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 gastrointestin 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 gastrointestin) 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*)))

Ordinal data scale (EcoReality score) for each experimental condition

Experimental Condition	Ordinal Data Scale
Taxon Match	1 = Mismatch 2 = Match
Donor Environment	1 = In-Lab in sterile environment 2 = Lab animal host in Non-Sterile Lab 3 = Captive Bred Wildlife (long time difference between capture and transplant) 4 = Wildlife brought into captivity (short time difference between capture and transplant) 5 = Free-Ranging Wildlife

Experimental Condition	Ordinal Data Scale
Donor Physiology	1 = Gene knockout/disease harbouring (non-microbial) 2 = Wildtype non-diseased
Transplanted Microbiome	1 = Single Strain 2 = Consortium, mixture of select strains 3 = Whole community
Transplant Method	1 = Active (e.g., suppository, oral gavage) 2 = Passive (e.g., mixed into food)
Recipient Microbiome	1 = Germ-Free 2 = Antibiotic Perturbed/Pathologic 3 = Whole community
Recipient Environment	1 = Lab animal host in Sterile Lab 2 = Lab animal host in Non-Sterile Lab 3 = Captive Bred Wildlife 4 = Wildlife brought into captivity 5 = Free-Ranging Wildlife
Recipient Physiology	1 = Gene knockout or disease harbouring (non-microbial) 2 = Wildtype or non-diseased
Housing Conditions	1 = Housed Singly 2 = Co-Housed
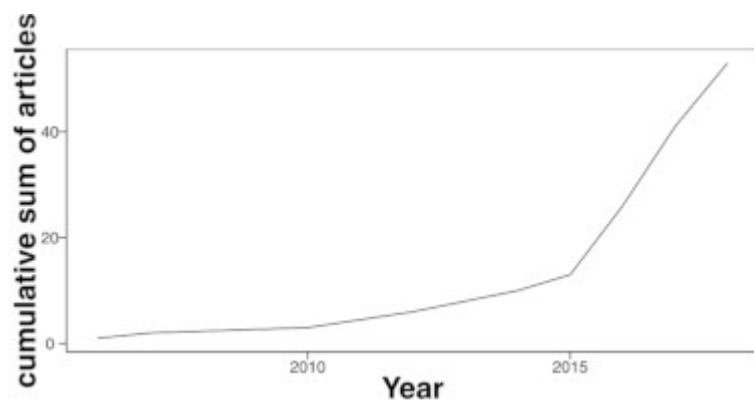
SI Figure 1 Cumulative sum of articles from our directed review between 2006 and 2018.

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_2019-03-25_Data.csv
- figs
  - 2019-03-07 CountAnimals.pdf – Figure 2 in manuscript
  - 2019-03-07 Eco-realityComparisons.pdf – Figure 3 in manuscript
  - 2019-03-07 Eco-realityAverageStandardOverTime.pdf – Figure 4 in manuscript
  - 2019-04-25 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
- GreysonGaitoetal_Intothewild_SupportingInformation.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