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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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ | 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
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ | 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

All data used in this study is publicly accessible data. Data cleaning and imputation was conducted using R (version 4.3.3). All code for the data cleaning and imputation can be found at GitHub, <https://doi.org/10.5281/zenodo.1496353893>.

Data analysis

R (version 4.3.3) was used for all statistical analyses and data visualisation. All code used for the analyses can be found at GitHub, <https://doi.org/10.5281/zenodo.1496353893>.

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](#)

All data used in this study were obtained from publicly accessible databases. We have complied with all data usage conditions and licensing agreements associated

with these databases. Population estimates were sourced from the United Nations Population Division [available at <https://population.un.org/wpp/> and downloaded on 02 Feb 2023]. Life table data were sourced from the Human Lifetable Database [available at <https://www.lifetable.de/> and downloaded on 03 August 2023]. Food supply data were sourced from the Food and Agriculture Statistical Database [available at <https://www.fao.org/faostat/en/> and downloaded on 11 August 2023]. Historical economic data were sourced from the Maddison Project Database [available at <https://www.rug.nl/ggdc/historicaldevelopment/maddison/releases/> and downloaded on 21 March 2022]. For any future analyses, it is recommended to obtain current data directly from the referenced sources for the most up-to-date information.

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	Data was stratified based on sex provided in source datasets. Analyses were conducted and reported separately using sex specific datasets.
Reporting on race, ethnicity, or other socially relevant groupings	Generalised additive mixed models included both linear and non-linear terms, as well as random effects, to control for variability between countries. The models included covariates such as time, gross domestic product (GDP) per capita, and other macronutrient supplies (fat and carbohydrate) to control for the influence of economic factors and other nutritional components on the observed associations. Survivorship observations were weighted based on their standard errors. Lower uncertainties were considered better representations of true long-term population survival rates. This approach helped to mitigate the impact of outliers and improve the reliability of the model estimates. Our analysis included statistical corrections to control for potential confounding by factors such as time, population size, and economic variables. These adjustments ensured that the observed associations between macronutrient supplies and age-specific mortality were not biased by these confounding factors.
Population characteristics	Age (in years from birth) was used as provided in source data.
Recruitment	Our study utilised existing national-level data from various sources, stated above, therefore there is no self-selection bias from participants choosing to be part of the study.
Ethics oversight	<i>Identify the organization(s) that approved the study protocol.</i>

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

Ecological, evolutionary & environmental sciences study design

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

Study description	Our study investigates the associations between national supplies of plant-based protein (PBP) and animal-based protein (ABP) and age-specific mortality across 101 countries from 1961 to 2018. Our analysis uses a comprehensive dataset that includes daily per capita food supply data, demographic data, and economic statistics. We examine the effects of ABP and PBP supplies, along with fat and carbohydrate supplies, on age-specific mortality. Interactions between these macronutrient supplies, time, country, and economic factors (GDP) are explored. Our study employs a hierarchical design, analyzing data at the country-year level and stratifying by sex. Generalized Additive Mixed Models (GAMMs) are used to account for non-linear relationships and random effects of country. The experimental units are country-year combinations, with a total of 4000 country-year-sex-specific life tables analyzed. Each unit includes data on macronutrient supplies, survivorship at ages 5 and 60, and GDP.
Research sample	The research sample for this study consists of national-level data of human populations from 101 countries, covering the period from 1961 to 2018. The data were sourced from several open source databases, as described above. Data is stratified by sex (male and female) and examines age-specific mortality, focusing on survivorship at ages 5 and 60. Statistical adjustments and modeling are used to account for potential confounding factors such as time, population size, and economic variables. Generalized Additive Mixed Models (GAMMs) are used to explore the interactive effects of animal-based protein (ABP), plant-based protein (PBP), fat, and carbohydrate supplies on age-specific mortality. The chosen sample allows for a comprehensive analysis of global patterns in macronutrient supply and their associations with age-specific mortality. The extensive temporal and geographic coverage of the data facilitates robust comparisons and insights into the nutritional environment's impact on health across different populations and time periods. The sample represents global human populations, providing insights into how national-level nutritional environments influence age-specific mortality rates worldwide. The use of existing datasets ensures a broad and diverse representation of different demographic and economic contexts.
Sampling strategy	The sampling procedure for this study involved collecting national-level data from 101 countries over the period from 1961 to 2018. The data sources have been noted above. Sample sizes were determined based on the availability of comprehensive and reliable data from the aforementioned sources. The chosen sample sizes are sufficient to provide meaningful and generalizable insights into the associations between national macronutrient supplies and age-specific mortality. The extensive and diverse dataset, combined with

robust statistical methods, ensures reliable findings that are relevant to a wide range of broader populations and contexts.

Specifically, the collated dataset includes 101 countries, providing a broad and diverse representation of global human populations. This extensive coverage allows for robust comparisons and insights into the nutritional environment's impact on health across different demographic and economic contexts. The data spans from 1961 to 2018, covering multiple decades. This long-term perspective enables the analysis of trends and changes over time, enhancing the identification and understanding of patterns and associations. The inclusion of complete entries for macronutrient supplies, survivorship at ages 5 and 60, and GDP across both sexes ensures that the analysis is based on a comprehensive and detailed dataset. This completeness supports the reliability and validity of the findings. Generalized Additive Mixed Models (GAMMs) were used to analyze the data, accounting for non-linear relationships and random effects of country. The models included interactions between macronutrient supplies, time, country, and economic factors, with statistical corrections to control for potential confounding variables.

Data collection

The data collection procedure for this study involved aggregating data from several reputable sources, described above. The FAO compiles FBS data by calculating the total quantities of food produced and imported, adjusting for changes in stocks, exports, and other factors to estimate the average food supply per person within a nation for each year. The HMD collects and standardizes life table data from official reports, statistical publications, and scientific datasets. The data includes age-specific mortality statistics, such as the proportion of individuals surviving to specific ages. The Maddison Project compiles historical and global economic data, providing comprehensive statistics on GDP for various countries and years. The UN Population Division provides detailed population estimates, which have been used to calculate standard errors for survivorship values and to assess the stochasticity and sampling variance of the estimated survival values.

All data used in this study were obtained from publicly accessible databases. We have complied with all data usage conditions and licensing agreements associated with these databases. Population estimates were sourced from the United Nations Population Division [available at <https://population.un.org/wpp/> and downloaded on 02 Feb 2023]. Life table data were sourced from the Human Lifetable Database [available at <https://www.lifetable.de/> and downloaded on 03 August 2023]. Food supply data were sourced from the Food and Agriculture Statistical Database [available at <https://www.fao.org/faostat/en/> and downloaded on 11 August 2023]. Historical economic data were sourced from the Maddison Project Database [available at <https://www.rug.nl/ggdc/historicaldevelopment/maddison/releases/> and downloaded on 21 March 2022]. For any future analyses, it is recommended to obtain current data directly from the referenced sources for the most up-to-date information.

Timing and spatial scale

The collected data from the specified sources were integrated to form a comprehensive dataset, providing yearly entries for each country within the dataset, spanning from 1961 to 2018. The collated data captures year-to-year variations and long-term trends in macronutrient supplies and mortality rates. This frequency is sufficient to observe significant changes and patterns without being overly granular, which could introduce noise and complicate the analysis. The collected data spans 101 countries, representing a wide range of geographic regions, economic statuses, and demographic profiles. This global scale ensures that the findings are broadly applicable and can provide insights into the nutritional environment's impact on health across diverse populations.

Data exclusions

Data were excluded for any country-year entry where complete food supply, GDP, population, and survivorship data was not available. Missing data was addressed through imputation methods to ensure no potential biases from missing data.

Reproducibility

All attempts to repeat the analyses were successful.

Randomization

Our analyses are based on existing observational data, used to identify associations between national macronutrient supplies and age-specific mortality, rather than testing the effects of an intervention through randomized controlled trials. Potential confounding factors have been accounted for through statistical controls and modeling techniques.

Blinding

Our study is based on observational data collected from existing national databases, and therefore did not involve the manipulation of variables or assigning of treatments to different groups. Since there were no interventions or treatments administered, there was no need to blind participants or researchers to the conditions of the study.

Did the study involve field work? ☐ Yes ☒ No

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

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, mosaicism, off-target gene editing) were examined.