

Corresponding author(s): Yi Liu

Last updated by author(s): Feb 25, 2026

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 The U.S. participants were recruited via Prolific, and the Chinese participants were recruited via Credamo.

Data analysis Data analysis was conducted in R (Version 4.4.2) using R Studio.

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 the materials and data, and associated analytic script have been deposited on the Open Science Framework (https://osf.io/2r3bz/?view_only=42c356cc123343de9a0adba5ed59aa9a).

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	Gender was assessed via self-report (male, female, other, prefer not to say). As gender was not a primary focus of the current study, it was included as a covariate in the main analyses. Additional analyses examining the effect of gender on beliefs about cooperation decline are presented in Supplementary Note 9, the significant results are also mentioned in the main text.
Reporting on race, ethnicity, or other socially relevant groupings	Participants also self-reported their ethnicity, political orientation, religion and religiosity, education level, and income. The exact survey questions are provided in Supplementary Material Sections 15 and 16 (English and Chinese versions, respectively). These variables were not central to the current research question. The distributions of ethnicity, education, and income are reported in Table 1. Exploratory analyses investigating the influence of education, income, religiosity, and political variables on perceived changes in cooperation are presented in Supplementary Note 9.
Population characteristics	628 American (308 males, 308 females, 10 others, and 2 preferred not to say; Mage = 43.90, SDage = 14.37) 449 Chinese (230 males, 219 females; Mage = 44.24, SDage = 13.37)
Recruitment	The U.S. participants were recruited via Prolific, and Credamo was used for the Chinese sample.
Ethics oversight	The study was approved by the ethics committee of the Faculty of Behavioural and Movement Sciences of the Vrije Universiteit Amsterdam (VCWE-2023-005).

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	Cross-country quantitative survey study
Research sample	We recruited participants aged 18 years or older who were currently residing in either the United States or China. Efforts were made to balance gender and age across predefined age brackets: For the U.S. sample: 18–24, 25–29, 30–34, 35–39, 40–44, 45–49, 50–54, 55–59, 60–64, and 65–69 years; For the Chinese sample: 18–25, 26–30, 31–35, 36–40, 41–45, 46–50, 51–55, as well as 56 and over. The difference brackets were made based on participant availability on the respective recruitment platforms.
Sampling strategy	The targeted sample size is based on a pilot study, in which we have collected and analyzed data from 100 American (1 participant was excluded because of the incompleteness of the answers) and 100 Chinese participants. For power analysis, we first focused on the effect sizes associated with our two confirmatory hypotheses. Using the simr package in R, we estimated that a total of 300 participants would be required to achieve 90% power to detect the interaction between Year and Country. We also conducted exploratory analyses testing several potential mediators. Power simulations using the lavaan and simsem packages indicated that a sample of 600 participants would yield approximately 88% power for detecting indirect effects. Given the number of mediators tested, we decided to double the sample size to increase sensitivity for detecting smaller effects. Data collection for the Chinese sample ended before reaching the planned sample size. Although the recruitment period was sufficiently long, there was limited availability of new participants in the final month. Nevertheless, the final sample was sufficiently powered for the confirmatory analyses.
Data collection	Data was collected via Prolific (U.S. sample) and Credamo (Chinese sample).
Timing	For the U.S. sample: August 3–27, 2023 For the Chinese sample: August 5, 2023–January 3, 2024
Data exclusions	As the completion time of the study is approximately 30 minutes, participants who spent less than 10 min or more than 90 minutes were considered invalid and excluded from the analyses.
Non-participation	A total of 1,166 participants took part in the study. Among them, 28 American (4%) and 61 Chinese (12%) participants were excluded due to incomplete survey responses.
Randomization	We have two groups. Specifically, participants in Group 1 answered questions related to their beliefs about people living in 1960,

Randomization

1980, 2000, and 2020, while participants in Group 2 answered questions about their beliefs about people living in 1970, 1990, 2010, and 2030. Participants were randomly assigned to these two groups.

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