# Data Files

Presented is the metadata corresponding to the data files in „Data“.

## anc\_evo\_growth\_metrics\_initial.tsv

Initial trait data for the ancestral and evolved populations of species in the 24 species community. For each species there are 8 replicates per predator absence/presence.

Rows: Observations per species and replicate

Columns:

Species contains the HAMBI identifier for each species (see “Community\_species\_list.csv” for matching species names).

Tetrahymena presence (yes) or absence (no) of the ciliate predator

bacteria\_history Evolutionary history of the prey. Either “anc” for ancestral or “evo” for evolved.

Replicate denotes one of eight replicates per species and predator absence/presence

auc\_log area under the curve (in units of log OD, and based on user-specified of time, estimate from fit)

gr maximum specific growth rate, estimate from fit

k\_lin carrying capacity (in units of OD, assumes that OD starts at 0, estimate from fit)

OD\_Min minimum optical density (600nm) measured after 96h of growth

OD\_Max maximum optical density (600nm) measured after 96h of growth -> the “carrying capacity” trait in predator absence

## [Ancestral Initial Traits AMiGA.txt](https://github.com/JmHof/Community_Experiment/blob/main/Data/Ancestral%20Initial%20Traits%20AMiGA.txt)

Initial trait data for the ancestral populations of species in the 24 species community. This file is a subset of “anc\_evo\_growth\_metrics\_initial.tsv” and contains median trait values from each 8 replicates.

Rows: each row represents observations for one of the 24 species.

Columns:

Species contains the HAMBI identifier for each species (see “Community\_species\_list.csv” for matching species names).

Prey\_history evolutionary history of the prey – “ANC” for ancestral

OD\_alone maximum optical density (600nm) measured after 96h of growth in absence of predators – median values from 8 replicates. -> the “carrying capacity” trait

OD\_with\_predator maximum Optical density (600nm) measured after 96h of growth in presence of predators – median values from 8 replicates.

Defence anti-predator defence calculated as log(OD\_with\_predator/OD\_alone)

## [Evolved Initial Traits AMiGA.txt](https://github.com/JmHof/Community_Experiment/blob/main/Data/Ancestral%20Initial%20Traits%20AMiGA.txt)

Initial trait data for the evolved populations of species in the 24 species community. This file is a subset of “anc\_evo\_growth\_metrics\_initial.tsv” and contains median trait values from each 8 replicates.

Rows: each row represents observations for one of the 24 species.

Columns:

Species contains the HAMBI identifier for each species (see “Community\_species\_list.csv” for matching species names).

Prey\_history evolutionary history of the prey – “EVO” for evolved.

OD\_alone maximum optical density (600nm) measured after 96h of growth in absence of predators. -> the “carrying capacity” trait

OD\_with\_predator maximum Optical density (600nm) measured after 96h of growth in presence of predators

Defence anti-predator defence calculated as log(OD\_with\_predator/OD\_alone)

## Bacterial\_densities.txt

Optical densities (600nm) measurements of microcosms during the community mis-match experiment.

Rows: observations per microcosm and time point (and transfer category)

Columns:

transfer\_category relative volume transferred to next batch culture (only “hi” = high relevant for this manuscript\*)

transfer\_volume\_ul absolute amount of volume in µl transferred to next batch culture (only “1800µl” (=”hi”) relevant for this manuscript\*)

replicate one of six microcosms per condition (only replicates A,C,E relevant for this manuscript\* because for others there is no trait data)

prey\_history evolutionary history of the prey. Either “anc” for ancestral or “evo” for evolved.

predator\_history evolutionary history of the predator. Either “anc” for ancestral or “evo” for evolved.

time\_days time in days after the start of the community mis-match experiment

bacteria\_od culture optical density (600nm)

## Ciliate\_cell\_counts.tsv

Cell density estimates of predators in microcosms during the community mis-match experiment.

Rows: observations per microcosm and time point (and transfer category)

Columns:

time\_days time in days after the start of the community mis-match experiment

replicate one of six microcosms per condition (only replicates A(=1),C(=3),E(=5) relevant for this manuscript\* because for others there is no trait data)

transfer\_volume absolute amount of volume in µl transferred to next batch culture (only “1800µl” (=”hi”) relevant for this manuscript\*)

prey\_history evolutionary history of the prey. Either “anc” for ancestral or “evo” for evolved.

predator\_history evolutionary history of the predator. Either “anc” for ancestral or “evo” for evolved.

cells\_mL predator density in cells per millilitre

## experiment\_clones\_traits.txt

Contains trait measurement of clones during the Community mis-match experiment

Rows: observations for each isolated clone

Columns:

Plate microtiter plate on which the sample was located

Well well on the microtiter plate in which the sample was

incubation\_length\_hours

length of incubation after which cloneOD and clone\_plus\_ciliateOD were assessed. “96” corresponds to 96h and was used for analysis

cloneOD maximum optical density (600nm) measured after 96h of growth in absence of predators. -> the “carrying capacity” trait

clone\_plus\_ciliateOD maximum Optical density (600nm) measured after 96h of growth in presence of predators

prey evolutionary history of the predator.

Predator evolutionary history of the predator.

Replicate replicate microcosm from which the clone was isolated.

ciliate\_detected indicates whether living predators were detected after 96h

experiment\_day time in days after the start of the community mis-match experiment

OD difference difference between clone\_plus\_ciliateOD and cloneOD

Defence anti-predator defence calculated as log(clone\_plus\_ciliateOD / cloneOD)

## [metadata.tsv](https://github.com/JmHof/Community_Experiment/blob/main/Data/metadata.tsv)

Meta data for 16s rRNA amplicon sequencing counts. This file was combined with “sequencing\_counts.tsv” to yield “sequencing\_counts and metadata.csv”.

Rows: represent each a sample per microcosm and time point in the sequencing pipeline – matches to sample names in “sequencing\_counts.tsv”

Columns:

Sample sample name in sequencing pipeline. see above

old\_sample\_number an old sample number (not relevant)

transfer\_volume absolute amount of volume in µl transferred to next batch culture (only “1800µl” (=”hi”) relevant for this manuscript\*)

replicate one of six microcosms per condition (only replicates A(=1),C(=3),E(=5) relevant for this manuscript\* because for others there is no trait data)

prey\_history evolutionary history of the prey. Either “ANC” for ancestral or “EVO” for evolved.

predator\_history evolutionary history of the predator. Either “ANC” for ancestral or “EVO” for evolved

time\_days time in days after the start of the community mis-match experiment

## sequencing\_counts.tsv

16s rRNA amplicon sequencing counts in microcosms of the community mis-match experiment.

Rows: represent each an observation per species, microcosm and time point

Columns:

Sample sample name in sequencing pipeline - matches to sample names in “metadata.tsv”

strainID HAMBI identifier for each species (see columns “genus” + “species” and “Community\_species\_list.csv” for matching species names).

genus matching genus to the HAMBI identifier in “strainID”

species matching species name to the HAMBI identifier in “strainID”

count counts from the corresponding species detected by 16s rRNA amplicon sequencing

## [sequencing\_counts and metadata.csv](https://github.com/JmHof/Community_Experiment/blob/main/Data/sequencing_counts%20and%20metadata.csv)

“[metadata.tsv](https://github.com/JmHof/Community_Experiment/blob/main/Data/metadata.tsv" \o "metadata.tsv)” and “sequencing\_counts.tsv” combined

## Community\_species\_list.csv

List of 24 species in the community

Rows: one per species

Columns:

strainID HAMBI identifier for each species (see columns “genus” + “species” and “Community\_species\_list.csv” for matching species names).

genus matching genus to the HAMBI identifier in “strainID”

species matching species name to the HAMBI identifier in “strainID”

## Predator\_selection\_species\_list.xlsx

List of the seven species used in the selection lines to generate the evolved predator population.

Rows: one per species

Columns:

strainID identifier for each species as specified by the source culture collection

genus matching genus to the identifier in “strainID”

species matching species name to the identifier in “strainID”

\*data for the presented manuscript/analysis was acquired alongside other samples that were not directly relevant to our analysis/hypothesis. However, this additional data is partly contained in the data files because this is the way I received the data. In the derived data files used for the analyses the non-relevant data is removed.