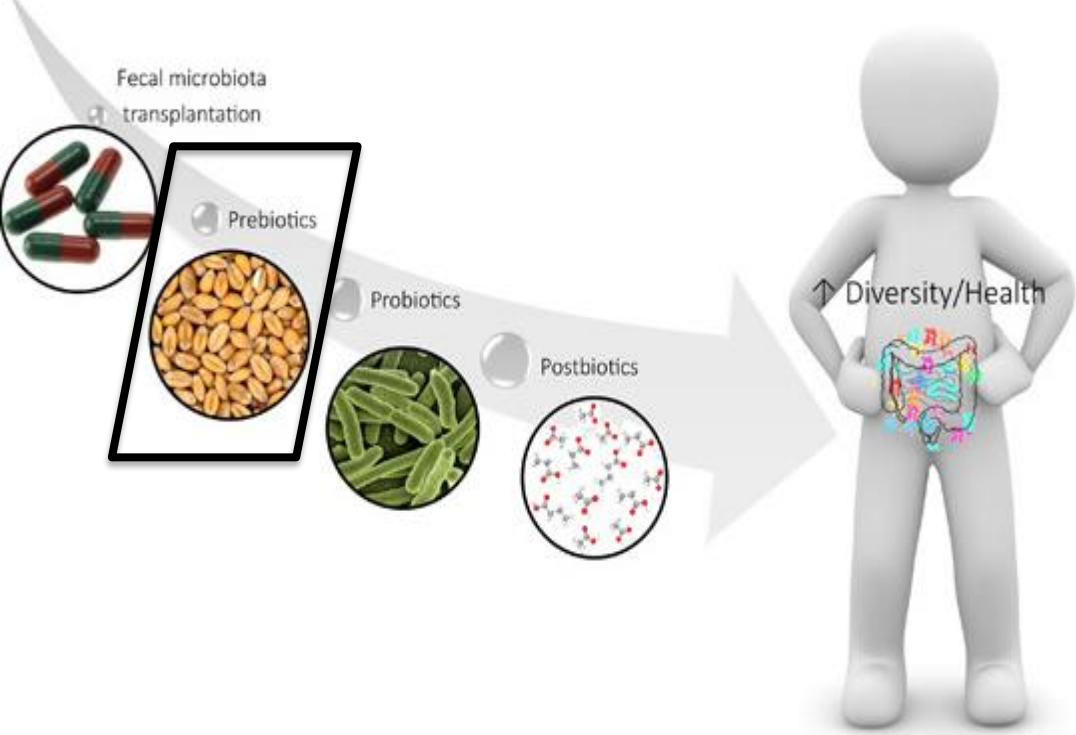


Conv.
 GF
 Colonised GF

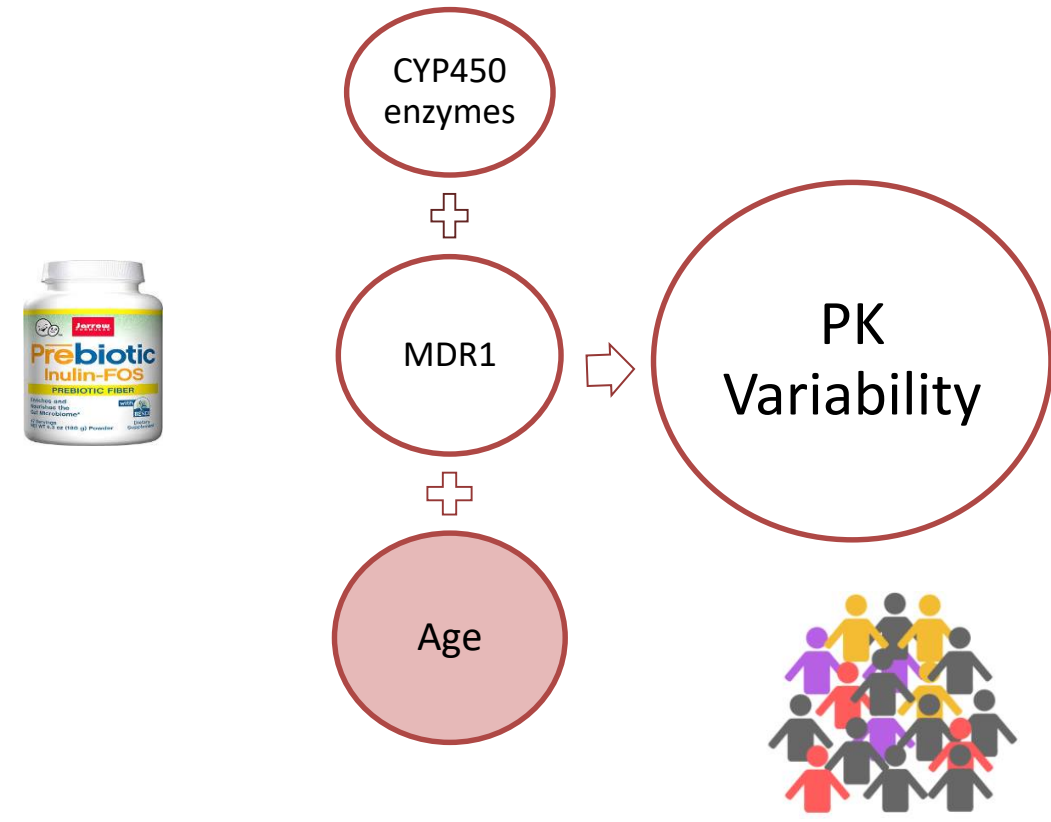
$*p > 0.05$; $**p < 0.01$; $***p < 0.001$
 One-way ANOVA
 $n = 5-6$ /group
 Conv=conventional
 GF=germ-free

Prebiotics → Modulate CYP/MDR expression?

1. Impact of Microbiota-Targeted Intervention on Host Metabolism?



2. If so, could prebiotics influence hepatic expression?



Impact of Microbiota-Targeted Intervention on Hepatic Genes?

Young Mice
(2months*)



Control

Prebiotic-Treated



Control

Standard Chow or
14 week treatment
Chow Supplemented with
10% FOS-Inulin

Euthanasia
& Liver
isolation

RT-qPCR

Middle-Aged Mice
(10months*)

e.g. dietary sources of inulin

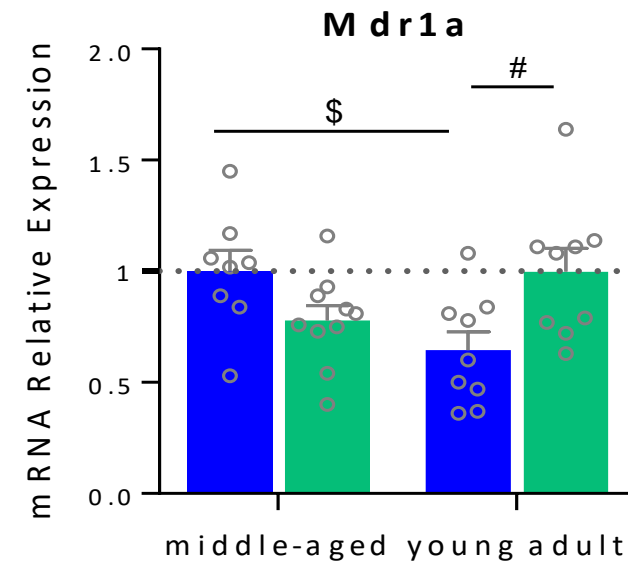
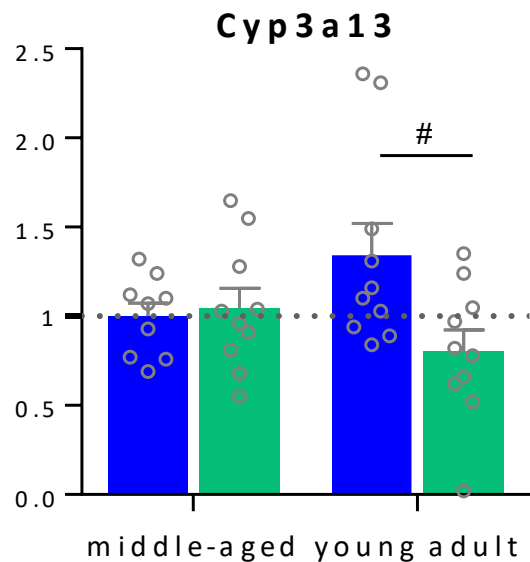
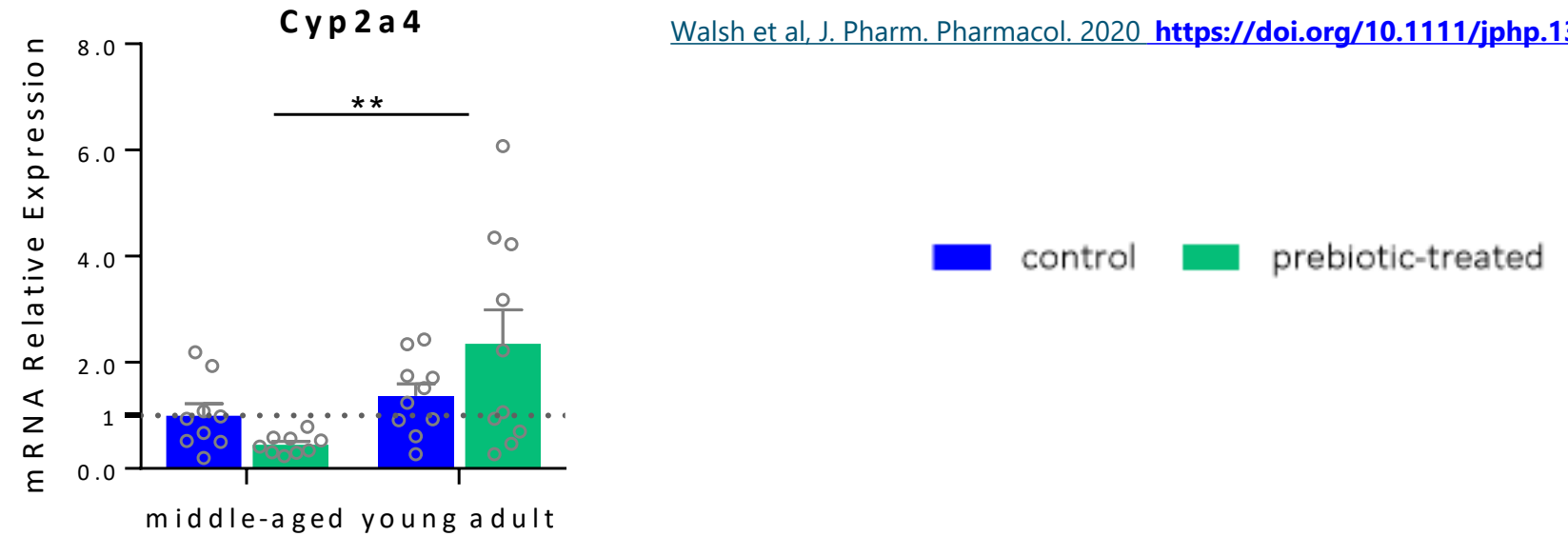


Male C57BL/6 (n=9-10/group)
*approx. age @ study start-date
FOS; fructooligosaccharide

Walsh et al, J. Pharm. Pharmacol. 2020 <https://doi.org/10.1111/jphp.13276>

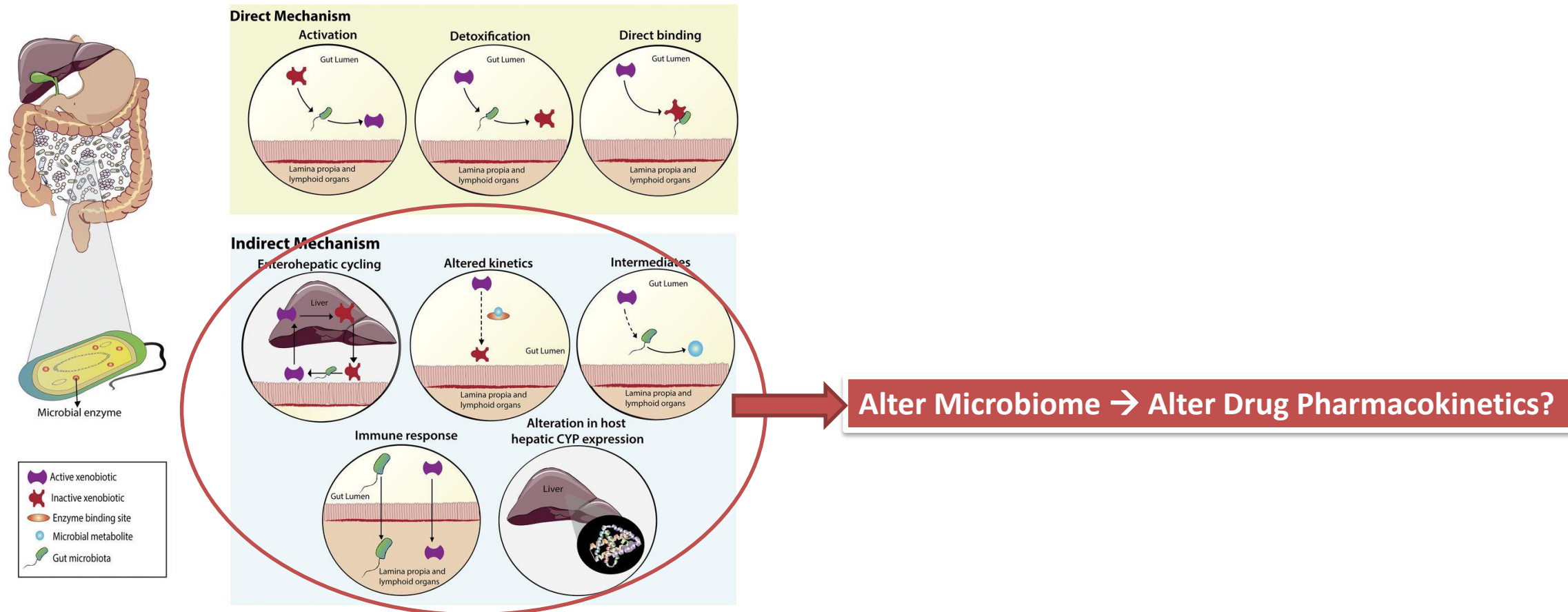
Prebiotic Mix alters Specific CYPs and MDR1 in Liver

Walsh et al, J. Pharm. Pharmacol. 2020 <https://doi.org/10.1111/jphp.13276>



*, p<0.05; **, p<0.01
n=9-10/group
Two-way ANOVA

Microbiome – Host metabolism interplay



Alter Gut Microbiome → alter Drug PK in vivo?

Probiotic-treated



Antibiotic-treated



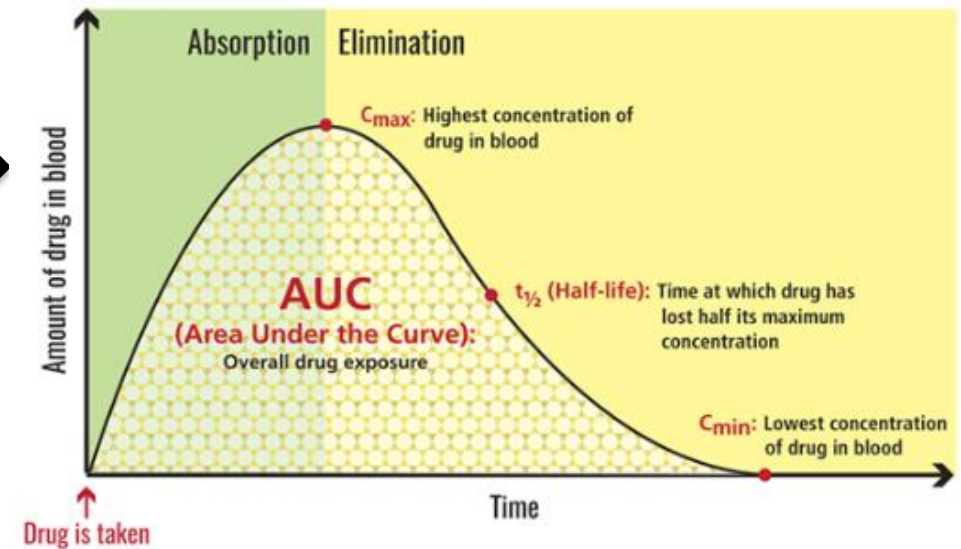
Vehicle



Single Oral
Drug Dose



Altered Drug Pharmacokinetics?????



Sprague Dawley Rats; n=7/group

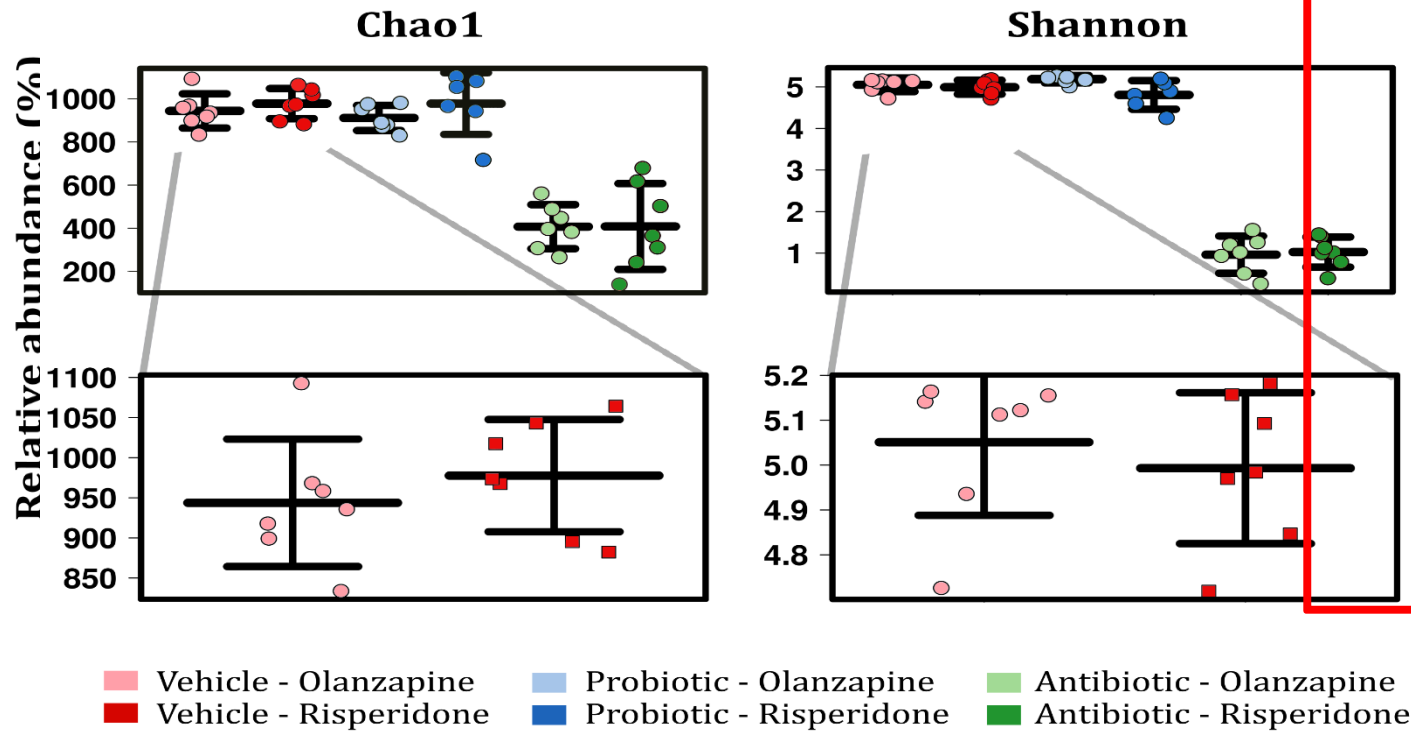
Antibiotic cocktail → ampicillin 1g/L; vancomycin 500mg/L; imipenem 250mg/L

Probiotic cocktail → VSL3 (5·10¹⁰ bacteria/kg/day)

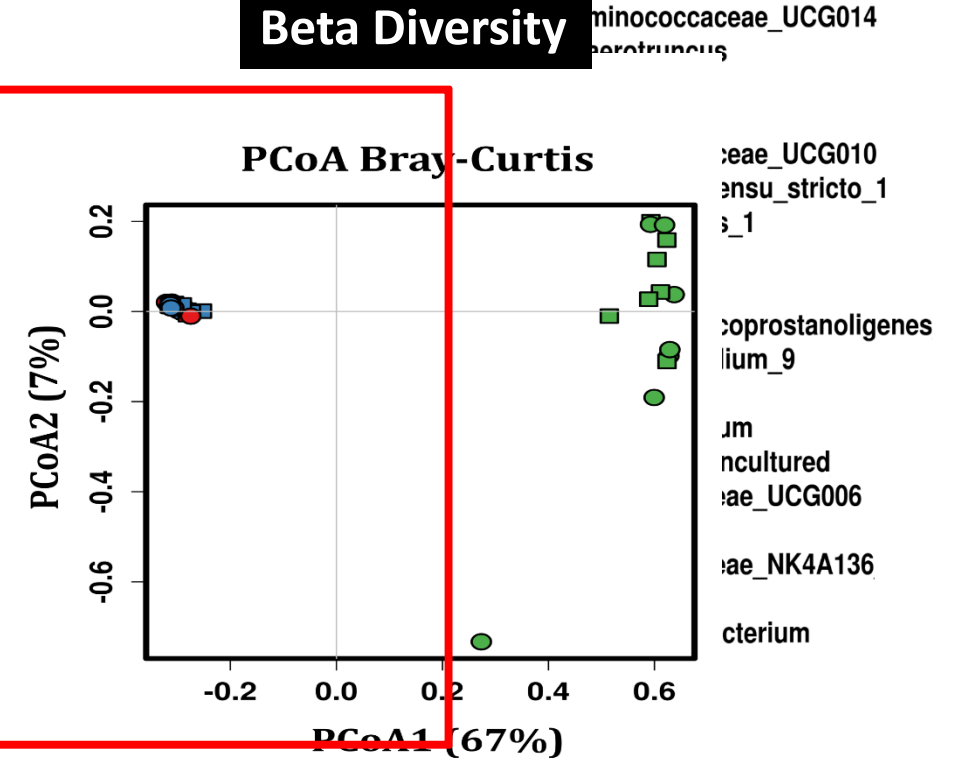
Walsh et al, under revision

Impact of Interventions on Microbial Signature

Changes in Composition (genus level) Alpha Diversity

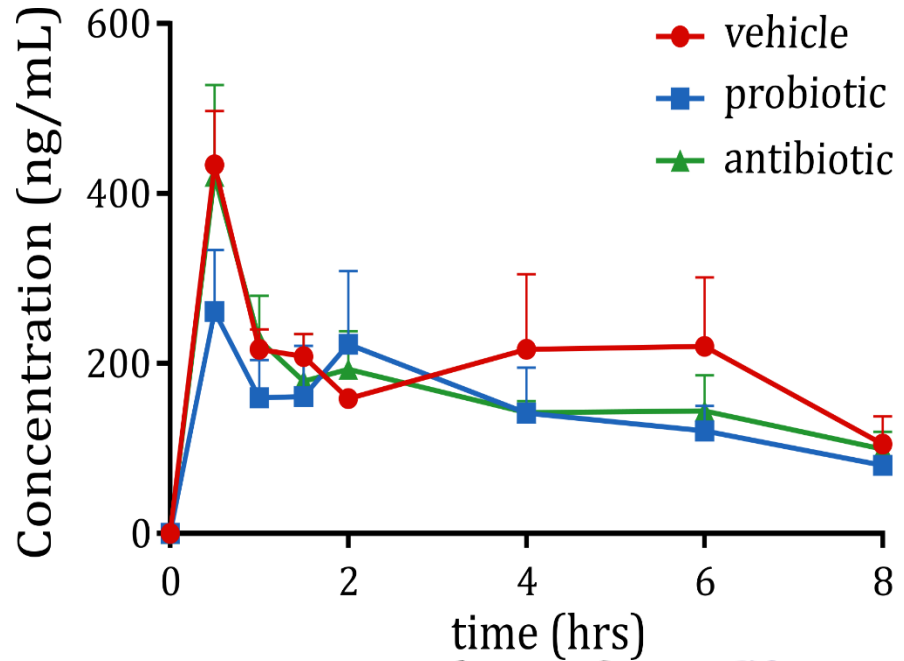


Beta Diversity

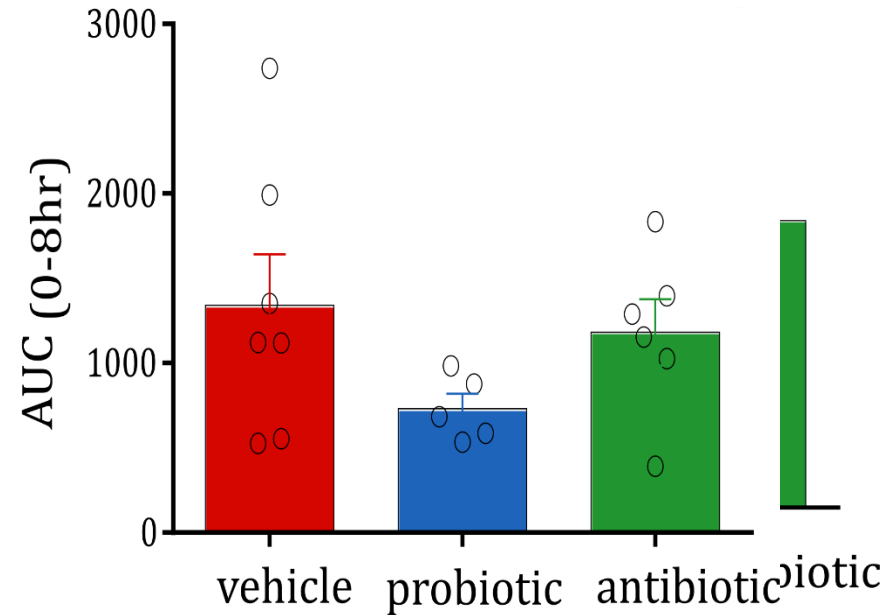


Microbiota-depletion Increases Systemic OLZ Absorption

Risperidone PK Profile



Risperidone AUC

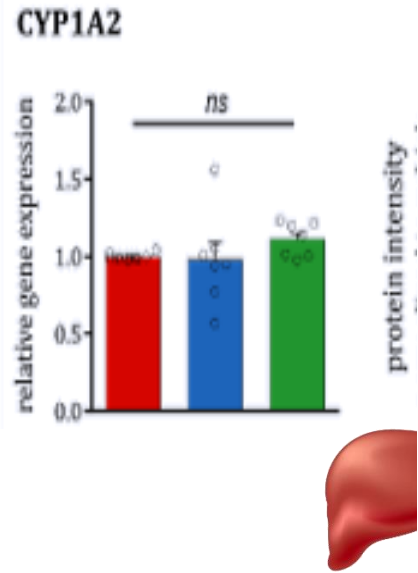


□ ABX=1.8x ↑ in Olanzapine Availability

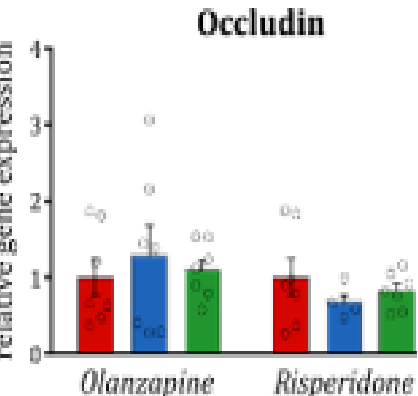
□ Microbiota-depletion alters PK after Single Olanzapine Dose

The Quest for Identifying Underlying Mechanism

1) ABX impact on hepatic gene expression?

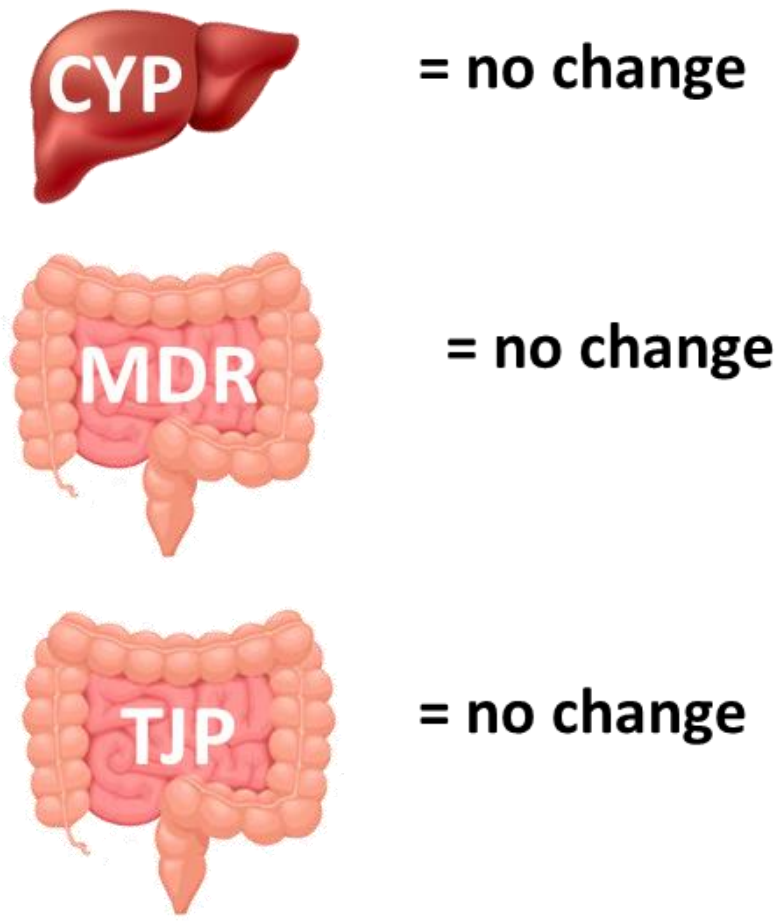


2) Altered efflux/loc

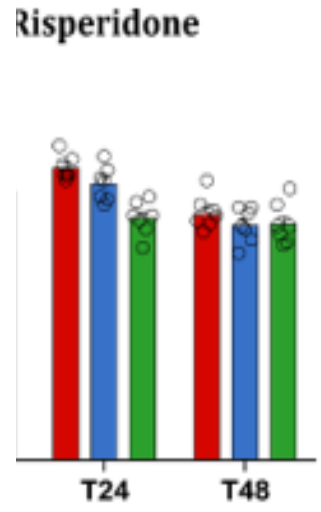
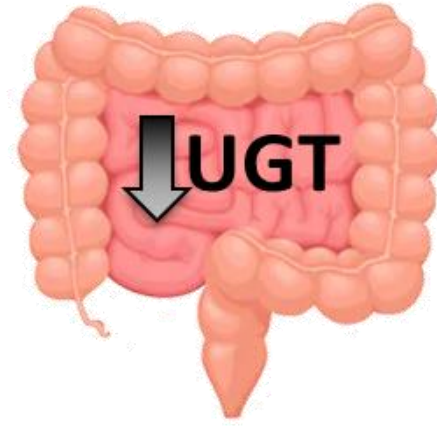


3) ABX impact on fecalase-mediated metabolism?

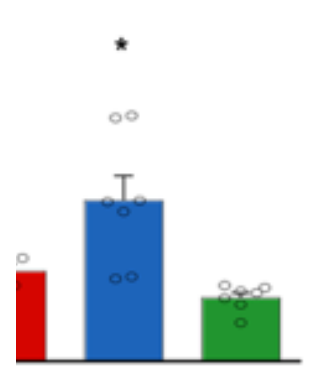
3. Microbiota Depletion Effects on OLZ → Mechanism



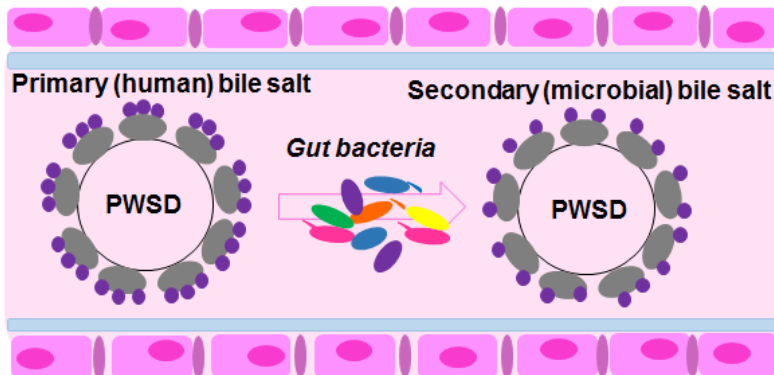
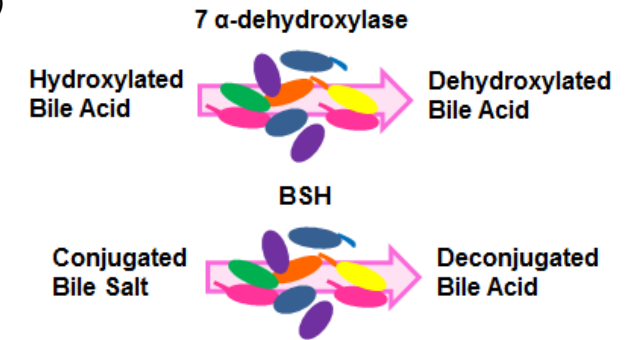
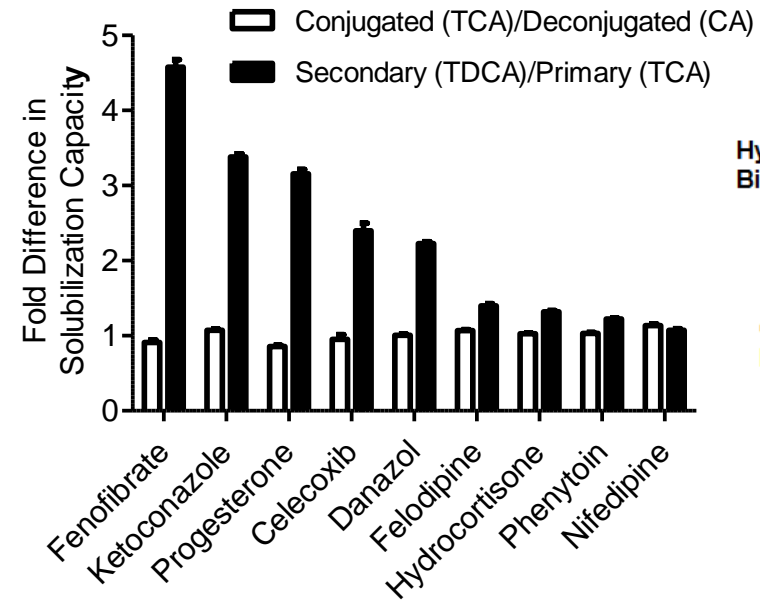
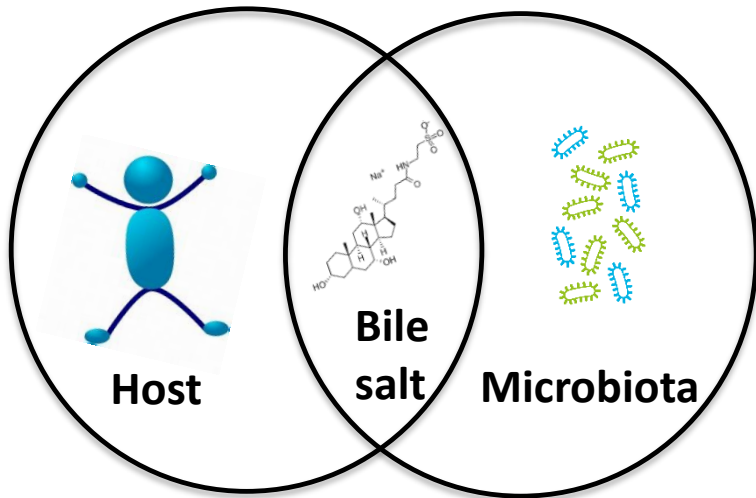
FIRST PASS METABOLISM



in duodenum?



Can Microbiota influence drug solubility?



molecular
pharmaceutics

Article

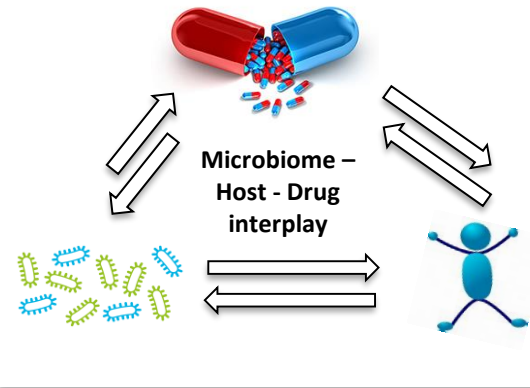
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Impact of Gut Microbiota-Mediated Bile Acid Metabolism on the Solubilization Capacity of Bile Salt Micelles and Drug Solubility

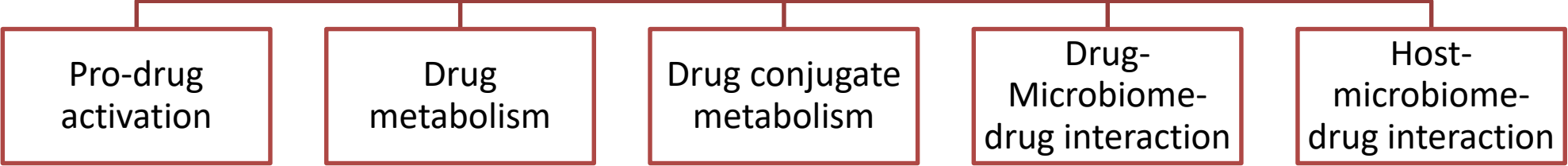
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Concluding comments



Influence of Microbiome on Drug Pharmacokinetics

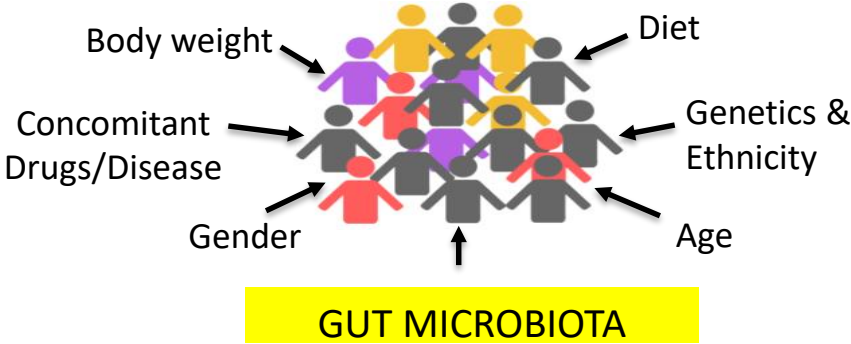


Direct drug PK effects

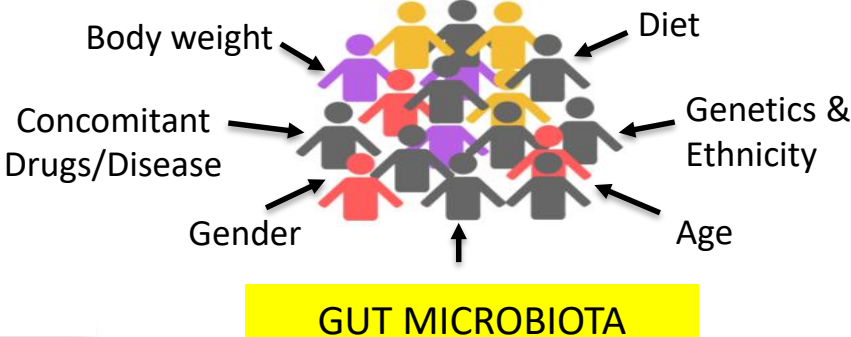
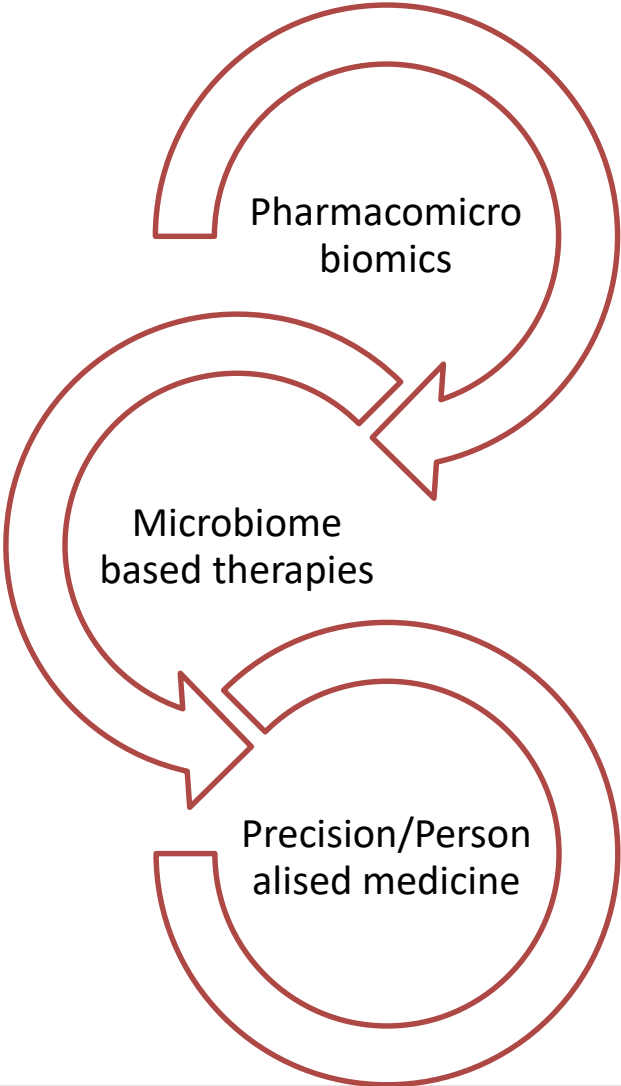
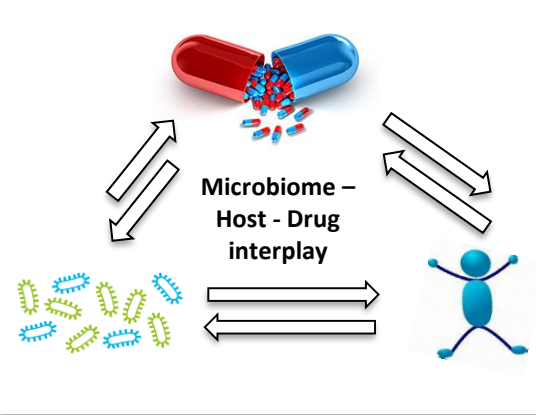
↑ Bioavailability ↑ Clearance ↓ Clearance

Indirect drug Pharmacokinetic effects

Inter-individual Variation in Drug Response



Concluding comments



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