

Supporting Information

Into the wild: microbiome transplant studies need broader ecological reality

Authors

Christopher J. Greyson-Gaito*^{1†}, Timothy J. Bartley^{1,2†}, Karl Cottenie^{1†}, William Jarvis^{3†}, Amy E.M. Newman^{1†}, Mason R. Stothart^{4†}

Affiliations

*Corresponding author - christopher@greyson-gaito.com

1. University of Guelph, Department of Integrative Biology, Guelph, ON, Canada
2. University of Toronto Mississauga, Mississauga, ON, Canada
3. University of Ottawa, Department of Biology, Ottawa, ON, Canada
4. University of Calgary, Calgary, AB, Canada

†All authors contributed equally

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)

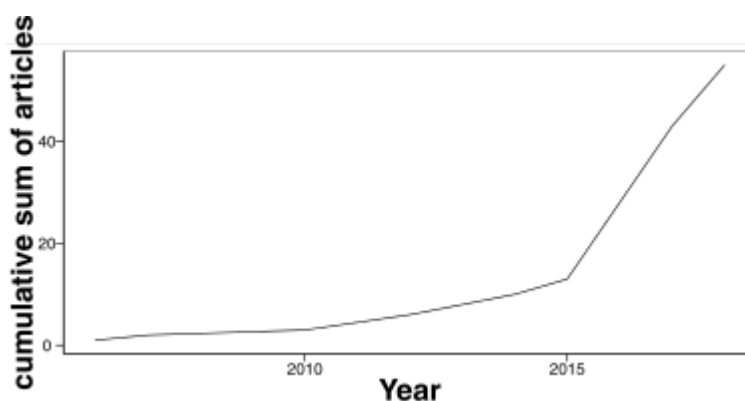


Figure S1 Cumulative sum of articles from our directed review between 2006 and 2018.

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 EcoRealTable_2019-10-09_Data.csv to whatever path is required on your computer.
- Run the script in RStudio or however you normally run R scripts