nature portfolio

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Last updated by author(s): Sep 9, 2024

Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☒	☐	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☒	☐	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☐	☒	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	No software was used.
Data analysis	The temporal-spatial hierarchical Bayesian model was used for exposure level estimates. The decomposition analysis was used to estimate the drivers of changes in CVD burden attributable to high fasting plasma glucose. All the data analysis was conducted using R version 4.2.0 and SAS version 9.4.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

The "minimum dataset" that are necessary to interpret, verify and extend the research in the article, can be found within the manuscript and its supplementary information. Age-sex-specific relative risks and theoretical minimum risk exposure level were available from Global burden of disease 2019 study (https://doi.org/10.1016/S0140-6736(20)30752-2). The original datasets generated or analyzed, or both, and the raw data for fasting plasma glucose levels and CVD deaths

are available under restricted access due to data privacy laws according to Chinese regulations, access can be obtained by submitting a collaboration request including information on the institution and a brief description of the project to wangzengwu@foxmail.com. An answer can be expected within 30 d. If the collaboration request is accepted, a data access agreement will be necessary and appropriate authorisations from the competent administrative authorities may be needed. In accordance with existing regulations, no personal identification data will be accessible. Source data are provided with this paper.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	We focused on the sex disparity in this study. Sex was used throughout this paper to discuss biological attribute differences. We obtained data from three large-scale, nationally representative and provincially studies, which considered sex in study design and sex was determined based on self-reporting. In this study, we estimated the cardiovascular disease burden attributable to high fasting plasma glucose by sex.
Reporting on race, ethnicity, or other socially relevant groupings	In this study, we didn't involve race, ethnicity, or other socially relevant groupings.
Population characteristics	"See above".
Recruitment	We obtained information on aggregated fasting plasma glucose levels from surveys at the population level that had been completed and did not contain any individual information. Please refer to survey-specific documentation for participant recruitment. This secondary data analysis did not recruit study participants. All data used in this study were aggregated and did not contain any individually identifiable information; therefore, no ethics approval or consent to participate was needed. Also, participant compensation was not involved.
Ethics oversight	All data used in this study were aggregated from three previous cross-sectional surveys and did not contain any individually identifiable information. The surveys included the China Chronic Disease and Risk Factor Surveillance , the China National Nutrition Survey, and the China Hypertension Survey, and received ethical approval from the ethical review committee of National Centre for Chronic and Noncommunicable Disease Control and Prevention, the ethical review committee of the Chinese Centre for Disease Control and Prevention, and the Ethics Committee of Fuwai Hospital, respectively. All participants obtained from these three surveys provided informed consent.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☒ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	This study was a quantitative population-based study, which combined three cross-sectional surveys and mortality surveillance data to quantitatively assess the CVD burden attributable to high fasting plasma glucose in China from 2010-2018.
Research sample	We obtained 791 373 participants aged 25 years and older in China from three large-scale studies, including the China Chronic Disease and Risk Factor Surveillance, the China National Nutrition Survey, and the China Hypertension Survey. The proportion of male was 44%.
Sampling strategy	The data were pooled from three large-scale, nationally representative and provincially studies. These three surveys were all using a stratified multistage random sampling method. The details were shown in previous publications. Please refer to survey-specific documentation for details.
Data collection	All the participants in the three surveys were invited to community health center, and blood samples were obtained in the morning after an overnight fast, which was one of the data sources used to assess fasting plasma glucose exposure levels.
Timing	The data included three waves of China Chronic Disease and Risk Factor Surveillance, one wave of the China National Nutrition Survey, and one wave of the China Hypertension Survey. In total, data were spread among the years in 2010, 2012, 2013, 2015 and 2018.
Data exclusions	We obtained information on aggregated fasting plasma glucose levels from surveys that did not contain any individual information. Thus, data exclusion is not applicable.
Non-participation	We obtained information on aggregated fasting plasma glucose levels from surveys that had been completed and did not contain any individual information. Please refer to survey-specific documentation for non-participation.

Randomization	We obtained information from surveys, not experiment. Thus, randomization is not applicable.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Plants

Seed stocks	*Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.*
Novel plant genotypes	*Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.*
Authentication	*Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosiacism, off-target gene editing) were examined.*