

Supporting Information

Into the wild: microbiome transplant studies need broader ecological reality

Authors

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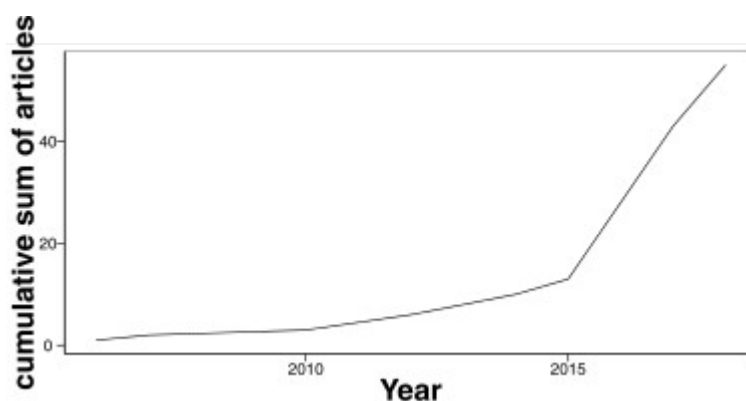
Search terms used for methodological literature search

- Google scholar
 - (transplant* AND microbio) (gut OR fecal OR feces OR gastrointestinal OR gastro-intestin* OR faecal OR faeces OR forces OR faecal) -human -patient -"homo sapiens" -man -woman -child*
- Web of Science
 - ((TOPIC:(transplant) AND TOPIC: (microbio))AND (TOPIC: (((((((gut OR fecal) OR feces) OR gastrointestinal) OR gastro-intestin) OR faecal) OR faeces) OR foeces) OR faecal) NOT TOPIC:((((human OR patient) OR homo sapiens) OR man) OR woman) OR child*)))

Table S1 Ordinal data scale (EcoReality score) for each experimental condition

Experimental Condition	Ordinal Data Scale
Taxon Match	1 = Mismatch (different species) 2 = Match (same species)
Donor Environment	1 = Lab animal host in sterile lab 2 = Lab animal host in non-sterile lab 3 = Captive bred wildlife (multiple generations bred in captivity) 4 = Wildlife brought into captivity (no generations bred in captivity) 5 = Free-ranging wildlife (capture and release)
Donor Physiology	1 = Gene knockout or disease harbouring (non-microbial) 2 = Wildtype non-diseased
Transplanted Microbiome	1 = Single strain 2 = Consortium, mixture of select strains

	3 = Whole community (no sorting or altering of community sampled for transplantation)
Transplant Method	1 = Active (microbiome sample forcefully added to recipient gut e.g., by a suppository or oral gavage) 2 = Passive (microbiome sample passively given to recipient e.g., mixed into food)
Recipient Microbiome	1 = Germ-free 2 = Antibiotic perturbed/pathologic 3 = Whole community (no experimental alteration of community)
Recipient Environment	1 = Lab animal host in sterile lab 2 = Lab animal host in non-sterile lab 3 = Captive bred wildlife (multiple generations bred in captivity) 4 = Wildlife brought into captivity (no generations bred in captivity) 5 = Free-ranging wildlife (capture and release)
Recipient Physiology	1 = Gene knockout or disease harbouring (non-microbial) 2 = Wildtype or non-diseased
Housing Conditions	1 = Housed singly (after microbiome transplantation) 2 = Co-housed (after microbiome transplantation with either other replicates in the experiment or with individuals of the same species that were not replicates. Co-housing could also have been used as the method of transplantation)



SI Figure 1 Cumulative sum of articles from our directed review between 2006 and 2018.

Data accessibility

The data, the above supporting information, and the R script for this manuscript are in a repository on GitHub. This repository can be cloned or downloaded straight from Github (https://github.com/cgreysongaito/Intothewild_Microbiome) or from Zenodo (<https://doi.org/10.5281/zenodo.2652255>).

Folder and file structure of Github repository (Intothewild_Microbiome)

- data
 - EcoRealTable_2019-10-09_Data.csv
- figs
 - 2019-10-09 CountAnimals.pdf – Figure 2 in manuscript
 - 2019-10-09 Eco-realityComparisons.pdf – Figure 3 in manuscript
 - 2019-10-09 Eco-realityAverageStandardOverTime.pdf – Figure 4 in manuscript
 - 2019-10-09 CumulativeSumArticles.pdf – Supporting Information Figure 1
- .gitignore – File containing files or folders that git should ignore
- IntotheWild_Microbiome_Greyson-Gaito_etal_2019.R – R script for analysis and figure creation
- SupportingInformation_Intothewild_GreysonGaitoetal.pdf – Supporting information (search terms, ordinal data scales, figure)
- LICENSE – Mozilla Public License 2.0
- README.md – Important information
- meta_transplant_microbiome.Rproj – R Project to increase ease of use

Instructions for use

- Download the whole repository (either by forking and cloning or by downloading a ZIP folder)
- In RStudio, open the project called meta_transplant_microbiome.Rproj and open the file IntotheWild_Microbiome_Greyson-Gaito_etal_2019.R
 - If not using RStudio, open the file IntotheWild_Microbiome_Greyson-Gaito_etal_2019.R and edit the path to the data file called Microbiome_Literature_Summaries.csv to whatever path is required on your computer.
- Run the script in RStudio or however you normally run R scripts