

STORMS Checklist for "Sugar-rich foods exacerbate antibiotic-induced microbiome disruption" by Dai *et al.*

Version:	1.03					
Number	Item	Recommendation	Item Source	Additional Guidance	Yes/No/NA	Comments or location in manuscript
<b>Abstract</b>						
1.0	Structured or Unstructured	Abstract should include information on background.	STORMS		Yes	Unstructured abstract
1.1	Study Design	State study design in abstract.	STORMS	See 3.0 for additional information on study design.	Yes	Cohort study
1.2	Sequencing methods	State the strategy used for metagenomic classification.	STORMS	For example, targeted 16S by nPCR or	Yes	targeted 16S amplicon sequencing
1.3	Specimens	Describe body site(s) studied.	STORMS		Yes	fecal microbiome
<b>Introduction</b>						
2.0	Background and Rationale	Summarize the underlying background, scientific	STORMS		Yes	
2.1	Hypotheses	State the pre-specified hypothesis. If the study is	STORMS		Yes	
<b>Methods</b>						
3.0	Study Design	Describe the study design.	STORMS	Observational (Case-Control, Cohort)	Yes	Cohort Study
3.1	Participants	State what the population of interest is, and the method by	STORMS	Examples of the population of interest	Yes	Methods, "Patients" subsection
3.2	Geographic location	State the geographic region(s) where participants were	MixS: geographic location (country)	Geographic location can be	Yes	Methods, "Patients" subsection
3.3	Relevant Dates	State the start and end dates for recruitment, follow-up, and	STORMS	Recruitment is the period in which	Yes	Methods, "Patients" subsection
3.4	Eligibility criteria	List any criteria for inclusion and exclusion of recruited	Modified STROBE	Among potential recruited participants	Yes	Methods, "Patients" subsection
3.5	Antibiotics Usage	List what is known about antibiotics usage before or	STORMS	If participants were excluded due to	Yes	Fig S5 and zenodo data supplement
3.6	Analytic sample size	Explain how the final analytic sample size was calculated	STORMS	Consider use of a flow diagram (see template)	Yes	Fig. S1
3.7	Longitudinal Studies	For longitudinal studies, state how many follow-ups were	STORMS	If there is less than follow-up, discuss the		Methods, "Patients" subsection
3.8	Matching	For matched studies, give matching criteria.	Modified STROBE	"Matched" refers to matching between	NA	
3.9	Ethics	State the name of the institutional review board that	STORMS		Yes	Methods, "Patients" subsection
4.0	Laboratory methods	State the laboratory/center where laboratory work was	STORMS	Provide a reference to complete lab protocols	Yes	Methods, "Human fecal microbiome analysis" subsection
4.1	Specimen collection	State the body site(s) sampled from and how specimens were collected.	MixS: sample collection device or method; host body site	Use terms from the Uber-anatomy Ontology ( <a href="https://www.ebi.ac.uk/ols/ontologies/uber">https://www.ebi.ac.uk/ols/ontologies/uber</a> ) to describe body sites in a standardized format.	Yes	Stool samples were collected from the feces (UBERON:0001988) of patients. Feces are the excreted waste products of the digestive system (UBERON:0001007), formed in the large intestine (UBERON:0000059) and stored in the rectum (UBERON:0001052) prior to defecation
4.2	Shipping	Describe how samples were stored and shipped to the	STORMS	Include length of time from collection to	Yes	Methods, "Human fecal microbiome analysis" subsection
4.3	Storage	Describe how the laboratory stored samples, including time	STORMS	State where each procedure or lot of	Yes	Methods "Fecal microbiome analysis" subsection
4.4	DNA extraction	Provide DNA extraction method, including kit and	MixS: nucleic acid extraction	If any DNA quantification methods	Yes	in the "Fecal microbiome analysis" section
4.5	Human DNA sequence	Describe whether human DNA sequence depletion or	STORMS		Yes	No depletion nor enrichment
4.6	Primer selection	Provide primer selection and DNA amplification methods as	MixS: per primers		Yes	Methods "Fecal microbiome analysis" subsection
4.7	Positive Controls	Describe any positive controls (mock communities) used.	STORMS	If used, should be deposited under	NA	Methods "Fecal microbiome analysis" subsection
4.8	Negative Controls	Describe any negative controls used.	STORMS	If used, should be deposited under	NA	Methods "Fecal microbiome analysis" subsection
4.9	Contaminant mitigation	Provide any laboratory or computational methods used to	STORMS	Includes filtering of reagents and other	Yes	Methods "Fecal microbiome analysis" subsection
4.10	Replication	Describe any biological or technical replicates included in the sequencing, including which	STORMS	Replication may be biological (redundant biological specimens)	Yes	Methods "Fecal microbiome analysis" subsection cites PMID 37295406
4.11	Sequencing strategy	Major divisions of strategy, such as shotgun or amplicon sequencing.	MixS: sequencing method	For amplicon sequencing (for example, 16S variable	Yes	Methods "Fecal microbiome analysis" subsection cites PMID 37295406
4.12	Sequencing methods	State whether experimental quantification was used.	STORMS	These include read length, sequencing	Yes	Methods "Fecal microbiome analysis" subsection
4.13	Batch effects	Detail any blocking or randomization used in study.	STORMS	Sources of batch effects include sample	No	
4.14	Metatranscriptomics	Detail whether any mRNA enrichment was performed and	STORMS	Provide details on any internal standards.	NA	
4.15	Metaproteomics	Detail which protease was used for digestion. Provide details on	STORMS	Provide details on any internal standards.	NA	
4.16	Metabolomics	Specify the analytic method used (such as nuclear magnetic	STORMS	Provide details on any internal standards.	NA	
5.0	Data sources/	For each non-microbiome variable, including the health	MixS: host disease status	State any sources of potential bias in	Yes	Methods
6.0	Research design for	Discuss any potential for confounding by variables that	STORMS	For causal inference, this item refers to	Yes	Methods, "Bayesian multilevel model" subsection
6.1	Selection bias	Discuss potential for selection or survival bias.	STORMS	Selection bias can occur when some	Yes	Discussion, third paragraph
7.0	Bioinformatic and	Describe any transformations to quantitative variables used in	STORMS	If a variable is analyzed using	Yes	Methods, "Bayesian multilevel model" subsection
7.1	Quality Control	Describe any methods to identify or filter low quality reads or samples.	MixS: sequence quality check	If samples were excluded based on quality or read depth.	Yes	Methods "Fecal microbiome analysis" subsection cites PMID 37295406
7.2	Sequence analysis	Describe any taxonomic, functional, or other	MixS: feature reduction		Yes	in the "Fecal microbiome analysis" section
7.3	Statistical methods	Describe all statistical methods.	Modified STROBE	Describe any statistical tests used.	Yes	Methods, "Bayesian multilevel model" subsection
7.4	Longitudinal analysis	If the study is longitudinal, include a section that explicitly	STORMS		NA	
7.5	Subgroup analysis	Describe any methods used to examine subgroups and	STROBE		Yes	Figure S10 (pre-transplant subgroup analysis)
7.6	Missing data	Explain how missing data were addressed.	STROBE	"Missing data" refers to participant	Yes	Methods, "Nutrition data collection and annotation"
7.7	Sensitivity analyses	Describe any sensitivity analyses.	STROBE		Yes	Figure S8, S9
7.8	Findings	State criteria used to select findings for reporting.	STORMS	For example, false discovery rate with	Yes	Methods, "Bayesian multilevel model" subsection
7.9	Software	Cite all software (including read mapping software) and	Modified STREGA	Installed packages, add-ons or libraries	Yes	Methods
8.0	Reproducible research	Make a statement about whether and how others can	STORMS	Any protected	Yes	Data availability statement just before references
8.1	Raw data access	State where raw data may be accessed, including	STORMS	Robust, long-term databases such as	Yes	NCBI SRA and zenodo ( <a href="https://zenodo.org/records/14538106">https://zenodo.org/records/14538106</a> ), as detailed in Data availability statement
8.2	Processed data access	State where processed data may be accessed.	STORMS	Unfiltered data should be provided.	Yes	NCBI SRA and zenodo ( <a href="https://zenodo.org/records/14538106">https://zenodo.org/records/14538106</a> ), as detailed in Data availability statement
8.3	Participant data access	State where individual participant data such as demographics and other	STORMS	If re-categorized, transformed, or otherwise derived	Yes	zenodo ( <a href="https://zenodo.org/records/14538106">https://zenodo.org/records/14538106</a> ), as detailed in Data availability statement
8.4	Source code access	State where code may be accessed.	STORMS	If a standard or formalized workflow	Yes	Github repository as linked to in the Data availability
8.5	Full results	Provide full results of all analyses in computer-readable	STORMS	For example, any fold-changes, $n$ -values, or	No	
<b>Results</b>						
9.0	Descriptive data	Give characteristics of study participants (e.g., dietary	STROBE	Typically reported in a table included in the	Yes	Table 1
10.0	Microbiome data	Report descriptive findings for microbiome analyses with all	STORMS	This includes measures of diversity	Yes	
10.1	Taxonomy	Identify taxonomy using standardized taxon	STORMS	If not using full taxonomic hierarchy	Yes	
10.2	Differential abundance	Report results of differential abundance analysis by the	STORMS	If there are more than two groups, include	NA	
10.3	Other data types	Report other data analyzed—e.g., metabolic functional	STORMS		Yes	
10.4	Other statistical analysis	Report any statistical data analysis not covered above.	STORMS	This could include subgroup analysis	Yes	
<b>Discussion</b>						
11.0	Key results	Summarise key results with reference to study objectives.	STROBE		Yes	
12.0	Interpretation	Give a cautious overall interpretation of results.	STROBE	Define or clarify any subjective terms such	Yes	
13.0	Limitations	Discuss limitations of the study, taking into account sources of	STROBE	Also consider limitations resulting	Yes	
13.1	Bias	Discuss any potential for bias to influence study findings.	STORMS	May include sampling method.	Yes	
13.2	Generalizability	Discuss the generalisability (external validity) of the study.	STROBE	To what populations or other settings do you	Yes	
14.0	Ongoing/future work	Describe potential future research or opinion research.	STORMS		Yes	
<b>Other information</b>						
15.0	Funding	Give the source of funding and the role of the funders for the	STROBE		Yes	
15.1	Acknowledgements	Include acknowledgements of those who contributed to the	STORMS	For general guidelines, see	Yes	
15.2	Conflicts of Interest	Include a conflicts of interest statement.	STORMS		Yes	
16.0	Supplements	Indicate where supplements may be accessed and what	STORMS		Yes	
17.0	Supplementary data	Provide supplementary data files of results with for all taxa	STORMS	Depending on the analysis performed	Yes	