Corresponding Author: Prof. Dominik N. Müller

Date: Sep 25, 2017

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work we publish. This form is published with all life science papers and is intended to promote consistency and transparency in reporting. All life sciences submissions use this form; while some list items might not apply to an individual manuscript, all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

Experimental design

1. Sample size

   Describe how sample size was determined.

   Power calculation is a prerequisite for any animal experiment according to the local animal law and was performed using G*Power Software Version 3.1.9.2. Effect sizes were calculated from previously published experiments.

2. Data exclusions

   Describe any data exclusions.

   Data exclusion criteria were pre-established. Technical failures were excluded. Outliers were excluded only after statistical testing. Outlier testing was performed using Grubbs' test (see statistics in Methods section).

3. Replication

   Describe whether the experimental findings were reliably reproduced.

   All findings shown have been reproduced in at least two independent experiments. The number of replicates is given in the respective figure legends. Individual values are shown in each figure.

4. Randomization

   Describe how samples/organisms/participants were allocated into experimental groups.

   Animals were randomly assigned to the respective body weight matched groups. For the clinical studies, participants were included if pre-specified exclusion criteria were absent. Randomization was not necessary for the clinical study because of the absence of different treatment groups (prospective longitudinal design).

5. Blinding

   Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

   Animals were randomly assigned to the respective body weight-matched groups, probiotic and control treatment were administered without knowledge of the treatment groups. The human pilot study was performed in an unblinded manner. Data analysis was performed by the investigators without knowledge of the treatment groups or treatment phase, respectively.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or the Methods section if additional space is needed).

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒	A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly.
☐	☒	A statement indicating how many times each experiment was replicated
☐	☒	The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
☒	☐	A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒	The test results (e.g. *p* values) given as exact values whenever possible and with confidence intervals noted
☐	☒	A summary of the descriptive statistics, including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☐	☒	Clearly defined error bars

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.

We state and cite all packages and software tools in the Methods section. Statistical analysis was performed using GraphPad Prism 6 and R (Version 3.1.1 R Foundation, Vienna, Austria) using the packages 'lme4' and 'nlme'. Furthermore the R 'survival', 'vegan', 'ape'; Python's scikit-learn module. Code used for the 16S rDNA data analysis has been uploaded to a github repository (https://github.com/almlab/analysis-salt-responsive). Software was obtained from publicly available sources; papers describing the software are cited in the text.

For all studies, we encourage code deposition in a community repository (e.g. GitHub). Authors must make computer code available to editors and reviewers upon request. The *Nature Methods* guidance for providing algorithms and software for publication may be useful for any submission.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

No unique materials have been used.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

Antibodies used for mouse flow cytometry analysis: aCD3ε-FITC clone 17A2, aCD3ε-VioBlue clone 17A2, aCD4-APC-Vio770 clone GK1.5, aCD4-Pacific Blue/FITC clone RM4-5, aCD25-VioBlue/FITC clone 7D4, aFoxP3-PerCP-Cy5.5 clone FJK-16s, aIFN-γ-PE-Cy7/APC clone XMG1.2 PE-Cy7/APC, aIL-17A-PE clone eBio17B7, aRORγt-APC clone REA278. Antibodies used for human flow cytometry analysis: aCD3-PerCP-Vio700 clone BW264/56, aIL-17A-APC-Vio770 clone CZ8-2361, aTNF-α-eFlour450 clone Mab11. Antibodies are also described in the Methods section. Specificity of the antibodies has been validated by using isotype controls and FMO controls.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

No eukaryotic cell lines were used, ony primary murine cells.

b. Describe the method of cell line authentication used.

No eukaryotic cell lines were used, ony primary murine cells.

c. Report whether the cell lines were tested for mycoplasma contamination.

No eukaryotic cell lines were used, ony primary murine cells.

d. If any of the cell lines used in the paper are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.

No commonly misidentified cell lines were used.

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

All animal experiments have been approved by local authorities, registration numbers are given in the Methods section. The following inbred mouse species were used: FVB/N, C57BL/6J. Supplier and age (10-12 weeks) of the mice as well as housing conditions are provided for each experiment in the Methods section. Only male mice were used.

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

Only healthy male participants were recruited. Study population was homogeneous with regard to age, ethnicity, socioeconomic status, weight, BMI, diet (omnivore) and blood pressure. Baseline characteristics are shown in the Supplementary Information, Table 1.

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Flow Cytometry Reporting Summary

Form fields will expand as needed. Please do not leave fields blank.

Data presentation

For all flow cytometry data, confirm that:

☒ 1. The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ 2. The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ 3. All plots are contour plots with outliers or pseudocolor plots.

☒ 4. A numerical value for number of cells or percentage (with statistics) is provided.

Methodological details

5. Describe the sample preparation.	Murine cells were isolated from the spleens and intestines as described in the Methods section. Human PBMC were isolated from peripheral venous blood as described in the Methods.
6. Identify the instrument used for data collection.	BD FACSCanto II system
7. Describe the software used to collect and analyze the flow cytometry data.	BD FACSDiva software was used for data collection and FlowJo v10 for data analysis.
8. Describe the abundance of the relevant cell populations within post-sort fractions.	Purity of the sorted T cell fractions was confirmed by flow cytometry resulting in a purity of the sorted cells of >95%.
9. Describe the gating strategy used.	A representative plot and gating is provided with every flow cytometry figure.

Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information. ☐