

Chronic exposure to antiepileptic drugs impacts the gut microbiome community and function

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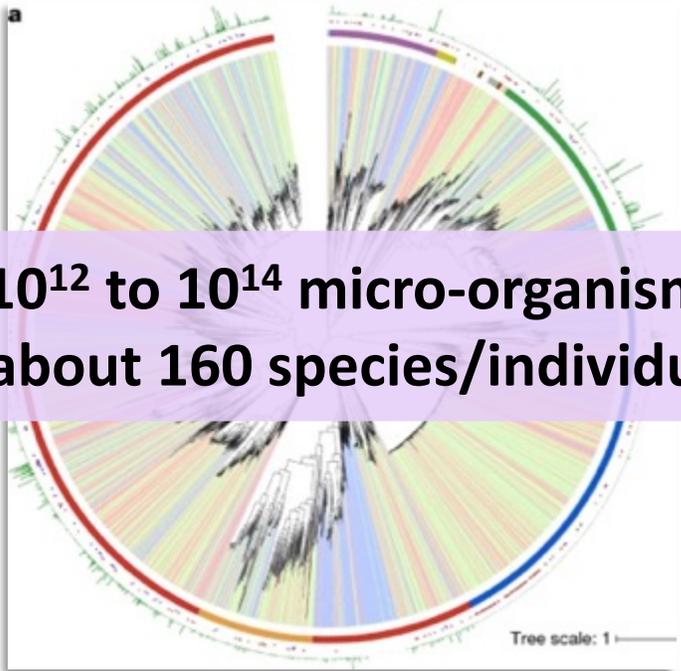
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The human microbiome evolves and adapts over time

Composition

- Phylum
- Actinobacteria
 - Bacteroidetes
 - Cyanobacteria
 - Firmicutes
 - Fusobacteria
 - Proteobacteria
 - Saccharibacteria
 - Spirochaetes
 - Synergistetes
 - Tenericutes
 - Verrucomicrobia



10¹² to 10¹⁴ micro-organisms about 160 species/individual

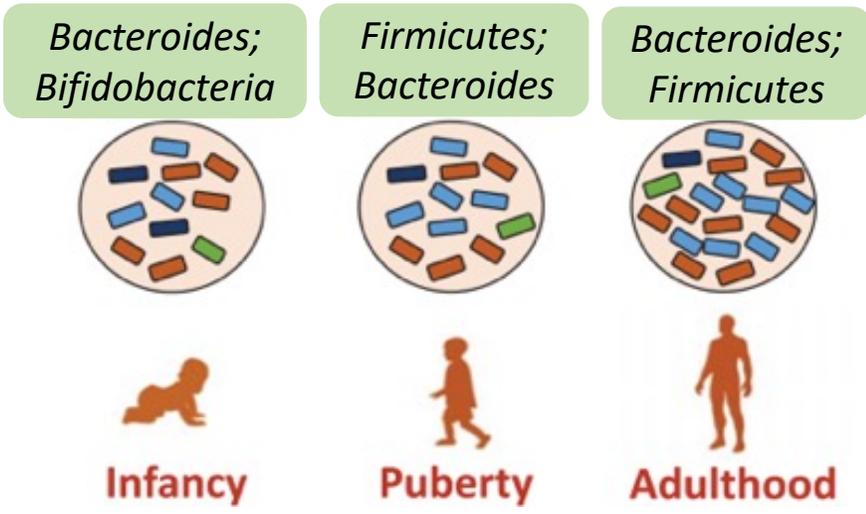
Almeida et al.(2019), Nature

Evolution

Core microbiome

Tentative relative proportions of microbial phyla

- Firmicutes
- Bacteroides
- Actinobacteria
- Proteobacteria



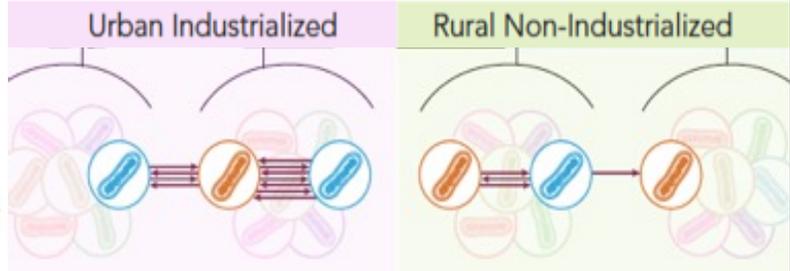
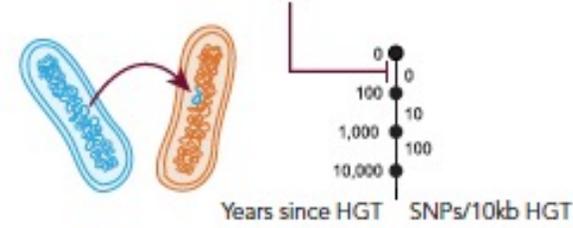
Ravinder et al. (2018), Nutrition and Healthy Aging

Adaptation

Microbiome



Horizontal gene transfer (HGT)



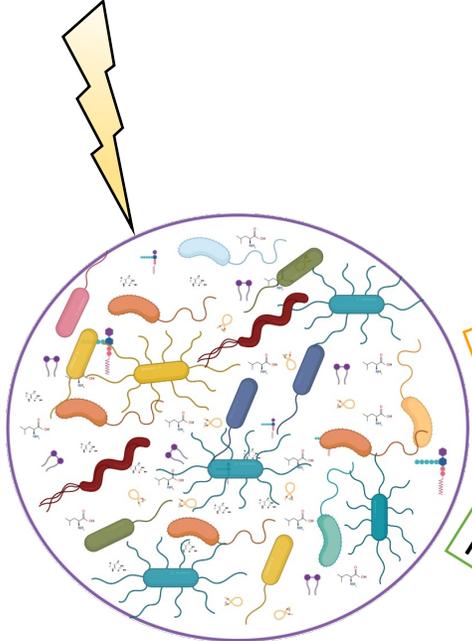
HGT is common in the human microbiome; Increases with industrialisation

Groussin et al. (2021) Cell

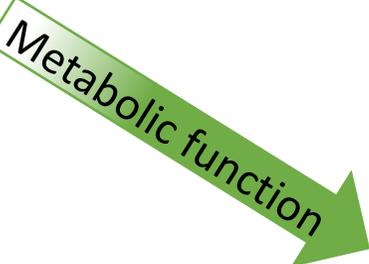
Xenobiotics alter complex microbial communities



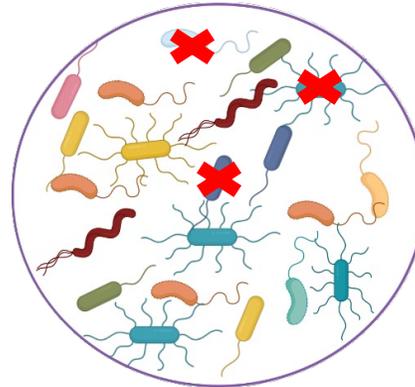
Xenobiotics



microbial communities

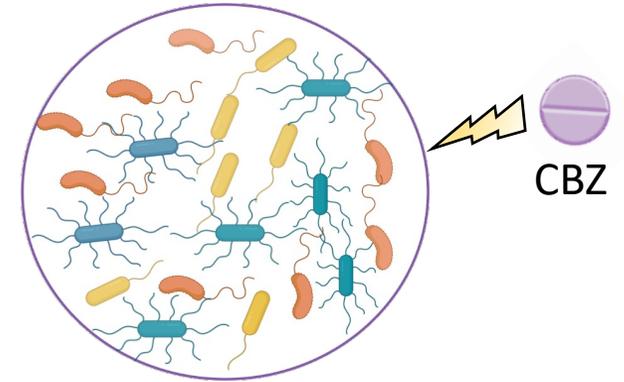


Anti-microbial properties of antipsychotics drugs



Maier et al.(2018), Nature

Shift in the microbial composition

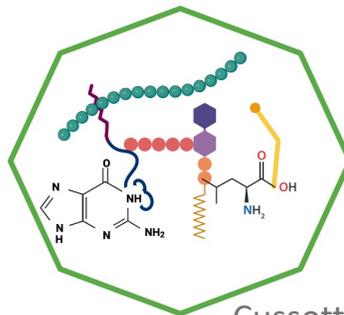


CBZ

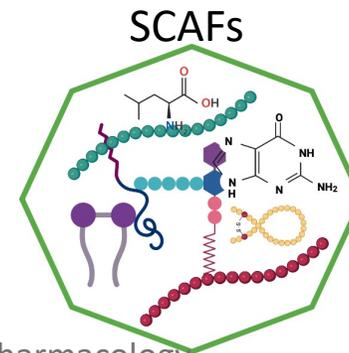
Environmental microbial communities

Zhang et al. (2020), Bioresource Technology

Zhang et al. (2020), Bioresource Technology



Valproate



Propionate and Butyrate

Isovalerate

Cussotto S et al.(2019), Psychopharmacology

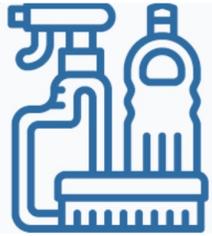
Children's gut microbiome are vulnerable to xenobiotics



Food



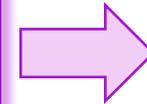
Pesticides



Cleaning supply



Drugs



Antiseizure drugs

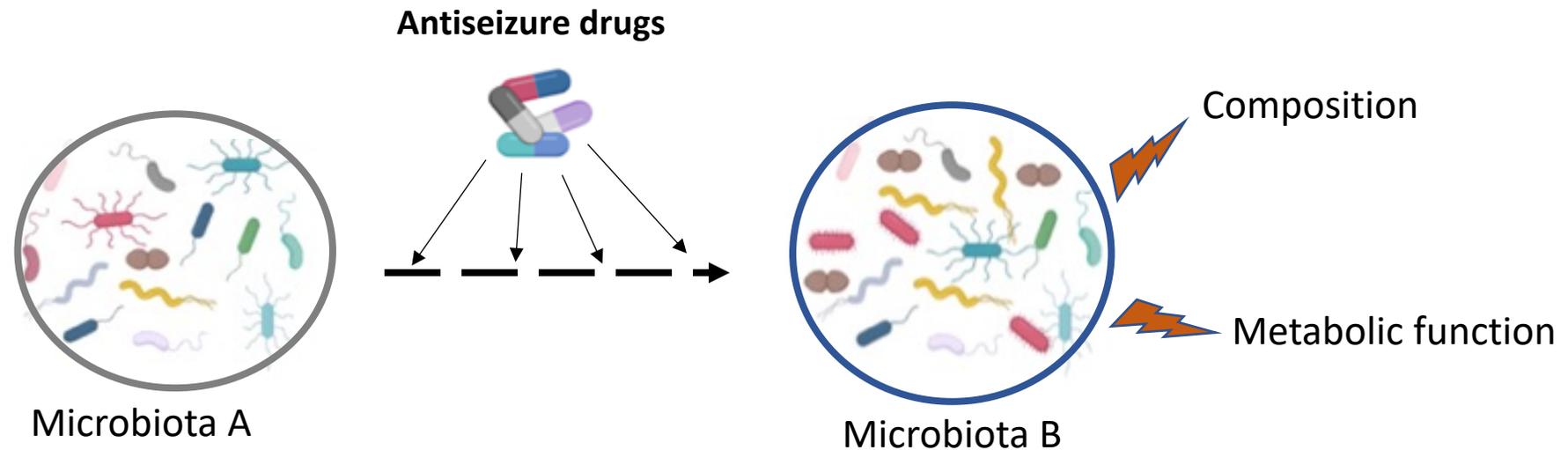


Industrial pollution

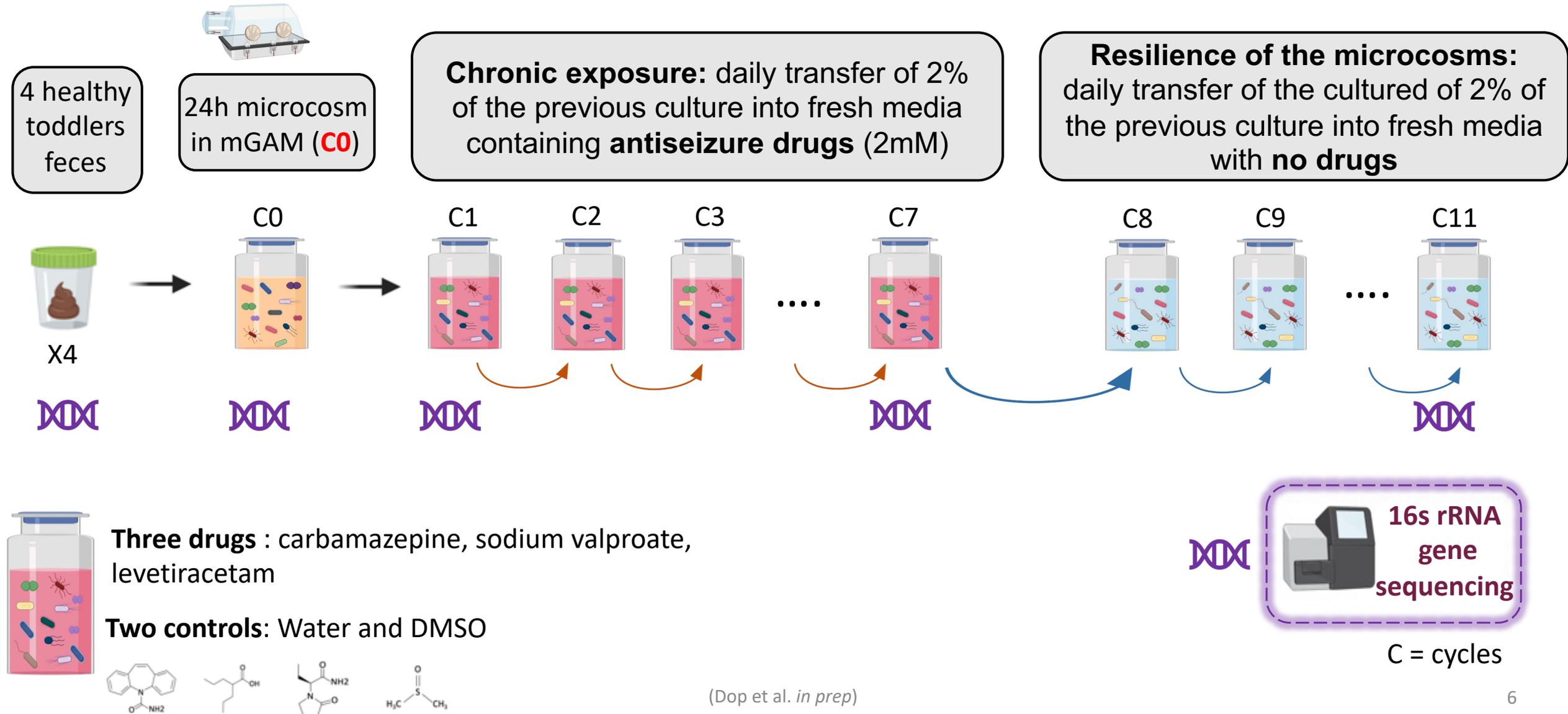


Cream/ shampoo

How does longitudinal exposure to antiseizure drugs (carbamazepine, sodium valproate, and levetiracetam) influence the early life gut microbiome structure and function?

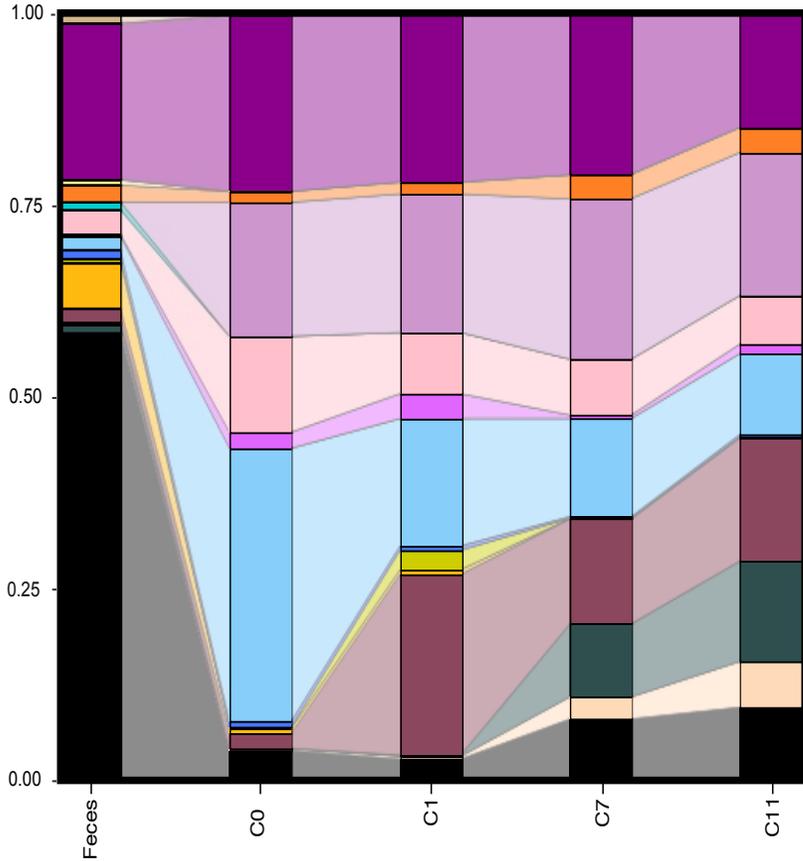


Our experimental approach relied on establishing semi-continuous microcosms

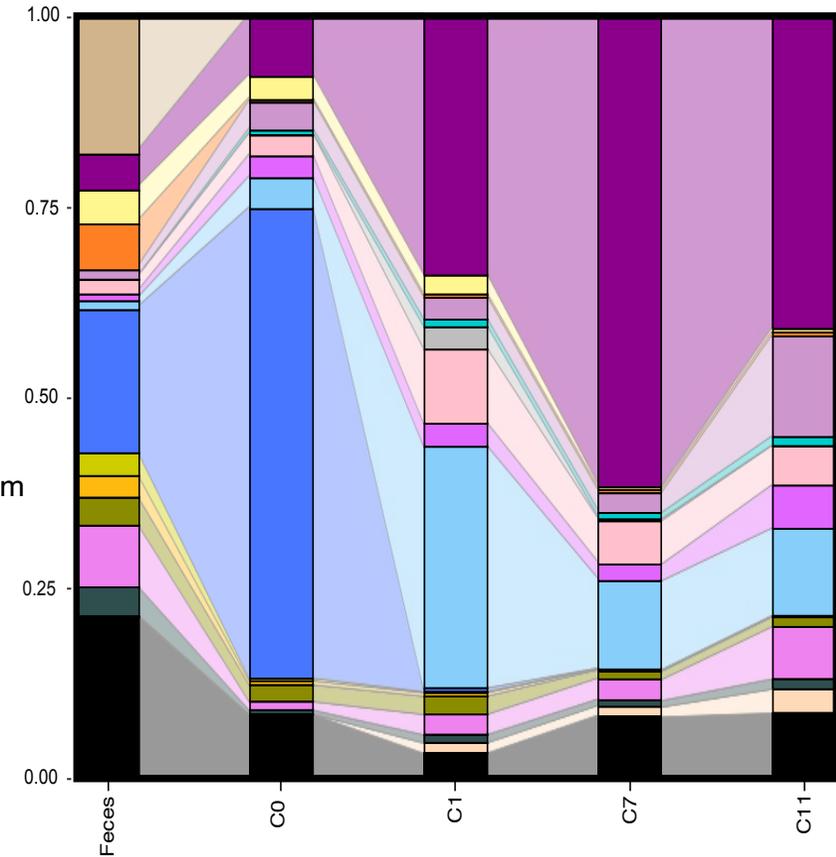


1. Feces composition was the main determinant of the microcosm structure during semi-continuous cultivation

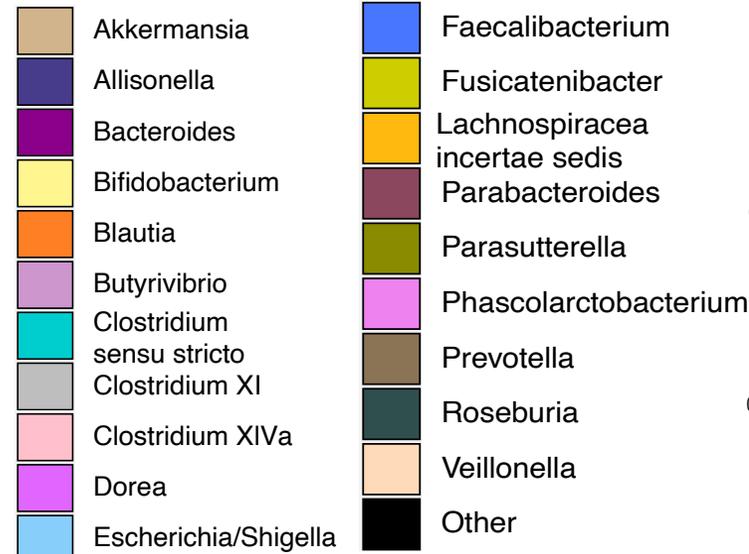
Feces A



Feces D



Genus

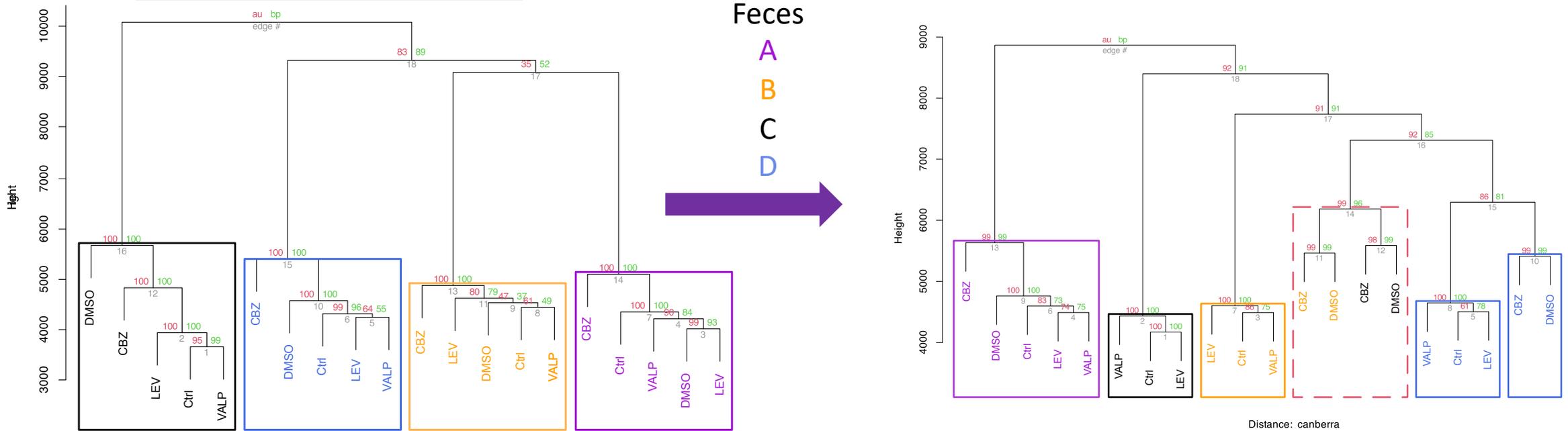


Medium and cultivation strategies generate compositionally different microcosms dependent on the initial feces composition

2. Among the three drugs, carbamazepine had the greatest impact on the microbial communities

Cycle 1 (acute exposure)

Cycle 7 (chronic exposure)



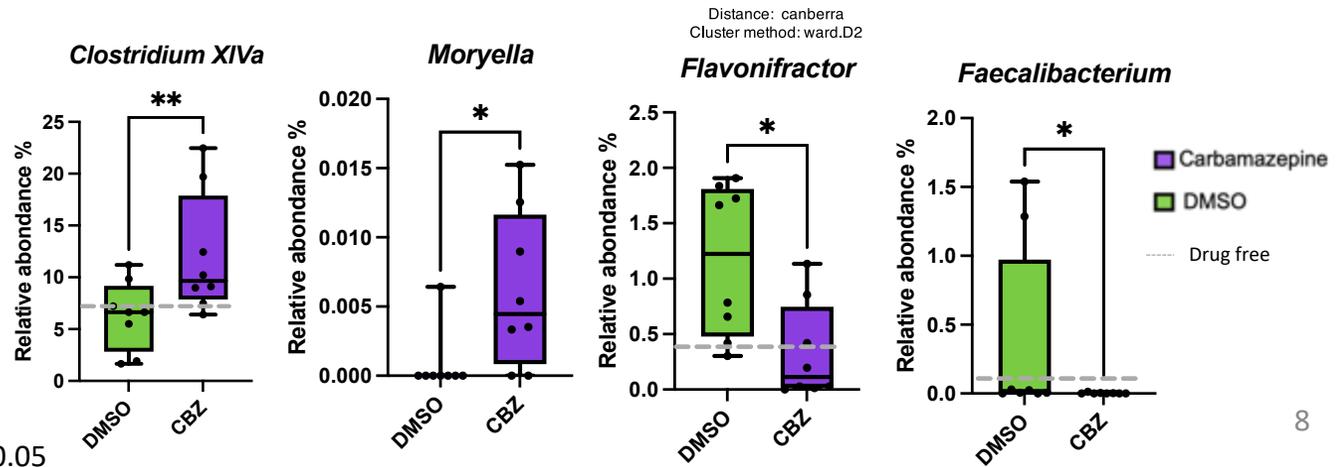
multiscale bootstrap resampling :

and Approximately unbiased (AU) probability values $\geq 95\%$

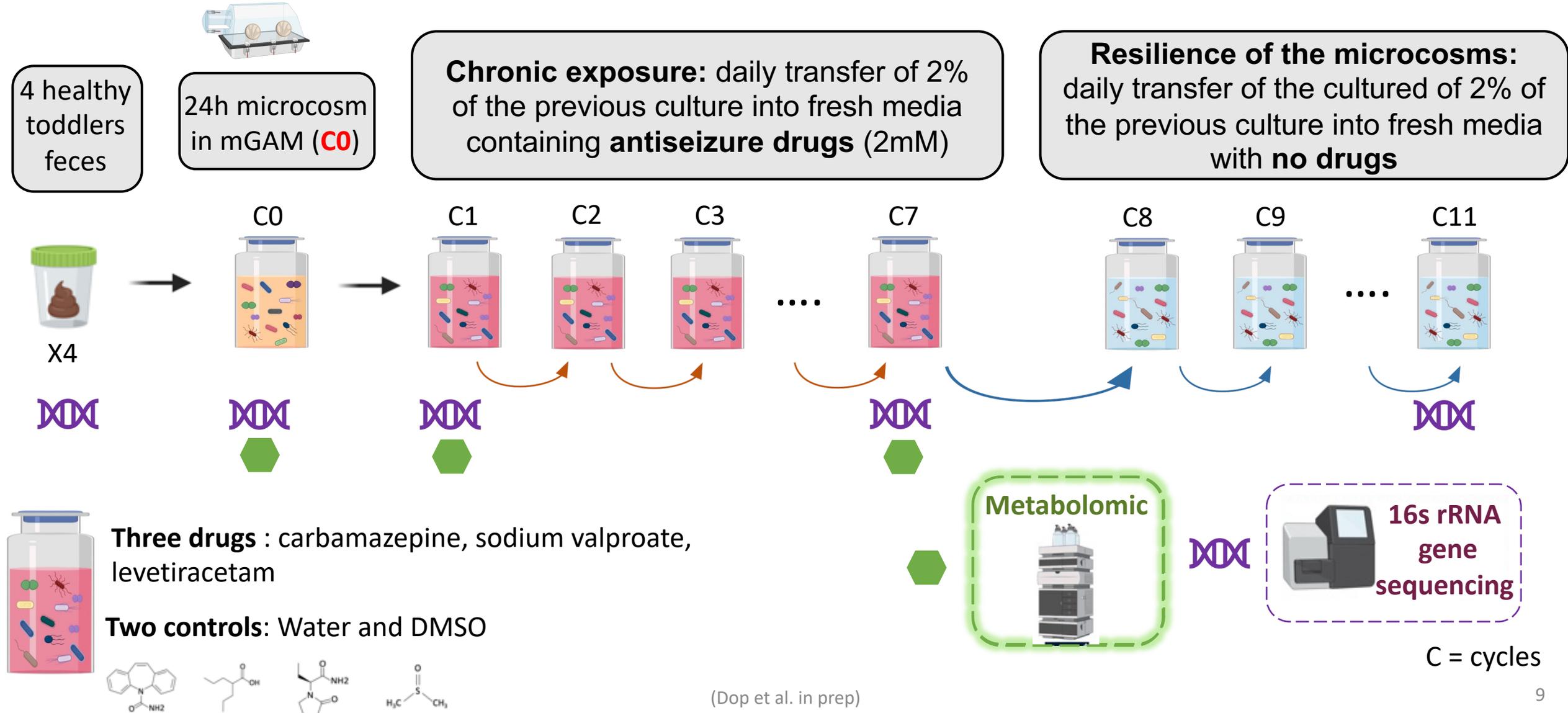
Compare to **acute exposure**, **chronic exposure** to carbamazepine had larger impact

(Dop et al. *in prep*)

Mann-Whitney = * $P < 0.1$ ** $P < 0.05$

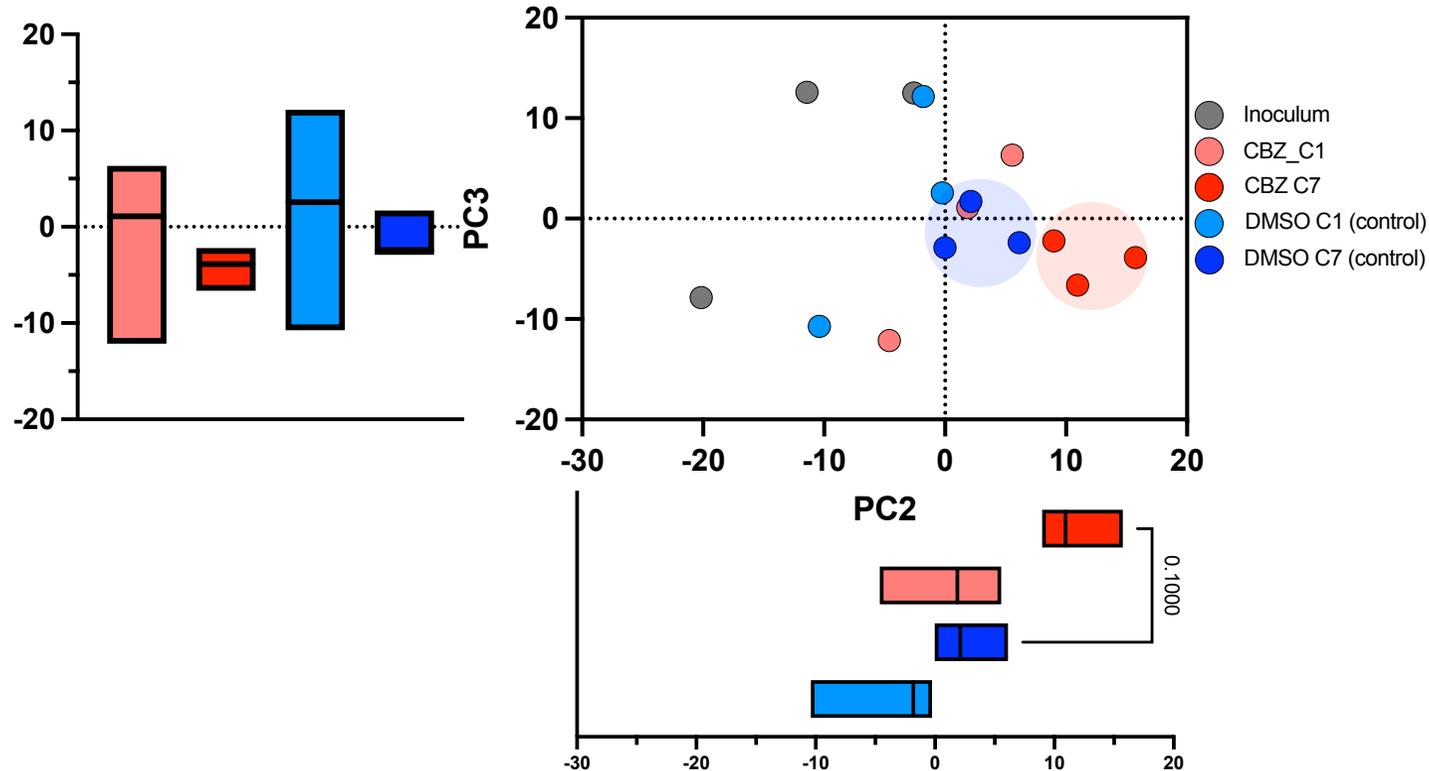


Our experimental approach relied on establishing semi-continuous microcosms



3. Chronic exposure to carbamazepine depleted 52 metabolites.

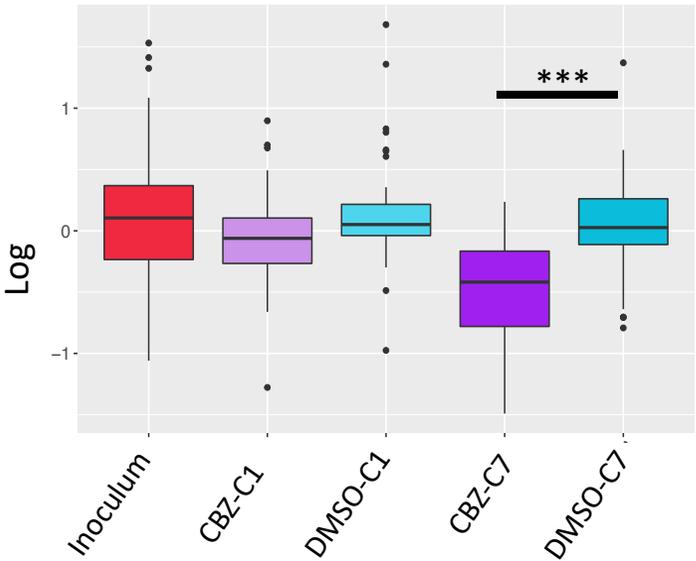
The impact of carbamazepine was greater on metabolomes on C7 than C1



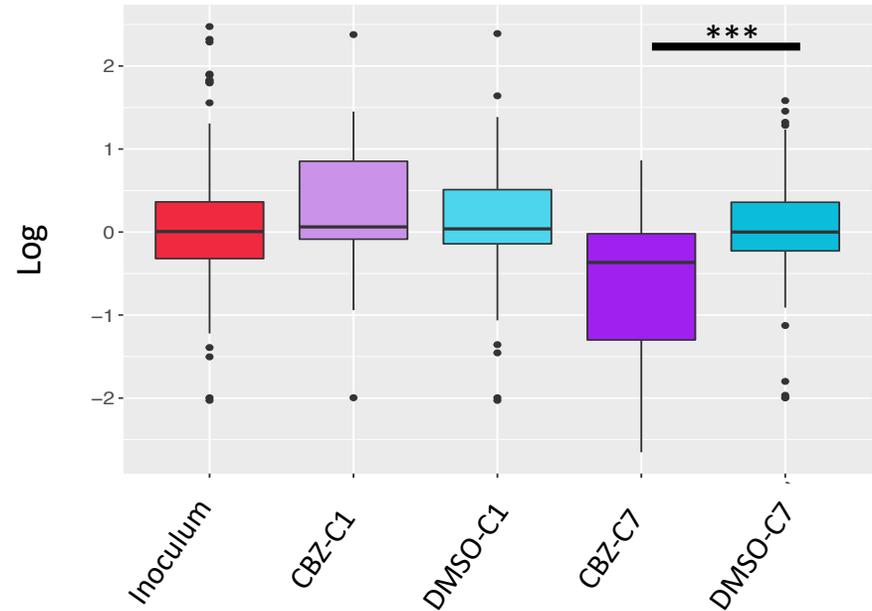
52 metabolites were significantly **lower** in CBZ treatment compared to DMSO control, and **11 metabolites** were significantly **higher**

4. Chronic exposure to carbamazepine leads to a decrease in dicarboxylic acid and dipeptides metabolites in the microcosms

Fatty Acid, Dicarboxylate sub-pathway



Dipeptide, Sub-pathway

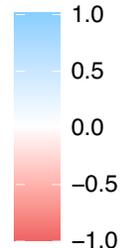


GROUP_NAME

- Inoculum
- Carbamazepine-C1
- DMSO -C1 (Control)
- Carbamazepine-C7
- DMSO -C7 (Control)

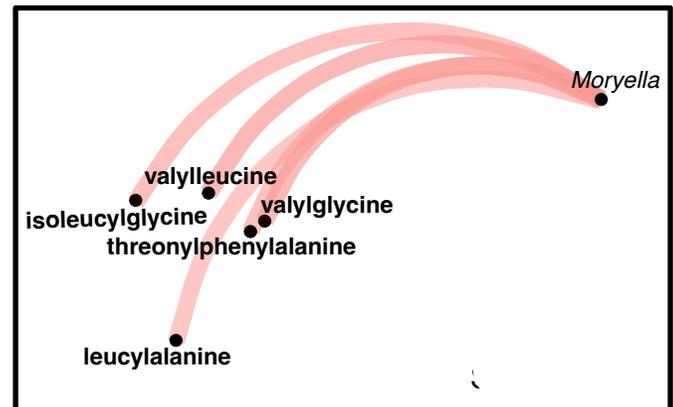
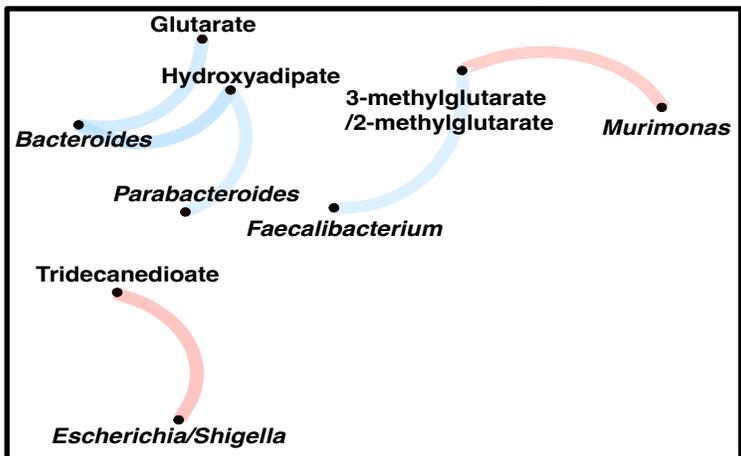
Dunn test = *** P < 0.01

Spearman correlation

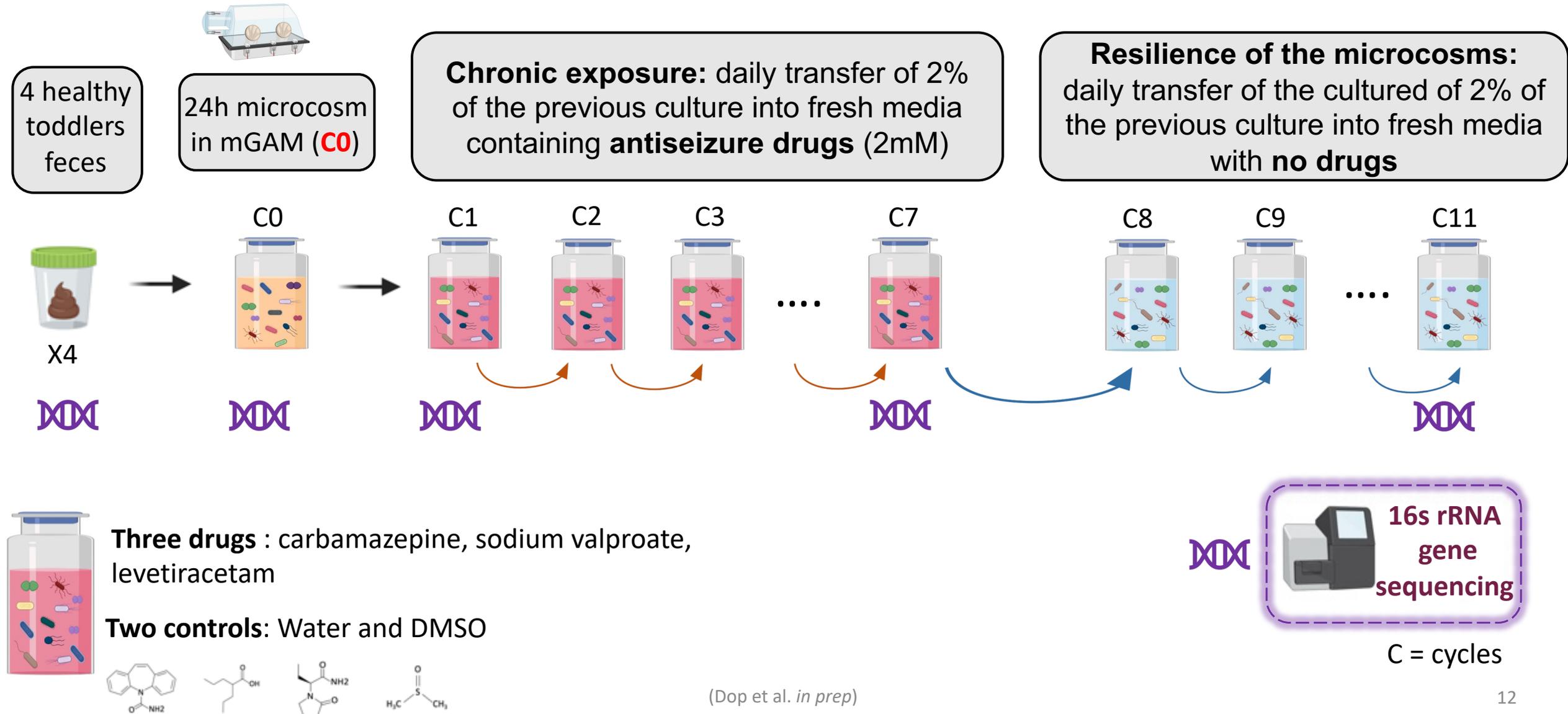


All correlation represented have a p < 0,05

(Dop et al. in prep)

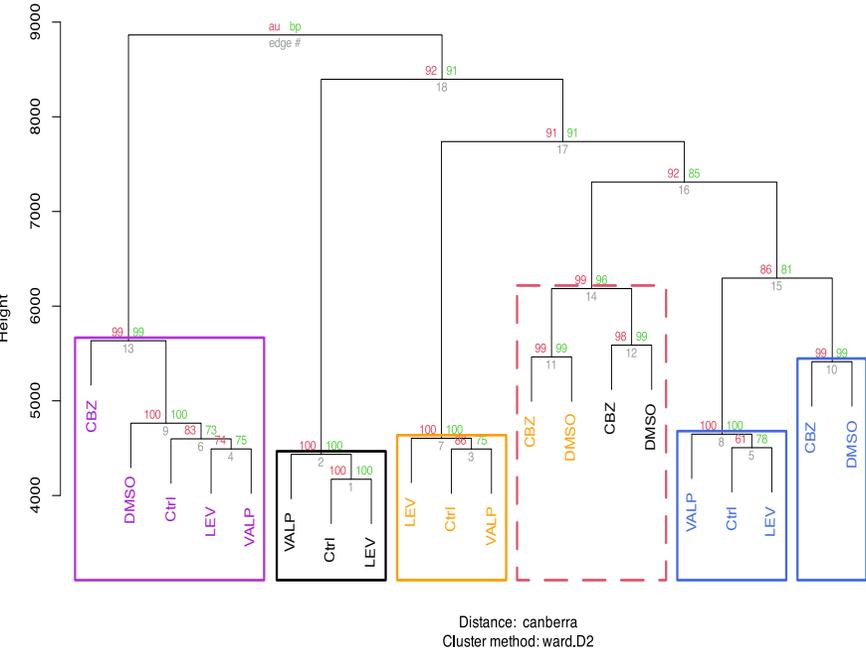


Our experimental approach relied on establishing semi-continuous microcosms



5. Drug-free cycles partially alleviate the impact of carbamazepine

Cycle 7 (chronic exposure)



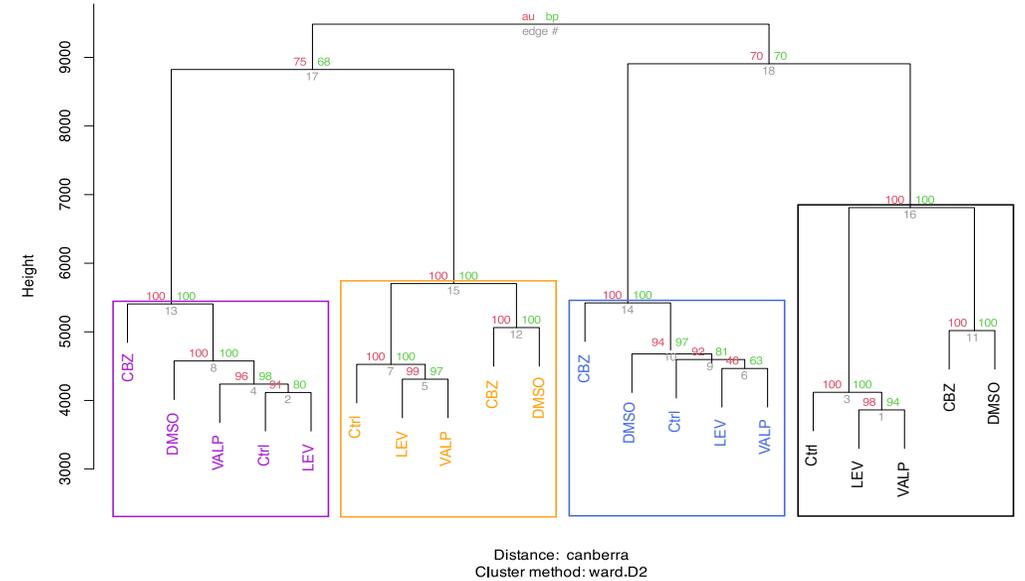
Feces

- A
- B
- C
- D

Drug-free
(4 days)



Cycle 11 (after 4 drug-free cycles)

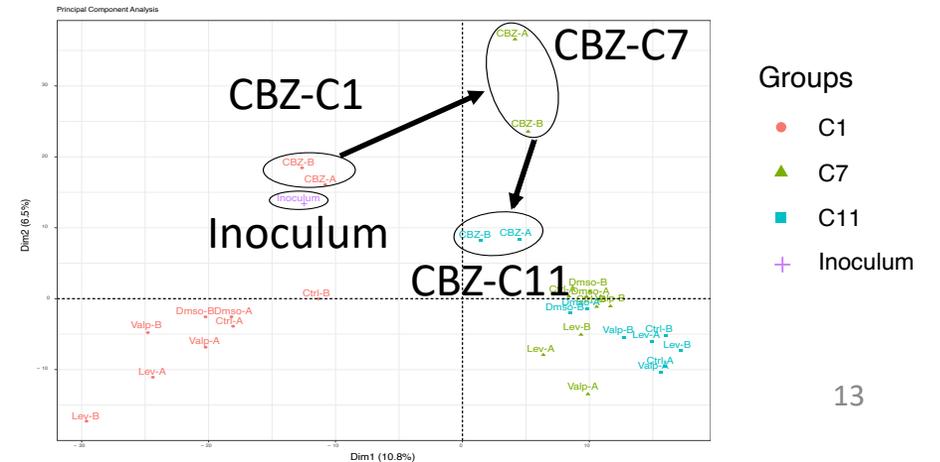


Feces

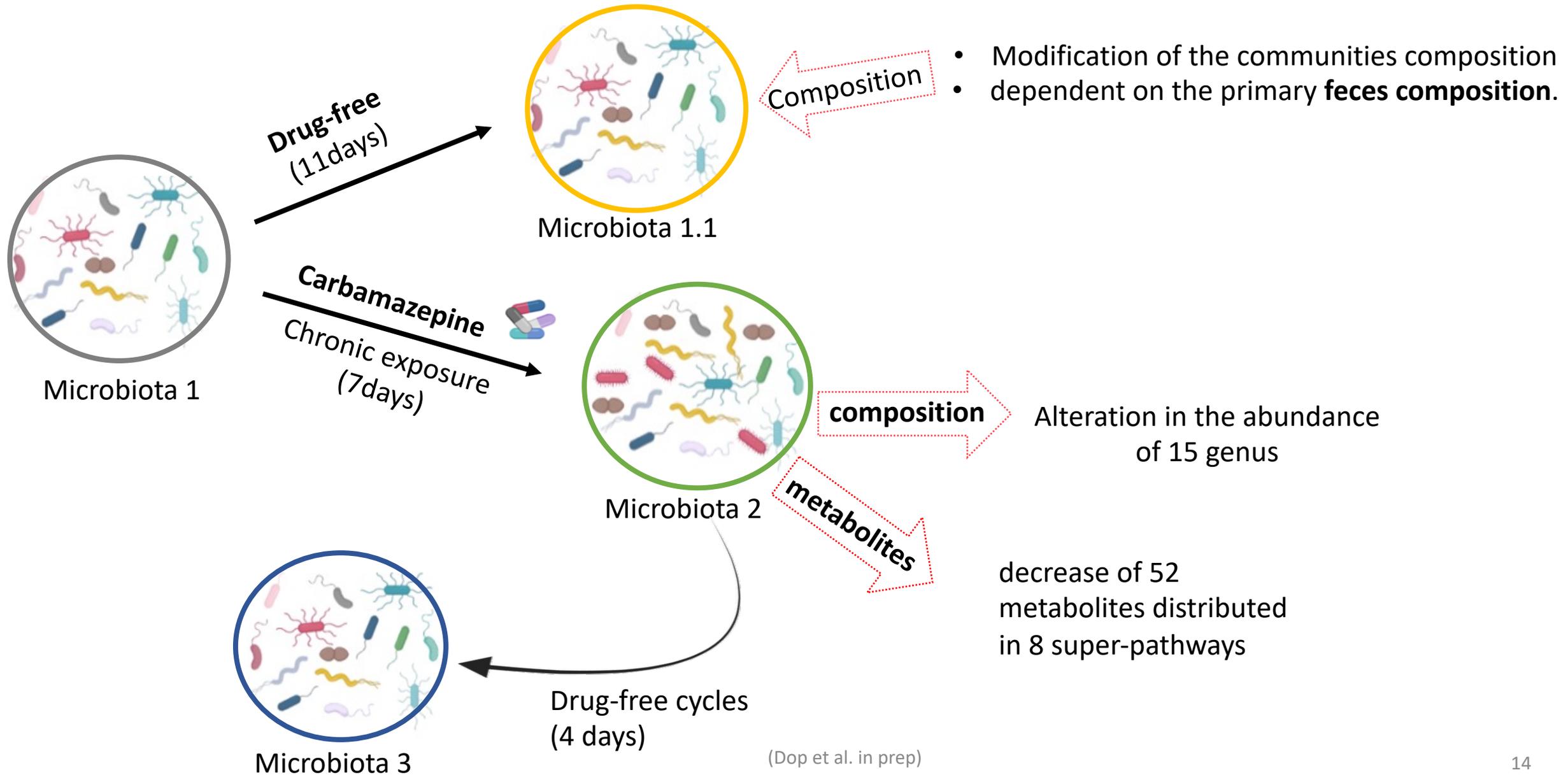
- A
- B
- C
- D

The **Drug-free cycles** allow the microcosm to **partially overcome** the carbamazepine repeated exposure

Feces A (PCA)



Take home message





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we're hiring for a Ph.D. position!

Where to join us!

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