

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

- 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

Estimates and corresponding data for the meta-analysis were collected from the original sources or by contacting the authors. All the obtained data were saved as csv files and edited in Microsoft Excel and R (open source packages used: tidyverse, meta, metafor, lfe, lme4, stargazer, ggpubr, jtools, RColorBrewer, rgeos, rnatuarearth). The meta-data and country-level data generated and analyzed are available in the Harvard Dataverse repository.

Data analysis

All data were edited and analyzed in R (open source packages used: tidyverse, meta, metafor, lfe, lme4, stargazer, ggpubr, jtools, RColorBrewer, rgeos, rnatuarearth). The complete codes used to generate and visualize the results reported in this study are available in the Harvard Dataverse repository.

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

The meta-data and country-level data generated during and/or analyzed during the current study are available in the Harvard Dataverse repository.

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](https://www.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 employs a meta-analysis approach to synthesize and quantify the impact of environmental change on internal and international migration based on 30 scientific papers published between 2006 and 2019. We focus on macro studies that estimate environmental effects using country-level data and exploiting variation both across countries and over time. Focusing on country-level studies allows us to ensure that coefficients are sufficiently comparable and to retrieve distributional information for key variables needed to harmonize the coefficients. We achieve comparability by standardizing the existing estimates using distributional information from the original study samples. Our analysis considers both the direction in which environmental changes influence migration as well as the magnitude of the effect. To obtain unified estimates of the size of environmental migration worldwide, we collect estimated coefficients from different studies that empirically investigate the relationship between different types of environmental factors and migration.
Research sample	The 30 considered quantitative studies estimate environmental effects on migration outcomes, typically using linear longitudinal models. The research sample of our meta-analysis are the coefficients estimated in these models (k=1803). These reflect the strength of the relationship between the considered environmental factors and migration. Coefficient estimates were obtained from the original studies and precision-weighted with the inverse of the estimated variance to down-weight highly uncertain estimates with large standard errors.
Sampling strategy	To identify the relevant sample, a thorough search for quantitative empirical studies was carried out. We started with a broad systematic search for quantitative empirical studies related to environmental migration. The literature search included journal articles, book chapters, books and working papers and was carried out in Web of Science and Scopus, two multidisciplinary online databases with extensive bibliographic information. In particular, we searched for studies which contained terms related to (i) migration, (ii) environmental change and hazards, (iii) and quantitative analysis (e.g. data, relationship, effect, statistics) in their title, abstract, or keywords. We also used the CliMig bibliographic database, which provides a comprehensive collection of resources on migration, the environment, and climate change. As an additional source, references provided in relevant papers and citation paths in Google Scholar were screened iteratively during the entire search process to complement the aforementioned databases and to identify any grey literature and working papers that were not captured by the Web of Science, Scopus and CliMig databases. From the initial set of studies, we selected all macro-level studies analyzing the impact of environmental factors on migration using country-level data and a linear estimation framework. The focus on macro studies ensures a sufficient comparability of the retrieved coefficients. The sample is further restricted to studies analyzing the relationships using longitudinal data, which can reliably infer causal associations between environmental changes and migration by exploiting variations in environmental variables over time.
Data collection	In addition to data on coefficients and estimation precision (t-statistics, SE), which were obtained from the original studies, distributional information about the environmental and migration variables were collected to standardize the effect estimates. The distributional information was retrieved from summary statistics tables in the original studies, by contacting the authors, or calculated from the original data sources. In particular, we obtain information on the standard deviations of the key migration and environmental variables, which allow us to ex-post transform the estimated linear coefficients into (beta) standardized effect sizes. In addition, we collected rich data about the specification and estimation of the original models as well as the measurement of input and output variables. Complementary data from the World Bank, the Major Episodes of Political Violence (MEPV) database, and the Uppsala Conflict Database (UCDP) were used to classify countries included in the study samples and to calculate compositional shares (e.g. percentage of agriculturally dependent countries in sample) to test whether the effect sizes differ by sample composition.
Timing	Data collection and preparation for this study took place between January 2018 and June 2019.
Data exclusions	The full set of studies (n=30) including all relationship estimates (k=1803) were included in our final meta-analytical sample.
Non-participation	All studies identified as relevant according to our inclusion/exclusion criteria were included in the meta-sample. Since our sample does not rely on human participants, non-participation was not an issue.
Randomization	Our main models controlled for a rich set of covariates ranging from the type of environmental factors considered in the study lines, the measurement of input and output variables, the composition of the sample used, and further model-specific controls. In addition, the main models include study fixed effects controlling for between-study heterogeneities. All results remain robust upon changes in the specification of our meta-regressions.

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 | Involvement 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 |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Human research participants |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data |

Methods

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|-------------------------------------|---|
| n/a | Involvement 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 |