

Reporting Summary

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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
<input type="checkbox"/>	<input checked="" type="checkbox"/> The exact sample size (<i>n</i>) for each experimental group/condition, given as a discrete number and unit of measurement
<input type="checkbox"/>	<input checked="" type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
<input type="checkbox"/>	<input checked="" type="checkbox"/> 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>
<input type="checkbox"/>	<input checked="" type="checkbox"/> A description of all covariates tested
<input type="checkbox"/>	<input checked="" type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
<input type="checkbox"/>	<input checked="" type="checkbox"/> 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)
<input type="checkbox"/>	<input checked="" type="checkbox"/> For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
<input type="checkbox"/>	<input checked="" type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
<input type="checkbox"/>	<input checked="" type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
<input type="checkbox"/>	<input checked="" type="checkbox"/> Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i>), 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	PsychoPy3 (version 2023.1.3) was used to present experimental stimuli and record participant response data. Electroencephalography (EEG) data were recorded by 64-channel Neuroscan equipment (NeuroScan 4.3.1, USA), following the international 10-20 system of EEG electrode placement.
Data analysis	Learning models were fitted, compared, and recovered by MATLAB2018b, while the model-based efficacy estimates were calculated in R-Studio. LMMs were performed in R-Studio. Hierarchical Drift Diffusion Model Model fit, comparison and posterior predictive checks were performed using the HDDM package (version 1.0.1) in Python (version 3.8). Bayesian hypothesis tests were conducted in R-Studio. The multilevel mediation analyses were performed using the MLmed macro (https://nrockwood.com/mlmed) in SPSS 25.00.

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 and analysis code used in this study are publicly available on the Open Science Framework (OSF): <https://osf.io/vpr9e/>.

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	Participants reported their assigned sex at birth (male or female) which was included as a control variable in the data analyses. No restrictions were applied regarding gender identity. Sex- and gender-based analyses were not performed, as this study was not designed to examine differences by sex or gender. In Experiment 1, there were 10 males and 22 females; in Experiment 2, there were 9 males and 25 females.
Reporting on race, ethnicity, or other socially relevant groupings	No data on race, ethnicity, or other socially relevant groupings were collected in this study. Consequently, analyses based on these variables were not performed.
Population characteristics	See above
Recruitment	All participants were recruited using a convenience sampling strategy, where voluntary participation was solicited through recruitment posters. This self-selection approach may introduce bias, as the sample may not fully represent the broader population, potentially limiting the generalizability of the findings.
Ethics oversight	The study protocol was approved by the Psychological Ethics Committee of Capital Normal University.

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	We conducted two quantitative experimental studies using the same within-participant design, with two social comparison conditions: downward and upward social comparison.
Research sample	Experiment 1 included 32 healthy participants (10 males; mean age = 22.75 ± 2.03 years). Experiment 2 initially included 42 participants, of whom 8 were excluded, leaving 34 participants (9 males; mean age = 22.12 ± 1.91 years). All participants had non-psychology backgrounds, normal or corrected-to-normal vision, and normal color perception.
Sampling strategy	All participants were recruited using a convenience sampling method. No formal a priori sample-size calculation was conducted; sample sizes were chosen based on prior studies. Post-hoc effect size analyses indicated that the final sample provided sufficient power.
Data collection	PsychoPy3 (version 2023.1.3) was used to present experimental stimuli and record participant response data. Electroencephalography (EEG) data were recorded by 64-channel Neuroscan equipment (NeuroScan 4.3.1, USA), following the international 10-20 system of EEG electrode placement. In Experiment 1, only the researcher and the participant were present during data collection. In Experiment 2, two research assistants were also present to assist with the experiment. The researcher was aware of all study hypotheses and experimental conditions.
Timing	Data for Experiment 1 were collected from May 7 to June 3, 2023. Data for Experiment 2 were collected from July 16 to December 5, 2023.
Data exclusions	In Experiment 1, no data were excluded from the analyses. In experiment 2, we excluded eight participants. Specifically, two

Data exclusions	participants were excluded due to crash of computer program, and four participants were excluded for not completing the formal experiment. Additionally, two participants were excluded due to insufficient data per condition (< 30 rounds) after removing the eyeblinks or muscle artifacts. These exclusion criteria were pre-established before data analysis.
Non-participation	Four participants in Experiment 2 did not complete the experiment due to fatigue. No other participants declined to participate.
Randomization	Participants were not assigned to separate experimental groups, as this study employed a within-participant design. The order of social comparison conditions was pseudo-randomized.

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
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input checked="" type="checkbox"/>	<input type="checkbox"/> Plants

Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> 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.