Reporting Summary

Nature Research 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 Research policies, see Authors & Referees 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.

- 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
- 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 computer task was programmed in Cogent with Matlab.

Data analysis
All statistical analyses for the behavioral data were carried out in R, using the packages 'ezANOVA', 'coxme', and 'lme4'.

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/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

Behavioral data and accompanying code for all behavioral analyses and figures can be found on the Open Science Framework (https://osf.io/c4qbr/). FMRI data and analysis code are available from the corresponding author on reasonable request.

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
Behavioural & social sciences study design

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

<table>
<thead>
<tr>
<th>Study description</th>
<th>This study constitutes a quantitative experimental design.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Research sample</td>
<td>The participant sample consistent primarily of students recruited from Columbia University.</td>
</tr>
<tr>
<td>Sampling strategy</td>
<td>We employed a convenience sampling approach.</td>
</tr>
<tr>
<td>Data collection</td>
<td>A computer was used to collect behavioral data. Electric stimulation was delivered using a BIOPAC STM100C. All fMRI data were acquired using a GE Discovery MR750 3.0 T scanner with 32-channel headcoil.</td>
</tr>
<tr>
<td>Timing</td>
<td>Indicate the start and stop dates of data collection. If there is a gap between collection periods, state the dates for each sample cohort.</td>
</tr>
<tr>
<td>Data exclusions</td>
<td>Data from one subject was lost due to computer error. One additional subject was excluded due to excessive movement during the scan (this was an established exclusion criteria). Our final sample consisted of 28 subjects.</td>
</tr>
<tr>
<td>Non-participation</td>
<td>No participants declined participation.</td>
</tr>
<tr>
<td>Randomization</td>
<td>This was a repeated measures design. Conditions were counterbalanced.</td>
</tr>
</tbody>
</table>

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.

<table>
<thead>
<tr>
<th>Materials &amp; experimental systems</th>
<th>Methods</th>
</tr>
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<tbody>
<tr>
<td>n/a</td>
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</tr>
<tr>
<td>✗ Antibodies</td>
<td>✗ ChIP-seq</td>
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<tr>
<td>✗ Eukaryotic cell lines</td>
<td>✗ Flow cytometry</td>
</tr>
<tr>
<td>✗ Palaeontology</td>
<td>✗ MRI-based neuroimaging</td>
</tr>
<tr>
<td>✗ Animals and other organisms</td>
<td></td>
</tr>
<tr>
<td>☒ Human research participants</td>
<td></td>
</tr>
<tr>
<td>☒ Clinical data</td>
<td></td>
</tr>
</tbody>
</table>

Human research participants

Policy information about studies involving human research participants

<table>
<thead>
<tr>
<th>Population characteristics</th>
<th>Participants were healthy, right-handed. 17 of 28 were female. Mean age was 25.4 ± 7.3 years.</th>
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</thead>
<tbody>
<tr>
<td>Recruitment</td>
<td>Participants were recruited according to the guidelines of the Columbia University Institutional Review Board after providing informed consent.</td>
</tr>
<tr>
<td>Ethics oversight</td>
<td>Columbia University Institutional Review Board.</td>
</tr>
</tbody>
</table>

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

Magnetic resonance imaging

Experimental design

<table>
<thead>
<tr>
<th>Design type</th>
<th>Task-based, event related design.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Design specifications</td>
<td>There were 96 trials per subject, each 11.75 seconds average in duration.</td>
</tr>
<tr>
<td>Behavioral performance measures</td>
<td>A single response was measured from subjects on each trial; the distance at which they made a response.</td>
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</tbody>
</table>
Acquisition

Imaging type(s) Functional and anatomical.
Field strength 3.0T
Sequence & imaging parameters For functional imaging, interleaved T2*-weighted gradient-echo echo planar imaging (EPI) sequences were used to produce 45 3-mm-thick oblique axial slices (TR = 2 s., TE = 25 ms, flip angle = 77, FOV = 192 x 192 mm, matrix = 64 x 64)
Area of acquisition Whole brain.
Diffusion MRI □ Used □ Not used

Preprocessing

Preprocessing software SPM8 software (Welcome Trust Centre for Neuroimaging, London, UK) implemented in Matlab 7 (The MathWorks Inc., Natick MA). Structural images were subjected to the unified segmentation algorithm implemented in SPM8, yielding discrete cosine transform spatial warping coefficients used to normalize each individual’s data into MNI space. Functional data were first corrected for slice timing difference, and subsequently realigned to account for head movements. Normalized data were finally smoothed with a 6-mm FWHM Gaussian kernel.
Normalization See above.
Normalization template See above.
Noise and artifact removal See above.
Volume censoring No volumes were censored.

Statistical modeling & inference

Model type and settings Preprocessed imaged were subjected to a two-level general linear model using SPM8. The first level contained the following regressors of interest, each convolved with the canonical two-gamma hemodynamic response function: a 2 s box-car function for the onset of the trial (during predator type cue presentation), a 4-8 s (duration jittered) box-car function from the onset to 2 s prior to participants’ flight decisions, a 2 s boxcar function for the time prior to participants’ flight decisions, and a 4-8 s (duration jittered) box-car function for the remainder of the trial. Mean-centered trait anxiety ratings were included as orthogonal regressors. In addition, nuisance regressors consisted of motion parameters determined during preprocessing, their first temporal derivative and discrete cosine transform-based temporal low frequency drift regressors with a cutoff of 192 s. Beta maps were used to create linear contrast maps, which were then subjected to second-level, random-effects one-sample t tests. In addition, A flexible factorial model was used to examine the main effects of predator type. The resulting statistical maps were thresholded at p < 0.05, and we corrected for multiple comparisons using false discovery rate correction (FDR whole brain corrected). The functional connectivity analysis was performed for the response phase (escape decision) using a generalized psychophysiological interactions (PPI) approach.
Effect(s) tested We tested contrasts between predator conditions and their modulation by trait anxiety.
Specify type of analysis: □ Whole brain □ ROI-based □ Both
Anatomical location(s) We determined vHPC as an independent seed region given background literature. The corresponding structural ROI was obtained using the WFU Pickatalas.
Statistic type for inference (See Eklund et al. 2016) Voxel-wise, see above.
Correction See above.

Models & analysis

n/a Involved in the study
□ Functional and/or effective connectivity
□ Graph analysis
□ Multivariate modeling or predictive analysis